

## REFERENCE TO A SEQUENCE LISTING SUBMITTED ON A COMPACT DISC

- [0001] This application includes a Sequence Listing, which is provided as an electronic document on a compact disc (CD-R). This compact disc contains the file "Final Sequence Listing.txt " (6,125,872 bytes, created on January 19, 2010), which is hereby incorporated by reference in its entirety.

## BACKGROUND OF THE INVENTION

### Field of the Invention

- [0002] This invention relates to the field of biology. In a particular embodiment, it relates to peptides, polynucleotides, and compositions useful to monitor or elicit an immune response to selected antigens, and methods of identifying such peptides and polynucleotides.

### Related Art

- [0003] HLA class I molecules are expressed on the surface of almost all nucleated cells. Following intracellular processing of antigens, epitopes from the antigens are presented as a complex with the HLA class I molecules on the surface of such cells. CTL recognize the peptide-HLA class I complex, which then results in the destruction of the cell bearing the HLA-peptide complex directly by the CTL and/or via the activation of non-destructive mechanisms *e.g.*, the production of interferon, that inhibit viral replication.
- [0004] **Human Immunodeficiency Virus.** Acquired immunodeficiency syndrome (AIDS) caused by infection with human immunodeficiency virus-1 (HIV-1) represents a major world health problem. Estimates indicate that about 16,000 people worldwide are infected with HIV each day.
- [0005] The development of anti-viral drugs has been a major advancement in reducing viral loads in HIV infected patients. Highly active retroviral therapy (HAART) has been shown to reduce viremia to nearly undetectable levels. However, current drug therapies are not practicable as a long term solution to the HIV epidemic. HAART therapy is severely limited due to poor tolerance for the drugs and the emergence of drug-resistant virus. Moreover, replication competent HIV

persists in the lymphoid tissue of patients who have responded to HAART, thus serving as a reservoir of virus. Lastly, current anti-retroviral drug therapies have little impact upon the global epidemic: almost 90% of the world's HIV infected population resides within countries lacking financial resources for these drugs. Thus, a need exists for an efficacious vaccine to both prevent and treat HIV infection.

[0006] Virus-specific, human leukocyte antigen (HLA) class I-restricted cytotoxic T lymphocytes (CTL) are known to play a major role in the prevention and clearance of virus infections in vivo (Oldstone *et al.*, *Nature* 321:239, 1989; Jamieson *et al.*, *J. Virol.* 61:3930, 1987; Yap *et al.*, *Nature* 273:238, 1978; Lukacher *et al.*, *J. Exp. Med.* 160:814, 1994; McMichael *et al.*, *N. Engl. J. Med.* 309:13, 1983; Sethi *et al.*, *J. Gen. Virol.* 64:443, 1983; Watari *et al.*, *J. Exp. Med.* 165:459, 1987; Yasukawa *et al.*, *J. Immunol.* 143:2051, 1989; Tigges *et al.*, *J. Virol.* 66:1622, 1993; Reddenhase *et al.*, *J. Virol.* 55:263, 1985; Quinnan *et al.*, *N. Engl. J. Med.* 307:6, 1982).

[0007] While immune correlates of protective immunity against HIV infection are not well defined, there is a growing body of evidence that suggests CTL are important in controlling HIV infection. HIV-specific CTL responses can be detected early in infection and the appearance of the responses corresponds to the time in infection at which initial viremia is reduced (Pantaleo *et al.*, *Nature* 370:463, 1994; Walker *et al.*, *Proc. Natl. Acad. Sci.* 86:9514, 1989). In addition, HIV replication in infected lymphocytes can be inhibited by incubation with autologous CTL (*see, e.g.*, Tsubota *et al.*, *J. Exp. Med.* 169:1421, 1989). These data are supported by recent studies that indicate CTL are required for controlling viral replication in a SIV/rhesus animal model (Schmitz *et al.*, *Science* 283:857, 1999), and additionally supported by studies that demonstrate that CTL exert selective pressure on HIV populations as evidenced by the eventual predominance of viruses with amino acid replacements in those regions of the virus to which CTL responses are directed (*see, e.g.*, Borrow *et al.*, *Nature Med.* 3:205-211, 1997; Price *et al.*, *Proc. Nat. Acad. Sci.* 94:12890-1895, 1997; Koenig *et al.*, *Nature Med.* 1:330-336, 1995; and Haas *et al.*, *J. Immunol.* 157:4212-4221, 1996).

[0008] Virus-specific T helper lymphocytes are also known to be critical for maintaining effective immunity in chronic viral infections. Historically, HTL responses were viewed as primarily supporting the expansion of specific CTL and B cell populations; however, more recent data indicate that HTL may directly contribute to the control of virus replication. For example, a decline in CD4<sup>+</sup> T cells and a corresponding loss in HTL function characterize infection with HIV (Lane *et al.*, *New Engl. J. Med.* 313:79, 1985). Furthermore, studies in HIV infected patients have also shown that there is an inverse relationship between virus-specific HTL responses and viral load, suggesting that HTL play a role in viremia (*see, e.g.*, Rosenberg *et al.*, *Science* 278:1447, 1997).

[0009] A fundamental challenge in the development of an efficacious HIV vaccine is the heterogeneity observed in HIV. The virus, like some other infectious agents including retroviruses, rapidly mutates during replication resulting in the generation of virus that can escape anti-viral therapy and immune recognition (Borrow et al., *Nature Med.* 3:205, 1997). In addition, HIV can be classified into a variety of subtypes that exhibit significant sequence divergence (*see, e.g.,* Lukashov *et al.*, *AIDS* 12:S43, 1998). In view of the heterogeneous nature of HIV, and the heterogeneous immune response observed with HIV infection, induction of a multi-specific cellular immune response directed simultaneously against multiple HIV epitopes appears to be important for the development of an efficacious vaccine against HIV. There is a need to establish such vaccine embodiments which elicit immune responses of sufficient breadth and vigor to prevent and/or clear HIV infection.

[0010] **Hepatitis B Virus.** Chronic infection by hepatitis B virus (HBV) affects at least 5% of the world's population and is a major cause of cirrhosis and hepatocellular carcinoma (Hoofnagle, J., *N. Engl. J. Med.* 323:337, 1990; Fields, B. and Knipe, D., In: *Fields Virology* 2:2137, 1990). The World Health Organization lists hepatitis B as a leading cause of death worldwide, close behind chronic pulmonary disease, and more prevalent than AIDS. Chronic HBV infection can range from an asymptomatic carrier state to continuous hepatocellular necrosis and inflammation, and can lead to hepatocellular carcinoma.

[0011] The immune response to HBV is believed to play an important role in controlling hepatitis B infection. A variety of humoral and cellular responses to different regions of the HBV nucleocapsid core and surface antigens have been identified. T cell mediated immunity, particularly involving class I human leukocyte antigen-restricted cytotoxic T lymphocytes (CTL), is believed to be crucial in combatting established HBV infection.

[0012] Several studies have emphasized the association between self-limiting acute hepatitis and multispecific CTL responses (Penna, A. et al., *J. Exp. Med.* 174:1565, 1991; Nayersina, R. et al., *J. Immunol.* 150:4659, 1993). Spontaneous and interferon-related clearance of chronic HBV infection is also associated with the resurgence of a vigorous CTL response (Guidotti, L. G. et al., *Proc. Natl. Acad. Sci. USA* 91:3764, 1994). In all such cases the CTL responses are polyclonal, and specific for multiple viral proteins including the HBV envelope, core and polymerase antigens. By contrast, in patients with chronic hepatitis, the CTL activity is usually absent or weak, and antigenically restricted.

- [0013] The crucial role of CTL in resolution of HBV infection has been further underscored by studies using HBV transgenic mice. Adoptive transfer of HBV-specific CTL into mice transgenic for the HBV genome resulted in suppression of virus replication. This effect was primarily mediated by a non-lytic, lymphokine-based mechanism (Guidotti, L. G. et al., *Proc. Natl. Acad. Sci. USA* 91:3764, 1994; Guidotti, L. G., Guilhot, S., and Chisari, F. V. *J. Virol.* 68:1265, 1994; Guidotti, L. G. et al., *J. Virol.* 69:6158, 1995; Gilles, P. N., Fey, G., and Chisari, F. V., *J. Virol.* 66:3955, 1992).
- [0014] As is the case for HLA class I restricted responses, HLA class II restricted T cell responses are usually detected in patients with acute hepatitis, and are absent or weak in patients with chronic infection (Chisari, F. V. and Ferrari, C., *Annu. Rev. Immunol.* 13:29, 1995). HLA Class II responses are tied to activation of helper T cells (HTLs) Helper T lymphocytes, which recognize Class II HLA molecules, may directly contribute to the clearance of HBV infection through the secretion of cytokines which suppress viral replication (Franco, A. et al., *J. Immunol.* 159:2001, 1997). However, their primary role in disease resolution is believed to be mediated by inducing activation and expansion of virus-specific CTL and B cells.
- [0015] In view of the heterogeneous immune response observed with HBV infection, induction of a multi-specific cellular immune response directed simultaneously against multiple epitopes appears to be important for the development of an efficacious vaccine against HBV. There is a need to establish vaccine embodiments that elicit immune responses that correspond to responses seen in patients that clear HBV infection. Epitope-based vaccines appear useful.
- [0016] **Hepatitis C Virus.** Hepatitis C virus (HCV) infection is a global human health problem with approximately 150,000 new reported cases each year in the U.S. alone. HCV is a single stranded RNA virus, and is the etiological agent identified in most cases of non-A, non-B post-transfusion and post-transplant hepatitis, and is a common cause of acute sporadic hepatitis (Choo *et al.*, *Science* 244:359, 1989; Kuo *et al.*, *Science* 244:362, 1989; and Alter *et al.*, in: *Current Perspective in Hepatology*, p. 83, 1989). It is estimated that more than 50% of patients infected with HCV become chronically infected and, of those, 20% develop cirrhosis of the liver within 20 years (Davis *et al.*, *New Engl. J. Med.* 321:1501, 1989; Alter *et al.*, in: *Current Perspective in Hepatology*, p. 83, 1989; Alter *et al.*, *New Engl. J. Med.* 327:1899, 1992; and Dienstag, J. L. *Gastroenterology* 85:430,



1983). Moreover, the only therapy available for treatment of HCV infection is interferon- $\alpha$ . Most patients are unresponsive, however, and among the responders, there is a high recurrence rate within 6-12 months of cessation of treatment (Liang *et al.*, *J. Med. Virol.* 40:69, 1993). Ribavirin, a guanosine analog with a broad spectrum activity against many RNA and DNA viruses, has been shown in clinical trials to be effective against chronic HCV infection when used in combination with interferon- $\alpha$  (*see, e.g.,* Poynard *et al.*, *Lancet* 352:1426-1432, 1998; Reichard *et al.*, *Lancet* 351:83-87, 1998). However, the response rate is still well below 50%.

[0017] Virus-specific, human leukocyte antigen (HLA) class I-restricted cytotoxic T lymphocytes (CTL) are known to play a major role in the prevention and clearance of virus infections *in vivo* (Oldstone *et al.*, *Nature* 321:239, 1989; Jamieson *et al.*, *J. Virol.* 61:3930, 1987; Yap *et al.*, *Nature* 273:238, 1978; Lukacher *et al.*, *J. Exp. Med.* 160:814, 1994; McMichael *et al.*, *N. Engl. J. Med.* 309:13, 1983; Sethi *et al.*, *J. Gen. Virol.* 64:443, 1983; Watari *et al.*, *J. Exp. Med.* 165:459, 1987; Yasukawa *et al.*, *J. Immunol.* 143:2051, 1989; Tigges *et al.*, *J. Virol.* 66:1622, 1993; Reddenhase *et al.*, *J. Virol.* 55:263, 1985; Quinnan *et al.*, *N. Engl. J. Med.* 307:6, 1982).

[0018] In view of the heterogeneous immune response observed with HCV infection, induction of a multi-specific cellular immune response directed simultaneously against multiple HCV epitopes appears to be important for the development of an efficacious vaccine against HCV. There is a need, however, to establish vaccine embodiments that elicit immune responses that correspond to responses seen in patients that clear HCV infection.

[0019] **Human Papillomavirus.** Human papillomavirus (HPV) is a member of the papillomaviridae, a group of small DNA viruses that infect a variety of higher vertebrates. More than 80 types of HPVs have been identified. Of these, more than 30 can infect the genital tract. Some types, generally types 6 and 11, may cause genital warts, which are typically benign and rarely develop into cancer. Other strains of HPV, "cancer-associated", or "high-risk" types, can more frequently lead to the development of cancer. The primary mode of transmission of these strains of HPV is through sexual contact.

[0020] The main manifestations of the genital warts are cauliflower-like condylomata acuminata that usually involve moist surfaces; keratotic and smooth papular warts, usually on dry surfaces; and subclinical "flat" warts, which are found on any mucosal or cutaneous

surface (Handsfield, H., *Am. J. Med.* 102(5A):16-20, 1997). These warts are typically benign but are a source of inter-individual spread of the virus (Ponten, J. & Guo, Z., *Cancer Surv.* 32:201-29, 1998). At least three HPV strains associated with genital warts have been identified: type 6a (see, *e.g.*, Hofmann, K.J., *et al.*, *Virology* 209(2):506-518, 1995), type 6b (see, *e.g.*, Hofmann *et al.*, *supra*) and type 11 (see, *e.g.*, Dartmann, K. *et al.*, *Virology* 151(1):124-130, 1986).

[0021] Cancer-associated HPVs have been linked with cancer in both men and women; they include, but are not limited to, HPV-16, HPV-18, HPV-31, HPV-45, HPV-33 and HPV-56. Other HPV strains, including types 6 and 11 as well as others, *e.g.*, HPV-5 and HPV-8, are less frequently associated with cancer. The high risk types are typically associated with the development of cervical carcinoma and premalignant lesions of the cervix in women, but are also associated with similar malignant and premalignant lesions at other anatomic sites within the lower genital or anogenital tract. These lesions include neoplasia of the vagina, vulva, perineum, the penis, and the anus. HPV infection has also been associated with respiratory tract papillomas, and rarely, cancer, as well as abnormal growth or neoplasia in other epithelial tissues. *See, e.g.* VIROLOGY, 2<sup>ND</sup> ED, Fields *et al.*, Eds. Raven Press, New York, 1990, Chapters 58 and 59, for a review of HPV association with cancer.

[0022] The HPV genome consists of three functional regions, the early region, the late region, and the “long control region”. The early region gene products control viral replication, transcription and cellular transformation. They include the HPV E1 and E2 proteins, which play a role in HPV DNA replication, and the E6 and E7 oncoproteins, which are involved in the control of cellular proliferation. The late region include the genes that encode the structural proteins L1 and L2, which are the major and minor capsid proteins, respectively. The “long control region” contains such sequences as enhancer and promoter regulatory regions.

[0023] HPV expresses different proteins at different stages of the infection, for example early, as well as late, proteins. Even in latent infections, however, early proteins are often expressed and are therefore useful targets for vaccine-based therapies. For example, high-grade dysplasia and cervical squamous cell carcinoma continue to express E6 and E7, which therefore can be targeted to treat disease at both early and late stages of infection.

[0024] Treatment for HPV infection is often unsatisfactory because of persistence of virus after treatment and recurrence of clinically apparent disease is common. The treatment

may require frequent visits to clinics and is not directed at elimination of the virus but at clearing warts. Because of persistence of virus after treatment, recurrence of clinically apparent disease is common.

[0025] Thus, a need exists for an efficacious vaccine to both prevent and treat HPV infection and to treat cancer that is associated with HPV infection. Effective HPV vaccines would be a significant advance in the control of sexually transmissible infections and could also protect against clinical disease, particularly cancers such as cervical cancer. (see, e.g., Rowen, P. & Lacey, C., *Dermatologic Clinics* 16(4):835-838, 1998).

[0026] Virus-specific, human leukocyte antigen (HLA) class I-restricted cytotoxic T lymphocytes (CTL) are known to play a major role in the prevention and clearance of virus infections *in vivo* (Oldstone *et al.*, *Nature* 321:239, 1989; Jamieson *et al.*, *J. Virol.* 61:3930, 1987; Yap *et al.*, *Nature* 273:238, 1978; Lukacher *et al.*, *J. Exp. Med.* 160:814, 1994; McMichael *et al.*, *N. Engl. J. Med.* 309:13, 1983; Sethi *et al.*, *J. Gen. Virol.* 64:443, 1983; Watari *et al.*, *J. Exp. Med.* 165:459, 1987; Yasukawa *et al.*, *J. Immunol.* 143:2051, 1989; Tigges *et al.*, *J. Virol.* 66:1622, 1993; Reddenhase *et al.*, *J. Virol.* 55:263, 1985; Quinnan *et al.*, *N. Engl. J. Med.* 307:6, 1982).

[0027] Virus-specific T helper lymphocytes are also known to be critical for maintaining effective immunity in chronic viral infections. Historically, HTL responses were viewed as primarily supporting the expansion of specific CTL and B cell populations; however, more recent data indicate that HTL may directly contribute to the control of virus replication. For example, a decline in CD4<sup>+</sup> T cells and a corresponding loss in HTL function characterize infection with HIV (Lane *et al.*, *New Engl. J. Med.* 313:79, 1985). Furthermore, studies in HIV infected patients have also shown that there is an inverse relationship between virus-specific HTL responses and viral load, suggesting that HTL plays a role in viremia (see, e.g., Rosenberg *et al.*, *Science* 278:1447, 1997).

[0028] The development of vaccines with prophylactic and therapeutic efficacy against HPV is ongoing. Early vaccine development was hampered by the inability to culture HPV. With the introduction of cloning techniques and protein expression, however, some attempts have been made to stimulate humoral and CTL response to HPV (See, e.g., Rowen, P. & Lacey, C., *Dermatologic Clinics* 16(4):835-838 (1998)). Studies to date, however, have been inconclusive.

[0029] Activation of T helper cells and cytotoxic lymphocytes (CTLs) in the development of vaccines has also been analyzed. Lehtinen, M., *et al.* for instance, has shown that some

peptides from the E2 protein of HPV type 16 activate T helper cells and CTLs (*Biochem. Biophys. Res. Commun.* 209(2):541-6 (1995). Similarly, Tarpey *et al.*, has shown that some peptides from HPV type 11 E7 protein can stimulate human HPV-specific CTLs *in vitro* (*Immunology* 81:222-227 (1994)) and Borysiewicz *et al.* have reported a recombinant vaccinia virus expressing HPV 16 and HPV 17 E6 and E7 that stimulated CTL responses in at least one patient (*Lancet* 347:1347-1357, 1996).

[0030]        ***Plasmodium falciparum* and Malaria.** Malaria, which is caused by infection with the parasite *Plasmodium falciparum* (PF), represents a major world health problem. Approximately 500 million people in the world are at risk from the disease, with approximately 200 million people actually harboring the parasites. An estimated 1 to 2 million deaths occur each year due to malaria. (Miller *et al.*, *Science* 234:1349, 1986).

[0031]        Fatal outcomes are not confined to first infections, and constant exposure is apparently a prerequisite for maintaining immunity. Naturally acquired sterile immunity is rare, if it exists at all. Accordingly, major efforts to develop an efficacious malaria vaccine have been undertaken.

[0032]        Human volunteers injected with irradiated PF sporozoites are resistant to subsequent sporozoite challenges, which demonstrates that development of a malaria vaccine is indeed immunologically feasible. Furthermore, these immune individuals developed a vigorous response, including antibodies, and cytotoxic T lymphocyte (CTL) and helper T lymphocyte (HTL) components, directed against multiple antigens. Reproducing the breadth and multiplicity of this response in a vaccine, however, is a task of large proportions. The epitope approach, as described herein, may represent a solution to this challenge, in that it allows the incorporation of various antibody, CTL and HTL epitopes, from various proteins, in a single vaccine composition.

[0033]        Anti-sporozoite antibodies are by themselves, in general, not completely efficacious in clearing the infection (Egan *et al.*, *Science* 236:453, 1987). However, high concentrations of antibodies directed against the repeated region of the major B cell antigen of the sporozoite/circumsporozoite protein (CSP) have been shown to prevent liver cell infection in certain experimental models (Egan *et al.*, *Science* 236:453, 1987; Potocnjak, P. *et al.*, *Science* 207:71, 1980). The present inventors have shown that constructs encompassing CSP-repeat B cell epitopes and the optimized helper epitope PADRE™ (San Diego, CA) are highly immunogenic, and can protect *in vitro* against

sporozoite invasion in both mouse and human liver cells, and protect mice *in vivo* against live sporozoite challenge (Franke *et al.*, *Vaccine* 17:1201-1205, 1999)

[0034] PF-specific CD4<sup>+</sup> T cells also have a role in malarial immunity beyond providing help for B cell and CTL responses. Experiments by Renia *et al.* (Renia, *et al.*, *Proc. Natl. Acad. Sci. USA* 88:7963, 1991) demonstrated that HTLs directed against the *Plasmodium yoelli* CS protein could in fact adoptively transfer protection against malaria.

[0035] Considerable data implicate CTLs in protection against pre-erythrocytic-stage malaria. CD8<sup>+</sup> CTLs can eliminate *Plasmodium berghei*- or *Plasmodium yoelii*-infected mouse hepatocytes from *in vitro* culture in a major histocompatibility complex (MHC)-restricted and antigen-restricted manner (Hoffman *et al.*, *Science* 244:1078-1081, 1989; Weiss *et al.*, *J. Exp. Med.* 171:763-773, 1990). Further, it has also been shown that the immunity that developed in mice vaccinated with irradiated sporozoites is also dependent upon the presence of CD8<sup>+</sup> T cells. These T cells accumulate in inflammatory liver infiltrates subsequent to challenge. Passive transfer of circumsporozoite (CSP)-specific CTL clones as long as three hours after inoculation of sporozoites (*i.e.*, after the parasites have left the bloodstream and infected liver cells) were capable of protecting animals against infection (Romero *et al.*, *Nature* 341:323, 1989).

[0036] It is notable that CTL-restricted responses directed against a single antigen are insufficient to protect mice with different MHC alleles, and a combination of multiple antigens was required even to protect mice from the most common laboratory strains of *Plasmodium*. These data indicate that a combination of epitopes from several antigens is necessary to elicit a protective CTL response.

[0037] Indirect evidence that CTLs are important in protective immunity against Pf in humans has also accumulated. It has been reported that cytotoxic CD8<sup>+</sup> T cells can be identified in humans immunized with PF sporozoites (Moreno, *et al.*, *Int. Immunol.* 3:997, 1991). Further, humans immunized with irradiated sporozoites or naturally exposed to malaria can generate a CTL response to the pre-erythrocytic-stage antigens, CSP, sporozoite surface protein 2 (SSP2), liver-stage antigen-1 (LSA-1), and exported protein-1 (Exp-1) (*see, e.g.* Malik *et al.*, *Proc. Natl. Acad. Sci. USA* 88, 3300-3304, 1991; Doolan *et al.*, *Int. Immunol.* 3:511-516, 1991; Hill *et al.*, *Nature* 360:434-439, 1992). Additionally, there is evidence that the polymorphism within the CSP may be the result of selection by CTLs of parasites that express variant forms (MCutchan and Water, *Immunol. Lett.* 25:23-26, 1990). This is based on the observation that the variation is nonsynonymous at the

nucleotide level, thereby indicating selective pressure at the protein level. The polymorphism primarily maps to identified CTL and T helper epitopes (Doolan *et al.*, *Int. Immunol.* 5:27-46, 1993); and CTL responses to some of the parasite variants do not cross-react (Hill *et al.*, *supra*). Finally, the MHC class I human leukocyte antigen (HLA)-Bw53 has been associated with resistance to severe malaria in The Gambia, and CTLs to a conserved epitope restricted by the HLA-Bw53 allele have been identified on *P. falciparum* LSA-1 (Hill *et al.*, *Nature* 352:595-600, 1991; Hill *et al.*, *Nature* 340:434-439, 1992). Since HLA-Bw53 is found in 15%-40% of the population of sub-Saharan Africa but in less than 1% of Caucasians and Asians, these data suggest evolutionary selection on the basis of protection against severe malaria.

[0038] Thus, antibody, and both HLA class I and class II restricted responses directed against multiple sporozoite antigens appear to be involved in generating protective immunity to malaria. Furthermore, several important antigenic epitopes against which humoral and cellular immunity is focused have already been exactly delineated.

[0039] In view of the heterogeneous immune response observed with PF infection, induction of a multi-specific cellular immune response directed simultaneously against multiple PF epitopes appears to be important for the development of an efficacious vaccine against PF. There is a need, however, to establish vaccine embodiments that elicit immune responses that correspond to responses seen in patients that clear PF infection.

[0040] **Epitope-Based Vaccines.** The use of epitope-based vaccines has several advantages over current vaccines. The epitopes for inclusion in such a vaccine are to be selected from conserved regions of viral or tumor-associated antigens, in order to reduce the likelihood of escape mutants. The advantage of an epitope-based approach over the use of whole antigens is that there is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. Furthermore, immunosuppressive epitopes that may be present in whole antigens can be avoided with the use of epitope-based vaccines.

[0041] Additionally, with an epitope-based vaccine approach, there is an ability to combine selected epitopes (CTL and HTL) and additionally to modify the composition of the epitopes, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches.

[0042] Another major benefit of epitope-based immune-stimulating vaccines is their safety. The possible pathological side effects caused by infectious agents or whole protein antigens, which might have their own intrinsic biological activity, is eliminated.

[0043] An epitope-based vaccine also provides the ability to direct and focus an immune response to multiple selected antigens from the same pathogen. Thus, patient-by-patient variability in the immune response to a particular pathogen may be alleviated by inclusion of epitopes from multiple antigens from that pathogen in a vaccine composition. A “pathogen” may be an infectious agent or a tumor associated molecule.

[0044] One of the most formidable obstacles to the development of broadly efficacious epitope-based immunotherapeutics has been the extreme polymorphism of HLA molecules. In the past, effective non-genetically biased coverage of a population has been a task of considerable complexity; such coverage has required that epitopes be used specific for HLA molecules corresponding to each individual HLA allele. Therefore, impractically large numbers of epitopes would be required in order to cover ethnically diverse populations. Recently, methods have been developed that allow the identification of epitopes that bind multiple HLA molecules. Therefore, epitope-based vaccines can be designed that contain epitopes which, either individually or in combination, bind a greater number of HLA molecules. The resulting epitope-based vaccines have a greater breadth of population coverage across one or more continents and even worldwide.

[0045] **Variation in Epitopes of Infectious Agents.** A challenge in the development of effective vaccines against infectious agents such as hepatitis B virus (HBV) (47, 60) hepatitis C virus (HCV) (61-63), human papilloma virus (HPV) (64, 65) *Plasmodium falciparum* (66), and human immunodeficiency virus (HIV-1) is the protein sequence variation associated with different isolates. This variation is the result of gene sequence mutations. When such mutations occur in regions encoding epitopes recognized by cytotoxic T-lymphocytes (CTL), they provide a mechanism for escape of the agent from immune system control.

[0046] HIV-1 represents an infectious agent with an especially high frequency of sequence variation. The sequence variation associated with HIV-1 proteins from related isolates, members of the same clades or types, as well as unrelated isolates, is well documented (1). Viral escape from CTL induced as the result of natural infection or vaccines was documented in nonhuman primate models where the mechanism behind this

escape was mutation of the primary anchor residues in dominant CTL epitopes (5-9). Viral escape from HIV-specific CTL has also been strongly implied by data obtained from HIV-1 infected individuals whose disease status change, including the transition from acute to chronic infection (10, 11), loss of stable control of viral replication and subsequent progression to AIDS (4, 12) or mother-to-child transmission (13). Thus, HIV-1 genetic and protein sequence variation represent a significant challenge to immune system-based control of viral replication, both within infected individuals and within populations.

[0047] While the public health need for a vaccine against HIV-1 is well recognized and accepted, the genetic variation of HIV-1 isolates represents a highly significant obstacle (1, 14-16). Several strategies have been proposed, some of which include:

(1) Designing vaccines on HIV-1 types prevalent within small, well defined populations or geographical regions, such as individual countries or regions, and producing multiple different vaccines for exclusive use within these countries or regions (16).

(2) Use of HIV-1 ancestral or consensus sequences based on HIV types present in larger target populations, such as groups of neighboring countries or continents (15, 17-19).

(3) Incorporation of viral gene products obtained from multiple different virus isolates, representing diversely different types or clades, into a single 'multi-valent' vaccine.

[0048] Related vaccine design concepts that incorporate many of the advantages associated with the approaches described above are the use of highly conserved regions or epitopes derived from these regions as the basis of the vaccine. The logic behind this approach is that conserved regions of the viral genome are those that have been maintained through the evolution of HIV-1 because changes impact gene product function and general viral fitness. This theory is consistent with analyses of HIV-1 protein sequence data which demonstrated that CTL epitopes are concentrated in conserved regions and that regions devoid of CTL epitopes are the most variable (20). Additional support comes from published reports describing CTL responses, induced as the result of



natural infection or vaccination, that recognize viral proteins or epitopes common to viral isolates from diverse types or clades (21-26). Broad function CTL responses are also known to be correlated with slower progression to AIDS, at least for certain carefully studied populations (27, 28). Despite these reports and the clustering of CTL epitopes in conserved regions of HIV-1 gene products, amino acid sequence variation of analogous regions and epitopes from different viral isolates, both within the same type or clade and from different types, remains significant. There are currently no rules guiding the selection of conserved regions of CTL epitopes for use in vaccines other than the use of amino acid sequence identity (29).

**[0049]** A clear understanding of how CTL recognize pathogen infected cells has emerged over the past decade. It is now well established that small fragments of pathogen-derived proteins are generated, defined as peptide epitopes generally 8-11 amino acids in length, which bind to HLA-A, -B, or -C (human Class I Major Histocompatibility Molecules) molecules expressed on the cell surface. Sequencing of naturally processed peptides bound to HLA molecules provided a means to identify the amino acid residues required for allele-specific epitope-peptide binding (30-32). Data obtained from X-ray crystallographic analysis of HLA-epitope peptide complexes, allowed for the identification and structural characterization of 'binding pockets' within the peptide binding cleft of HLA molecules. More refined epitope anchor motif definitions were then developed using data obtained from *in vitro* peptide-MHC binding assays. It is now well known that the main anchor residues typically occur at position 2 and the carboxyl terminus of peptides 8-11 amino acids in length, thus positions 8, 9, 10 or 11 (33-40). The definition of epitope peptide binding anchor motifs is the key to most, if not all, epitope prediction methods.

**[0050]** Initial CTL epitope identification methods were developed using common HLA alleles, such as HLA-A2.1. Motifs defined using different HLA molecules were found to be similar and this led to the definition of HLA supertype families (41). The biological effect of this supertype relationship was first demonstrated for HIV-1 epitopes in a study where the HLA-A3 and -A11 epitope peptide binding patterns repertoires were demonstrated to be overlapping, not only with each other but also with HLA-A31, -A33 and -A\*6801 (42). This binding specificity was defined as the HLA-A3 supertype. A significant overlap in peptide binding patterns was also demonstrated amongst several serologically distant HLA-B alleles (43, 44), and multiple HLA-A2 alleles (45, 46),

resulting in the definition of the HLA-B7 and HLA-A2 supertype families. Recognition of epitopes by CTL in a supertype manner has since been demonstrated to occur naturally in infectious diseases and cancer (47-53).

[0051] While only two positions within CTL epitopes are typically characterized as the primary binding anchor positions, the amino acids that can serve as the anchor residues are more variable. The preferred and tolerated amino acids that can serve as anchor residues for the HLA-A2, -A3 and -B7 supertype families of epitopes are listed in Table 1. It is possible for analogous HIV-1 epitope peptides derived from different isolates, which differ with respect to the amino acids used as anchor residues, to bind to HLA molecules similarly. This type of variation can be as conserved since it is likely that CTL produced against one epitope would recognize the related epitope. Thus, variation limited to changes in anchor residues that result in sufficient epitope peptide binding to HLA molecules does not result in immune escape from CTL. Epitopes that contain this type of variation can be identified using the appropriately designed motif search algorithms.

[0052] The TCR of CTL has been reported to be somewhat flexible or promiscuous with respect to recognition of epitope peptides bound to HLA molecules. For HIV-1, this flexibility was demonstrated as CTL recognition of related, but slightly variable, epitopes by single clones of CTL produced following natural infection (54, 55). Similar flexibility of CTL epitope recognition was demonstrated using rhesus macaques and natural infection with SIV or immunization (56, 57). This observation is not unique to HIV-1 and SIV but rather the TCR appears to have evolved to allow promiscuous recognition of peptide epitope bound to MHC molecules (58).

[0053] Selective replacement of certain amino acids in CTL epitope peptides, amino acids thought to represent TCR contact points, is not only tolerated but can increase the recognition of the epitopes by CTL clones (59). The types of amino acid substitutions that can be incorporated, typically amino acids that are similar in chemical properties are best tolerated, and their positions, independent of primary anchor positions, within a selected number of CTL epitopes from tumor associated antigens were also defined.

[0054] For HIV-1 and other infectious agents, reproducible methods for predicting the CTL recognition of related variant epitopes that occur amongst isolates have not been developed. Nor have methods for identifying CTL epitopes that are most likely to induce broadly functional responses when used in vaccine. Thus, there exists a need to develop

such methods to overcome the challenge associated with protein sequence variation in HIV and other infectious agents.

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## SUMMARY OF THE INVENTION

[0055] The present invention is directed to methods for selecting a variant of a peptide epitope which induces a CTL response against another variant(s) of the peptide epitope, by determining whether the variant comprises only conserved residues, as defined herein, at non-anchor positions in comparison to the other variant(s).

[0056] In some embodiments, antigen sequences from a population of an infectious agent, said antigens comprising variants of a peptide epitope, are optionally aligned (manually or by computer) along their length, preferably their full length. Variant(s) of a peptide epitope (preferably naturally occurring variants), each 8-11 amino acids in length and comprising the same MHC class I supermotif or motif, are identified manually or with the aid of a computer. In some embodiments, a variant is optionally chosen which comprises preferred anchor residues of said motif and/or which occurs with high frequency within the population of variants. In other embodiments, a variant is randomly chosen. The randomly or otherwise chosen variant is compared to from one to all the remaining variant(s) to determine whether it comprises only conserved residues in the non-anchor positions relative to from one to all the remaining variant(s).

[0057] The present invention is also directed to variants identified by the methods above; peptides comprising such variants; nucleic acids encoding such variants and peptides; cells comprising such variants, and/or peptides, and/or nucleic acids; compositions comprising such variants, and/or peptides, and/or nucleic acids, and/or cells; as well as therapeutic and diagnostic methods for using such variants, peptides, nucleic acids, cells, and compositions.

## BRIEF DESCRIPTION OF THE DRAWINGS/FIGURES

- [0058] FIGS. 1A-1E. Recognition of variant peptides by CTL generated against a single epitope. Variant peptides were identified from 167 HIV strains for 5 HIV epitopes, 3 HLA-A2 restricted (Env 134, A, Gag 386, B, and Vpr 62, C) and 2 HLA-A11 restricted (Pol 98, D, and Env 47, E). These are listed according to their relationship to a previously determined parent (P) into single anchor substitutions (A), single non-anchor substitutions (NA) or multiple substitutions (M). Binding of each variant peptide is also shown. The number of viral sequences containing each variant peptide is shown in the column labeled # Isolates, and is reported for the total sequences, Clade B sequences (B), and Clade C sequences (C). Finally, the ability of CTL primed against the parent peptide to recognize the variant peptides is shown in the bar graphs.
- [0059] FIGS. 2A-2C. Characterization of the peptide-specific T cell lines. A. FACS analysis of the TCRs expressed by peptide -stimulated cells after 0, 1, and 5 peptide stimulations, using a panel of commercially available mAb for mouse TCR 2-14. B-C. Peptide affinity. Parent and variant peptides were titrated against CTL that had been stimulated 5 times with the parent peptide.
- [0060] FIGS. 2A-2B. Recognition of a panel of variant peptides by PBL from an HIV-infected individual.
- [0061] FIG 4. Prediction of immunological conservation. Gag 271 variants and their binding are shown, along with the number of isolates that express each variant. Immunological recognition was predicted for each variant based on two different choices in the immunizing peptide. On the right, the immunogenicity for each variant is shown.

## DETAILED DESCRIPTION OF THE INVENTION

### *Definitions*

- [0062] The invention can be better understood with reference to the following definitions:
- [0063] An "antigen" refers to a polypeptide encoded by the genome of an infectious agent, or other another source, but preferably an infectious agent in the present invention.

Examples of HIV antigens include Env, Gag, Nef, Pol, Tat, Rev, Vif, Vpr, Vpu, p17, p24, p2, p7, p1, p6, Protease, RT, Integrase, and gp160 (preferably Env, Gag, Nef, Pol, Tat, Rev, Vif, Vpr, Vpu). Examples of HBV antigens include Core, Env, and Pol. Examples of HCV antigens include Core, E1, E2, Ns1, Ns2, Ns3, Ns4, and Ns5. Examples of HPV antigens include E1, E2, E3, E4, E5, E6, E7, L1, and L2. Examples of *Plasmodium falciparum* antigens include CSP, SSP2, Exp1, and LSA1.

[0064] Throughout this disclosure, "binding data" results are often expressed in terms of "IC<sub>50</sub>'s." IC<sub>50</sub> is the concentration of peptide in a binding assay at which 50% inhibition of binding of a reference peptide is observed. Given the conditions in which the assays are run (*i.e.*, limiting HLA proteins and labeled peptide concentrations), these values approximate K<sub>D</sub> values. Assays for determining binding are described in detail, *e.g.*, in PCT publications WO 94/20127 and WO 94/03205, and other publications such as Sidney *et al.*, *Current Protocols in Immunology* 18.3.1 (1998); Sidney, *et al.*, *J. Immunol.* 154:247 (1995); and Sette, *et al.*, *Mol. Immunol.* 31:813 (1994). It should be noted that IC<sub>50</sub> values can change, often dramatically, if the assay conditions are varied, and depending on the particular reagents used (*e.g.*, HLA preparation, *etc.*). For example, excessive concentrations of HLA molecules will increase the apparent measured IC<sub>50</sub> of a given ligand.

[0065] Alternatively, binding is expressed relative to a reference peptide. Although as a particular assay becomes more, or less, sensitive, the IC<sub>50</sub>'s of the peptides tested may change somewhat, the binding relative to the reference peptide will not significantly change. For example, in an assay run under conditions such that the IC<sub>50</sub> of the reference peptide increases 10-fold, the IC<sub>50</sub> values of the test peptides will also shift approximately 10-fold. Therefore, to avoid ambiguities, the assessment of whether a peptide is a good (*i.e.* high), intermediate, weak, or negative binder is generally based on its IC<sub>50</sub>, relative to the IC<sub>50</sub> of a standard peptide. The Tables included in this application present binding data in a preferred biologically relevant form of IC<sub>50</sub> nM.

[0066] Binding may also be determined using other assay systems including those using: live cells (*e.g.*, Ceppellini *et al.*, *Nature* 339:392 (1989); Christnick *et al.*, *Nature* 352:67 (1991); Busch *et al.*, *Int. Immunol.* 2:443 (1990); Hill *et al.*, *J. Immunol.* 147:189 (1991); del Guercio *et al.*, *J. Immunol.* 154:685 (1995)), cell free systems using detergent lysates (*e.g.*, Cerundolo *et al.*, *J. Immunol.* 21:2069 (1991)), immobilized purified MHC (*e.g.*, Hill *et al.*, *J. Immunol.* 152, 2890 (1994); Marshall *et al.*, *J. Immunol.* 152:4946 (1994)), ELISA systems (*e.g.*, Reay *et al.*, *EMBO J.* 11:2829 (1992)), surface plasmon resonance (*e.g.*, Khilko *et al.*, *J. Biol. Chem.* 268:15425 (1993)), high flux soluble phase assays (Hammer *et al.*, *J. Exp. Med.* 180:2353 (1994)), and measurement of class I MHC stabilization or assembly (*e.g.*, Ljunggren *et al.*, *Nature* 346:476 (1990));



Schumacher *et al.*, *Cell* 62:563 (1990); Townsend *et al.*, *Cell* 62:285 (1990); Parker *et al.*, *J. Immunol.* 149:1896 (1992)).

- [0067] As used herein, “high affinity” with respect to HLA class I molecules is defined as binding with an  $IC_{50}$  or  $K_D$  value, of 50 nM or less, “intermediate affinity” is binding with an  $IC_{50}$  or  $K_D$  value of between 50 and about 500 nM, weak affinity is binding with an  $IC_{50}$  or  $K_D$  value of between about 500 and about 5000 nM. “High affinity” with respect to binding to HLA class II molecules is defined as binding with an  $IC_{50}$  or  $K_D$  value of 100 nM or less; “intermediate affinity” is binding with an  $IC_{50}$  or  $K_D$  value of between about 100 and about 1000 nM.
- [0068] A “computer” or “computer system” generally includes: a processor and related computer programs; at least one information storage/retrieval apparatus such as a hard drive, a disk drive or a tape drive; at least one input apparatus such as a keyboard, a mouse, a touch screen, or a microphone; and display structure, such as a screen or a printer. Additionally, the computer may include a communication channel in communication with a network. Such a computer may include more or less than what is listed above.
- [0069] “Cross-reactive binding” indicates that a peptide is bound by more than one HLA molecule; a synonym is degenerate binding.
- [0070] A “cryptic epitope” elicits a response by immunization with an isolated peptide, but the response is not cross-reactive *in vitro* when intact whole protein, which comprises the epitope, is used as an antigen.
- [0071] The term “derived” when used to discuss an epitope is a synonym for “prepared.” A derived epitope can be isolated from a natural source, or it can be synthesized in accordance with standard protocols in the art. Synthetic epitopes can comprise artificial amino acids “amino acid mimetics,” such as D isomers of natural occurring L amino acids or non-natural amino acids such as cyclohexylalanine. A derived/prepared epitope can be an analog of a native epitope.
- [0072] A “diluent” includes sterile liquids, such as water and oils, including those of petroleum, animal, vegetable or synthetic origin, such as peanut oil, soybean oil, mineral oil, sesame oil and the like. Water is a preferred diluent for pharmaceutical compositions. Saline solutions and aqueous dextrose and glycerol solutions can also be employed as diluents, particularly for injectable solutions.
- [0073] A “dominant epitope” is an epitope that induces an immune response upon immunization with a whole native antigen (see, *e.g.*, Sercarz, *et al.*, *Annu. Rev. Immunol.* 11:729-766, 1993). Such a response is cross-reactive *in vitro* with an isolated peptide epitope.
- [0074] An “epitope” is the collective features of a molecule, such as primary, secondary and tertiary peptide structure, and charge, that together form a site recognized by an immunoglobulin, T cell receptor or HLA molecule. Alternatively, an epitope can be defined as a set of amino acid residues which is involved in recognition by a particular immunoglobulin, or in the context of T

cells, those residues necessary for recognition by T cell receptor proteins and/or Major Histocompatibility Complex (MHC) receptors. Epitopes are present in nature, and can be isolated, purified or otherwise prepared/derived by humans. For example, epitopes can be prepared by isolation from a natural source, or they can be synthesized in accordance with standard protocols in the art. Synthetic epitopes can comprise artificial amino acids, "amino acid mimetics," such as D isomers of naturally-occurring L amino acids or non-naturally-occurring amino acids such as cyclohexylalanine. Throughout this disclosure, epitopes may be referred to in some cases as peptides. The variants of the invention are set forth in Tables 6-9 and Figures 1A-4.

[0075] It is to be appreciated that proteins or peptides that comprise a variant of the invention as well as additional amino acid(s) are still within the bounds of the invention. In certain embodiments, the peptide comprises a fragment of an antigen. A "fragment of an antigen" or "antigenic fragment" or simply "fragment" is a portion of an antigen which has 100% identity with a wild type antigen or naturally-occurring variant thereof. The fragment may or may not comprise an epitope of the invention. The fragment may be less than or equal to 600 amino acids, less than or equal to 500 amino acids, less than or equal to 400 amino acids, less than or equal to 250 amino acids, less than or equal to 100 amino acids, less than or equal to 85 amino acids, less than or equal to 75 amino acids, less than or equal to 65 amino acids, or less than or equal to 50 amino acids in length. In certain embodiments, a fragment is e.g., less than 101 or less than 51 amino acids in length, in any increment down to 5 amino acids in length. For example, the fragment may be 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, or 100 amino acids in length.

[0076] In certain embodiments, there is a limitation on the length of a peptide of the invention. The embodiment that is length-limited occurs when the protein/peptide comprising an epitope of the invention comprises a region (i.e., a contiguous series of amino acids) having 100% identity with a native sequence. In order to avoid the definition of epitope from reading, e.g., on whole natural molecules, there is a limitation on the length of any region that has 100% identity with a native peptide sequence. Thus, for a peptide comprising an epitope of the invention and a region with 100% identity with a native peptide sequence, the region with 100% identity to a native sequence generally has a length of: less than or equal to 600 amino acids, often less than or equal to 500 amino acids, often less than or equal to 400 amino acids, often less than or equal to 250 amino acids, often less than or equal to 100 amino acids, often less than or equal to 85 amino acids, often less than or equal to 75 amino acids, often less than or equal to 65 amino acids, and often less than or equal to 50 amino acids. In certain embodiments, an "epitope" of the invention

is comprised by a peptide having a region with less than 51 amino acids that has 100% identity to a native peptide sequence, in any increment down to 5 amino acids.

[0077] Accordingly, peptide or protein sequences longer than 600 amino acids are within the scope of the invention, so long as they do not comprise any contiguous sequence of more than 600 amino acids that have 100% identity with a native peptide sequence. For any peptide that has five contiguous residues or less that correspond to a native sequence, there is no limitation on the maximal length of that peptide in order to fall within the scope of the invention. It is presently preferred that a peptide of the invention (*e.g.*, a peptide comprising an epitope of the invention) be less than 600 residues long in any increment down to eight amino acid residues.

[0078] A peptide epitope occurring with "high frequency" is one that occurs in at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, or at least 90% of the infectious agents in a population. A "high frequency" peptide epitope is one of the more common in a population, preferably the first most common, second most common, third most common, or fourth most common in a population of variant peptide epitopes.

[0079] "Human Leukocyte Antigen" or "HLA" is a human class I or class II Major Histocompatibility Complex (MHC) protein (*see, e.g.*, Stites, *et al.*, IMMUNOLOGY, 8<sup>TH</sup> ED., Lange Publishing, Los Altos, CA (1994).

[0080] An "HLA supertype or HLA family", as used herein, describes sets of HLA molecules grouped on the basis of shared peptide-binding specificities. HLA class I molecules that share somewhat similar binding affinity for peptides bearing certain amino acid motifs are grouped into such HLA superotypes. The terms HLA superfamily, HLA supertype family, HLA family, and HLA xx-like molecules (where "xx" denotes a particular HLA type), are synonyms. See Tables 1-4.

[0081] As used herein, "high affinity" with respect to HLA class I molecules is defined as binding with an  $IC_{50}$ , or  $K_D$  value, of 50 nM or less; "intermediate affinity" is binding with an  $IC_{50}$  or  $K_D$  value of between about 50 and about 500 nM; "weak affinity" is binding with an  $IC_{50}$  or  $K_D$  value between about 500 and about 5000 nM. "High affinity" with respect to binding to HLA class II molecules is defined as binding with an  $IC_{50}$  or  $K_D$  value of 100 nM or less; "intermediate affinity" is binding with an  $IC_{50}$  or  $K_D$  value of between about 100 and about 1000 nM. See "binding data."

[0082] An " $IC_{50}$ " is the concentration of peptide in a binding assay at which 50% inhibition of binding of a reference peptide is observed. Given the conditions in which the assays are run (*i.e.*, limiting HLA proteins and labeled peptide concentrations), these values approximate  $K_D$  values. See "binding data."

[0083] The terms "identical" or percent "identity," in the context of two or more peptide sequences or antigen fragments, refer to two or more sequences or subsequences that are the same

or have a specified percentage of amino acid residues that are the same, when compared and aligned for maximum correspondence over a comparison window, as measured using a sequence comparison algorithm or by manual alignment and visual inspection.

[0084] An "immunogenic" peptide or an "immunogenic" epitope or "peptide epitope" is a peptide that comprises an allele-specific motif or supermotif such that the peptide will bind an HLA molecule and induce a CTL and/or HTL response. Thus, immunogenic peptides of the invention are capable of binding to an appropriate HLA molecule and thereafter inducing a cytotoxic T lymphocyte (CTL) response, or a helper T lymphocyte (HTL) response, to the peptide.

[0085] An "infectious agent" refers to a disease-causing microorganism, including viruses, bacteria, fungi, and protozoa against which a cellular immune response, preferably a CTL response, plays a role in acquired immunity. Examples of infectious agents include viruses such as human immunodeficiency virus (HIV), hepatitis B virus (HBV), hepatitis C virus (HCV), human papillomoma virus (HPV), Influenza virus, Dengue virus, Epstein-Barr virus, bacteria such as *Mycobacterium tuberculosis* and *Chlamydia*, fungi such as *Candida albicans*, *Cryptococcus neoformans*, *Coccidioides spp.*, *Histoplasma spp.*, and *Aspergillus fumigatis*, protozoa such as *Plasmodium spp.*, including *P. falciparum*, *Trypanosoma spp.*, *Schistosoma spp.*, *Leishmania spp.* and the like. Preferred infectious agents include HIV, HBV, HCV, HPV, Epstein-Barr virus, *Plasmodium falciparum*, Influenza virus and Dengue virus.

[0086] The phrases "isolated" or "biologically pure" refer to material which is substantially or essentially free from components which normally accompany the material as it is found in its native state. Thus, isolated peptides in accordance with the invention preferably do not contain materials normally associated with the peptides in their *in situ* environment. An "isolated" epitope refers to an epitope that does not include the whole sequence of the antigen or polypeptide from which the epitope was derived. Typically the "isolated" epitope does not have attached thereto additional amino acids that result in a sequence that has 100% identity with a native sequence. The native sequence can be a sequence such as a tumor-associated antigen from which the epitope is derived. Thus, the term "isolated" means that the material is removed from its original environment (e.g., the natural environment if it is naturally occurring). For example, a naturally-occurring polynucleotide or peptide present in a living animal is not isolated, but the same polynucleotide or peptide, separated from some or all of the coexisting materials in the natural system, is isolated. Such a polynucleotide could be part of a vector, and/or such a polynucleotide or peptide could be part of a composition, and still be "isolated" in that such vector or composition is not part of its natural environment. Isolated RNA molecules include *in vivo* or *in vitro* RNA

transcripts of the DNA molecules of the present invention, and further include such molecules produced synthetically.

[0087] "Major Histocompatibility Complex" or "MHC" is a cluster of genes that plays a role in control of the cellular interactions responsible for physiologic immune responses. In humans, the MHC complex is also known as the human leukocyte antigen (HLA) complex. For a detailed description of the MHC and HLA complexes, see, Paul, FUNDAMENTAL IMMUNOLOGY, 3<sup>RD</sup> ED., Raven Press, New York (1993).

[0088] The term "motif" refers to a pattern of residues in an amino acid sequence of defined length, preferably a peptide of less than about 15 amino acids in length, or less than about 13 amino acids in length, usually from about 8 to about 13 amino acids (*e.g.*, 8, 9, 10, 11, 12, or 13) for a class I HLA motif and from about 6 to about 25 amino acids (*e.g.*, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25) for a class II HLA motif, which is recognized by a particular HLA molecule. Motifs are typically different for each HLA protein encoded by a given human HLA allele. These motifs often differ in their pattern of the primary and secondary anchor residues. See Tables 1-3.

[0089] A "native" or a "wild type" sequence refers to a sequence found in nature.

[0090] A "negative binding residue" or "deleterious residue" is an amino acid which, if present at certain positions (typically not primary anchor positions) in a peptide epitope, results in decreased binding affinity of the peptide for the peptide's corresponding HLA molecule.

[0091] The term "peptide" is used interchangeably with "oligopeptide" in the present specification to designate a series of residues, typically L-amino acids, connected one to the other, typically by peptide bonds between the  $\alpha$ -amino and carboxyl groups of adjacent amino acids.

[0092] A "PanDR binding" peptide or "PADRE<sup>®</sup>" peptide (Epimmune, San Diego, CA) is a member of a family of molecules that binds more than one HLA class II DR molecule. The pattern that defines the PADRE<sup>®</sup> family of molecules can be referred to as an HLA Class II supermotif. A PADRE<sup>®</sup> molecule binds to HLA-DR molecules and stimulates *in vitro* and *in vivo* human helper T lymphocyte (HTL) responses. For a further definition of the PADRE<sup>®</sup> family, see copending application US serial Nos. 09/709,774, filed November 11, 2000; and 09/707,738, filed November 6, 2000; PCT publication Nos WO 95/07707, and WO 97/26784; U.S. Patent Nos. 5,736,142 issued April 7, 1998; 5,679,640, issued October 21, 1997; and 6,413,935, issued July 2, 2002.

[0093] "Pharmaceutically acceptable" refers to a generally non-toxic, inert, and/or physiologically compatible composition or component of a composition.

- [0094] A “pharmaceutical excipient” or “excipient” comprises a material such as an adjuvant, a carrier, pH-adjusting and buffering agents, tonicity adjusting agents, wetting agents, preservatives, and the like. A “pharmaceutical excipient” is an excipient which is pharmaceutically acceptable.
- [0095] A "primary anchor residue" is an amino acid at a specific position along a peptide sequence which is understood to provide a contact point between the immunogenic peptide and the HLA molecule. One, two or three, primary anchor residues within a peptide of defined length generally defines a “motif” for an immunogenic peptide. These residues are understood to fit in close contact with peptide binding grooves of an HLA molecule, with their side chains buried in specific pockets of the binding grooves themselves. In one embodiment of an HLA class I motif, the primary anchor residues are located at position 2 (from the amino terminal position) and at the carboxyl terminal position of a peptide epitope in accordance with the invention. The primary anchor positions for each motif and supermotif of HLA Class I are set forth in Tables 1-2. For example, analog peptides can be created by altering the presence or absence of particular residues in these anchor positions. Such analogs are used to modulate the binding affinity of an epitope comprising a particular motif or supermotif. A “preferred primary anchor residue” is an anchor residue of a motif or supermotif that is associated with optimal binding. Preferred primary anchor residues are indicated in bold-face in Tables 1-2. A “tolerated primary anchor residue” is an anchor residue of a motif or supermotif that is associated with binding to a lesser extent than a preferred residue. Tolerated primary anchor residues are indicated in italicized text in Tables 1-2.
- [0096] “Promiscuous recognition” by a TCR is where a distinct peptide is recognized by the various T cell clones in the context of various HLA molecules. Promiscuous binding by an HLA molecule is synonymous with cross-reactive binding.
- [0097] A “protective immune response” or “therapeutic immune response” refers to a CTL and/or an HTL response to an antigen derived from an antigen of an infectious agent, which in some way prevents or at least partially arrests disease symptoms, side effects or progression. The immune response may also include an antibody response which has been facilitated by the stimulation of helper T cells.
- [0098] By “ranking” the variants in a population of peptide epitopes is meant ordering each variant by its frequency of occurrence relative to the other variants.
- [0099] The term "residue" refers to an amino acid or amino acid mimetic incorporated into a peptide or protein by an amide bond or amide bond mimetic.
- [00100] A "secondary anchor residue" is an amino acid at a position other than a primary anchor position in a peptide which may influence peptide binding. A secondary anchor residue occurs at a significantly higher frequency amongst HLA-bound peptides than would be expected by random

distribution of amino acids at a given position. A secondary anchor residue can be identified as a residue which is present at a higher frequency among high or intermediate affinity binding peptides, or a residue otherwise associated with high or intermediate affinity binding. The secondary anchor residues are said to occur at "secondary anchor positions." For example, analog peptides can be created by altering the presence or absence of particular residues in these secondary anchor positions. Such analogs are used to finely modulate the binding affinity of an epitope comprising a particular motif or supermotif. The terminology "fixed peptide" is generally used to refer to an analog peptide that has changes in primary anchor position; not secondary.

**[00101]** A "subdominant epitope" is an epitope which evokes little or no response upon immunization with a whole antigen or a fragment of the whole antigen comprising a subdominant epitope and a dominant epitope, which comprise the epitope, but for which a response can be obtained by immunization with an isolated peptide, and this response (unlike the case of cryptic epitopes) is detected when whole antigen or a fragment of the whole antigen comprising a subdominant epitope and a dominant epitope is used to recall the response *in vitro* or *in vivo*.

**[00102]** A "supermotif" is a peptide binding specificity shared by HLA molecules encoded by two or more HLA alleles. Preferably, a supermotif-bearing peptide is recognized with high or intermediate affinity (as defined herein) by two or more HLA antigens.

**[00103]** "Synthetic peptide" refers to a peptide that is obtained from a non-natural source, *e.g.*, is man-made. Such peptides may be produced using such methods as chemical synthesis or recombinant DNA technology. "Synthetic peptides" include "fusion proteins."

**[00104]** As used herein, a "vaccine" is a composition used for vaccination, *e.g.*, for prophylaxis or therapy, that comprises one or more peptides of the invention. There are numerous embodiments of vaccines in accordance with the invention, such as by a cocktail of one or more peptides; one or more peptides of the invention comprised by a polyepitopic peptide; or nucleic acids that encode such peptides or polypeptides, *e.g.*, a minigene that encodes a polyepitopic peptide. The "one or more peptides" can include any whole unit integer from 1-150, *e.g.*, at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135, 140, 145, or 150 or more peptides of the invention. The peptides or polypeptides can optionally be modified, such as by lipidation, addition of targeting or other sequences. HLA class I-binding peptides of the invention can be linked to HLA class II-binding peptides, *e.g.*, a PADRE® universal HTL-binding peptide, to facilitate activation of both cytotoxic T lymphocytes and helper T lymphocytes. Vaccines can comprise peptide pulsed antigen presenting cells, *e.g.*, dendritic cells.

**[00105]** A "variant of a peptide epitope" refers to a peptide that is identified from a different viral strain at the same position in an aligned sequence, and that varies by one or

more amino acids from the parent peptide epitope. Examples of peptide epitope variants include those shown in Tables 6-9 and Figures 1A-4. A “variant of an antigen” refers to an antigen that comprises at least one variant of a peptide epitope. Examples of antigen variants include those listed by sequence and/or accession number in Tables 10-22. A “variant of an infectious agent” refers to an infectious agent whose genome encodes at least one variant of an antigen. Variants of infectious agents are related viral, bacterial, fungal, or protozoan strains or isolates that vary in sequence but cause the same disease symptoms. Examples of infectious agent variants include HIV Clade A, B, and C subtypes, HBV subtypes adr, ayr, adw, and ayw, HCV types 1, 2, 3, 4, 5, and 6, HPV strains 1-92 (preferably strains 16, 18, 31, 33, 45, 52, 56, and 58) (see Table 10, listing accession numbers for the complete genome sequences of 167 HIV variants; Table 22, showing an alignment of the complete polyprotein sequences of 50 HCV variants) (see also, *Human Retroviruses and AIDS 2000: A Compilation and Analysis of Nucleic Acid and Amino Acid Sequences*, Kuiken CL, et al., Eds. Theoretical Biology and Biophysics Group, Los Alamos National Laboratory, Los Alamos, NM).

[00106] The nomenclature used to describe peptides/proteins follows the conventional practice wherein the amino group is presented to the left (the N-terminus) and the carboxyl group to the right (the C-terminus) of each amino acid residue. When amino acid residue positions are referred to in a peptide epitope they are numbered in an amino to carboxyl direction with position one being the position closest to the amino terminal end of the epitope, or the peptide or protein of which it may be a part. In the formulae representing selected specific embodiments of the present invention, the amino- and carboxyl-terminal groups, although not specifically shown, are in the form they would assume at physiologic pH values, unless otherwise specified. In the amino acid structure formulae, each residue is generally represented by standard three letter or single letter designations. The L-form of an amino acid residue is represented by a capital single letter or a capital first letter of a three-letter symbol, and the D-form for those amino acids having D-forms is represented by a lower case single letter or a lower case three letter symbol. However, when three letter symbols or full names are used without capitals, they may refer to L amino acids. Glycine has no asymmetric carbon atom and is simply referred to as "Gly" or "G". The amino acid sequences of peptides set forth herein are generally designated using the standard single letter symbol. (A, Alanine; C, Cysteine; D, Aspartic Acid; E, Glutamic Acid; F, Phenylalanine; G, Glycine; H, Histidine; I, Isoleucine; K, Lysine; L, Leucine; M, Methionine; N, Asparagine; P, Proline; Q, Glutamine; R, Arginine; S, Serine; T, Threonine; V, Valine; W, Tryptophan; and Y, Tyrosine.) In addition to these symbols, “B” in the single letter abbreviations used herein



designates  $\alpha$ -amino butyric acid. In some embodiments,  $\alpha$ -amino butyric acid may be replaced with cysteine.

Acronyms used herein are as follows:

APC:	Antigen presenting cell
CD3:	Pan T cell marker
CD4:	Helper T lymphocyte marker
CD8:	Cytotoxic T lymphocyte marker
CEA:	Carcinoembryonic antigen (see, e.g., SEQ ID NO: 363)
CTL:	Cytotoxic T lymphocyte
DC:	Dendritic cells. DC functioned as potent antigen presenting cells by stimulating cytokine release from CTL lines that were specific for a model peptide derived from hepatitis B virus. <i>In vivo</i> experiments using DC pulsed <i>ex vivo</i> with an HBV peptide epitope have stimulated CTL immune responses <i>in vivo</i> following delivery to naïve mice.
DLT:	Dose-limiting toxicity, an adverse event related to therapy.
DMSO:	Dimethylsulfoxide
ELISA:	Enzyme-linked immunosorbant assay
E:T:	Effector:Target ratio
G-CSF:	Granulocyte colony-stimulating factor
GM-CSF:	Granulocyte-macrophage (monocyte)-colony stimulating factor
HBV:	Hepatitis B virus
HER2/neu:	A tumor associated antigen; c-erbB-2 is a synonym (see, e.g., SEQ ID NO: 364)
HLA:	Human leukocyte antigen
HLA-DR:	Human leukocyte antigen class II
HPLC:	High Performance Liquid Chromatography
HTC:	Helper T Cell
HTL:	Helper T Lymphocyte. A synonym for HTC.
ID:	Identity
IFN $\gamma$ :	Interferon gamma
IL-4:	Interleukin-4
IV:	Intravenous
LU <sub>30%</sub> :	Cytotoxic activity for 10 <sup>6</sup> effector cells required to achieve 30% lysis of a target cell population, at a 100:1 (E:T) ratio.
MAb:	Monoclonal antibody
MAGE:	Melanoma antigen (see, e.g., SEQ ID NO: 365 and 366 for MAGE2 and MAGE3)
MLR:	Mixed lymphocyte reaction
MNC:	Mononuclear cells
PB:	Peripheral blood
PBMC:	Peripheral blood mononuclear cell
ProGP <sup>TM</sup> :	Progenipoietin <sup>TM</sup> product (Searle, St. Louis, MO), a chimeric flt3/G-CSF receptor agonist.
SC:	Subcutaneous
S.E.M.:	Standard error of the mean
QD:	Once a day dosing
TAA:	Tumor Associated Antigen
TNF:	Tumor necrosis factor
WBC:	White blood cells

[00107] The following describes the peptides, nucleic acid molecules, compositions, and methods of the invention in more detail.

#### Methods of Identifying Candidate Peptide Epitopes

[00108] The present invention is directed to methods for selecting a variant of a peptide epitope which induces a CTL response against another variant(s) of the peptide epitope, by determining whether the variant comprises only conserved residues, as defined herein, at non-anchor positions in comparison to the other variant(s).

[00109] In some embodiments, antigen sequences from a population of an infectious agent, said antigens comprising variants of a peptide epitope, are optionally aligned (manually or by computer) along their length, preferably their full length. Variant(s) of a peptide epitope (preferably naturally occurring variants), each 8-11 amino acids in length and comprising the same MHC class I supermotif or motif, are identified manually or with the aid of a computer. In some embodiments, a variant is optionally chosen which comprises preferred anchor residues of said motif and/or which occurs with high frequency within the population of variants. In other embodiments, a variant is randomly chosen. The randomly or otherwise chosen variant is compared to from one to all the remaining variant(s) to determine whether it comprises only conserved residues in the non-anchor positions relative to from one to all the remaining variant(s).

[00110] The present invention is also directed to variants identified by the methods above; peptides comprising such variants; nucleic acids encoding such variants and peptides; cells comprising such variants, and/or peptides, and/or nucleic acids; compositions comprising such variants, and/or peptides, and/or nucleic acids, and/or cells; as well as therapeutic and diagnostic methods for using such variants, peptides, nucleic acids, cells, and compositions.

[00111] In some embodiments, the invention is directed to a method for identifying a candidate peptide epitope which induces a HLA class I CTL response against variants of said peptide epitope, comprising

- a) identifying, from a particular antigen of an infectious agent, variants of a peptide epitope 8-11 amino acids in length, each variant comprising primary anchor residues of the same HLA class I binding motif; and

- b) determining whether one of said variants comprises only conserved non-anchor residues in comparison to at least one remaining variant, thereby identifying a candidate peptide epitope.

[00112] In some embodiments, (b) comprises identifying a variant which comprises only conserved non-anchor residues in comparison to at least 25%, at least 50%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, or at least 99% of the remaining variants.

[00113] In some embodiments, the invention is directed to a method for identifying a candidate peptide epitope which induces a HLA class I CTL response against variants of said peptide epitope, comprising

- a) identifying, from a particular antigen of an infectious agent, variants of a peptide epitope 8-11 amino acids in length, each variant comprising primary anchor residues of the same HLA class I binding motif;
- b) determining whether each of said variants comprises conserved, semi-conserved or non-conserved non-anchor residues in comparison to each of the remaining variants; and
- c) identifying a variant which comprises only conserved non-anchor residues in comparison to at least one remaining variant.

[00114] In some embodiments, (c) comprises identifying a variant which comprises only conservative non-anchor residues in comparison to at least 25%, at least 50%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, or at least 99% of the remaining variants.

[00115] In some embodiments, the invention is directed to a method for identifying a candidate peptide epitope which induces a HLA class I CTL response against variants of said peptide epitope, comprising

- a) identifying, from a particular antigen of an infectious agent, a population of variants of a peptide epitope 8-11 amino acids in length, each peptide epitope comprising primary anchor residues of the same HLA class I binding motif;
- b) choosing a variant selected from the group consisting of:
  - i) a variant which comprises preferred primary anchor residues of said motif; and

- ii) a variant which occurs with high frequency within the population of variants; and
- c) determining whether the variant of (b) comprises only conserved non-anchor residues in comparison to at least one remaining variant, thereby identifying a candidate peptide epitope.

**[00116]** In some embodiments, (c) comprises identifying a variant which comprises only conservative non-anchor residues in comparison to at least 25%, at least 50%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, or at least 99% of the remaining variants.

**[00117]** In some embodiments, the invention is directed to method for identifying a candidate peptide epitope which induces a HLA class I CTL response against variants of said peptide epitope, comprising

- a) identifying, from a particular antigen of an infectious agent, a population of variants of a peptide epitope 8-11 amino acids in length, each peptide epitope comprising primary anchor residues of the same HLA class I binding motif;
- b) choosing a variant selected from the group consisting of:
  - i) a variant which comprises preferred primary anchor residues of said motif; and
  - ii) a variant which occurs with high frequency within the population of variants; and
- c) determining whether the variant of (b) comprises conserved, semi-conserved or non-conserved non-anchor residues in comparison to each of the remaining variants; and
- d) identifying a variant which comprises only conserved non-anchor residues in comparison to at least one remaining variant.

**[00118]** In some embodiments, (d) comprises identifying a variant which comprises only conservative non-anchor residues in comparison to at least 25%, at least 50%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, or at least 99% of the remaining variants.

**[00119]** In some embodiments, (a) comprises aligning the sequences of said antigens.

- [00120] In some embodiments, (b) comprises choosing a variant which comprises preferred primary anchor residues of said motif.
- [00121] In some embodiments, (b) comprises choosing a variant which occurs with high frequency within said population.
- [00122] In some embodiments, (b) comprises ranking said variants by frequency of occurrence within said population.
- [00123] In some embodiments, (b) comprises choosing a variant which comprises preferred primary anchor residues of said motif and which occurs with high frequency within said population.
- [00124] In some embodiments, (b) comprises ranking said variants by frequency of occurrence within said population.
- [00125] In some embodiments, the identified variant comprises the fewest conserved anchor residues in comparison to each of the remaining variants.
- [00126] In some embodiments, the remaining variants comprise 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 220, 240, 260, 280, or 300 variants.
- [00127] In some embodiments, the infectious agent is selected from the group consisting of: HIV, HBV, HCV, HPV, *Plasmodium falciparum*, Influenza virus, and Dengue virus, Epstein-Barr virus, *Mycobacterium tuberculosis*, *Chlamydia*, *Candida albicans*, *Cryptococcus neoformans*, *Coccidioides spp.*, *Histoplasma spp.*, *Aspergillus fumigatis*, *Plasmodium spp.*, *Trypanosoma spp.*, *Schistosoma spp.*, and *Leishmania spp.*
- [00128] In some embodiments, the infectious agent is selected from the group consisting of: HIV, HBV, HCV, HPV, *Plasmodium falciparum*, Influenza virus, and Dengue virus.
- [00129] In some embodiments, the infectious agent is HIV and the antigen is selected from the group consisting of: Gag, Env, Pol, Nef, Rev, Tat, Vif, Vpr, and Vpu.
- [00130] In some embodiments, the infectious agent is HBV and the antigen is selected from the group consisting of: Pol, Env, Core, and NS1/Env2.
- [00131] In some embodiments, the infectious agent is HCV and the antigen is selected from the group consisting of: Core, E1, E2, NS1, NS2, NS3, NS4, and NS5.
- [00132] In some embodiments, the infectious agent is HPV and the antigen is selected from the group consisting of: E1, E2, E3, E4, E5, E6, E7, L1, and L2.

- [00133] In some embodiments, the infectious agent is *Plasmodium falciparum* and the antigen is selected from the group consisting of: CSP, SSP2, EXP1, LSA1.
- [00134] In some embodiments, the selected variant and the at least one remaining variant comprise different primary anchor residues of the same motif or supermotif.
- [00135] In some embodiments, the motif or supermotif is selected from the group consisting of those in Tables 1-2.
- [00136] In some embodiments, the conserved non-anchor residues are at any of positions 3-7 of said variant.
- [00137] In some embodiments, the variant comprises only 1-3 conserved non-anchor residues compared to at least one remaining variant.
- [00138] In some embodiments, the variant comprises only 1-2 conserved non-anchor residues compared to at least one remaining variant.
- [00139] In some embodiments, the variant comprises only 1 conserved non-anchor residue compared to at least one remaining variant.
- [00140] In some embodiments, the infectious agent is HPV, and further wherein, the HPV infectious agent is selected from the group consisting of HPV strains 16, 18, 31, 33, 45, 52, 56, and 58.
- [00141] In some embodiments, the variants are a population of naturally occurring variants.
- [00142] **Optional Alignment.** Optionally, antigen sequences, either full-length or partial, may be aligned manually or by computer. Convenient computer programs for aligning multiple sequences include Omega, Oxford software, version 1.1.3, using ClustalW alignment, using an open gap penalty of 10.0, extend gap penalty of 0.05, and delay divergent sequences of 40.0 (See, e.g., Table 21); and BLASTP 2.2.5 (Nov-16-2002) (Altschul, S.F., et al., Nucleic Acids Res. 25:3389-3402 (1997)) using a cutoff = 3e-88 (to select human sequences) (see, e.g., Table 20). Alternatively, alignments may be obtained through publicly available sources such as published journal articles and published patent documents or as disclosed herein (see, e.g., Tables 10-22).
- [00143] **HLA Class I Motifs Indicative of CTL Inducing Peptide Epitopes.** A large fraction of HLA class I and class II molecules can be classified into a relatively few supertypes, each respective supertype characterized by largely overlapping peptide binding repertoires, and consensus structures of the main peptide binding pockets. Thus,

peptides of the present invention are preferably identified by the primary residues of any one of several HLA-specific amino acid motifs, or if the presence of the motif corresponds to the ability to bind several allele-specific HLA antigens, a supermotif (*see, e.g.*, Tables 1-2). The preferred primary residues are indicated in bold, while the tolerated primary residues are indicated by italics.

[00144] The primary anchor residues of the HLA class I peptide epitope supermotifs and motifs are summarized in Tables 1-2. Preferred primary anchors are shown in bold, while tolerated primary anchors are shown in italics. Primary and secondary anchor positions for HLA Class I are summarized in Table 3. Allele-specific HLA molecules that fall within the various HLA class I supertypes are listed in Table 4. In some cases, patterns of amino acid residues are present in both a motif and a supermotif. The relationship of a particular motif and any related supermotif is indicated in the description of the individual motifs.

[00145] Thus, the peptide motifs and supermotifs described below, and summarized in Tables 1-2, provide guidance for the identification and use of peptide epitopes comprising primary anchor residues of motifs or supermotifs in accordance with the invention.

[00146] Allele-specific HLA molecules that comprise HLA class I supertype families are listed in Table 4.

[00147] **HLA-A1 supermotif.** The HLA-A1 supermotif is characterized by the presence in peptide ligands of a small (T or S) or hydrophobic (L, I, V, or M) primary anchor residue in position 2, and an aromatic (Y, F, or W) primary anchor residue at the C-terminal position of the epitope. The corresponding family of HLA molecules that bind to the A1 supermotif (*i.e.*, the HLA-A1 supertype) is comprised of at least A\*0101, A\*2601, A\*2602, A\*2501, and A\*3201 (*see, e.g.*, DiBrino, M. *et al.*, *J. Immunol.* 151:5930, 1993; DiBrino, M. *et al.*, *J. Immunol.* 152:620, 1994; Kondo, A. *et al.*, *Immunogenetics* 45:249, 1997). Other allele-specific HLA molecules predicted to be members of the A1 superfamily are shown in Table 4. Peptides binding to each of the individual HLA proteins can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the supermotif.

[00148] **HLA-A2 supermotif.** Primary anchor specificities for allele-specific HLA-A2.1 molecules (*see, e.g.*, Falk *et al.*, *Nature* 351:290-296, 1991; Hunt *et al.*, *Science* 255:1261-1263, 1992; Parker *et al.*, *J. Immunol.* 149:3580-3587, 1992; Ruppert *et al.*, *Cell* 74:929-937, 1993) and cross-reactive binding among HLA-A2 and -A28 molecules have been

described. (See, e.g., Fruci *et al.*, *Human Immunol.* 38:187-192, 1993; Tanigaki *et al.*, *Human Immunol.* 39:155-162, 1994; Del Guercio *et al.*, *J. Immunol.* 154:685-693, 1995; Kast *et al.*, *J. Immunol.* 152:3904-3912, 1994 for reviews of relevant data.) These primary anchor residues define the HLA-A2 supermotif; which presence in peptide ligands corresponds to the ability to bind several different HLA-A2 and -A28 molecules. The HLA-A2 supermotif comprises peptide ligands with L, I, V, M, A, T, or Q as a primary anchor residue at position 2 and L, I, V, M, A, or T as a primary anchor residue at the C-terminal position of the epitope.

[00149] The corresponding family of HLA molecules (*i.e.*, the HLA-A2 supertype that binds these peptides) is comprised of at least: A\*0201, A\*0202, A\*0203, A\*0204, A\*0205, A\*0206, A\*0207, A\*0209, A\*0214, A\*6802, and A\*6901. Other allele-specific HLA molecules predicted to be members of the A2 superfamily are shown in Table 4. As explained in detail below, binding to each of the individual allele-specific HLA molecules can be modulated by substitutions at the primary anchor and/or secondary anchor positions, preferably choosing respective residues specified for the supermotif.

[00150] The motifs comprising the primary anchor residues V, A, T, or Q at position 2 and L, I, V, A, or T at the C-terminal position are those most particularly relevant to the invention claimed herein.

[00151] **HLA-A3 supermotif.** The HLA-A3 supermotif is characterized by the presence in peptide ligands of A, L, I, V, M, S, or, T as a primary anchor at position 2, and a positively charged residue, R or K, at the C-terminal position of the epitope, *e.g.*, in position 9 of 9-mers (see, e.g., Sidney *et al.*, *Hum. Immunol.* 45:79, 1996). Exemplary members of the corresponding family of HLA molecules (the HLA-A3 supertype) that bind the A3 supermotif include at least A\*0301, A\*1101, A\*3101, A\*3301, and A\*6801. Other allele-specific HLA molecules predicted to be members of the A3 supertype are shown in Table 4. As explained in detail below, peptide binding to each of the individual allele-specific HLA proteins can be modulated by substitutions of amino acids at the primary and/or secondary anchor positions of the peptide, preferably choosing respective residues specified for the supermotif.

[00152] **HLA-A24 supermotif.** The HLA-A24 supermotif is characterized by the presence in peptide ligands of an aromatic (F, W, or Y) or hydrophobic aliphatic (L, I, V, M, or T) residue as a primary anchor in position 2, and Y, F, W, L, I, or M as primary anchor at the C-terminal position of the epitope (see, e.g., Sette and Sidney, *Immunogenetics*, in press,



1999). The corresponding family of HLA molecules that bind to the A24 supermotif (*i.e.*, the A24 supertype) includes at least A\*2402, A\*3001, and A\*2301. Other allele-specific HLA molecules predicted to be members of the A24 supertype are shown in Table 4. Peptide binding to each of the allele-specific HLA molecules can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the supermotif.

**[00153] HLA-B7 supermotif.** The HLA-B7 supermotif is characterized by peptides bearing proline in position 2 as a primary anchor, and a hydrophobic or aliphatic amino acid (L, I, V, M, A, F, W, or Y) as the primary anchor at the C-terminal position of the epitope. The corresponding family of HLA molecules that bind the B7 supermotif (*i.e.*, the HLA-B7 supertype) is comprised of at least twenty six HLA-B proteins including: B\*0702, B\*0703, B\*0704, B\*0705, B\*1508, B\*3501, B\*3502, B\*3503, B\*3504, B\*3505, B\*3506, B\*3507, B\*3508, B\*5101, B\*5102, B\*5103, B\*5104, B\*5105, B\*5301, B\*5401, B\*5501, B\*5502, B\*5601, B\*5602, B\*6701, and B\*7801 (*see, e.g.*, Sidney, *et al.*, *J. Immunol.* 154:247, 1995; Barber, *et al.*, *Curr. Biol.* 5:179, 1995; Hill, *et al.*, *Nature* 360:434, 1992; Rammensee, *et al.*, *Immunogenetics* 41:178, 1995 for reviews of relevant data). Other allele-specific HLA molecules predicted to be members of the B7 supertype are shown in Table 4. As explained in detail below, peptide binding to each of the individual allele-specific HLA proteins can be modulated by substitutions at the primary and/or secondary anchor positions of the peptide, preferably choosing respective residues specified for the supermotif.

**[00154] HLA-B27 supermotif.** The HLA-B27 supermotif is characterized by the presence in peptide ligands of a positively charged (R, H, or K) residue as a primary anchor at position 2, and a hydrophobic (F, Y, L, W, M, I, A, or V) residue as a primary anchor at the C-terminal position of the epitope (*see, e.g.*, Sidney and Sette, *Immunogenetics*, in press, 1999). Exemplary members of the corresponding family of HLA molecules that bind to the B27 supermotif (*i.e.*, the B27 supertype) include at least B\*1401, B\*1402, B\*1509, B\*2702, B\*2703, B\*2704, B\*2705, B\*2706, B\*3801, B\*3901, B\*3902, and B\*7301. Other allele-specific HLA molecules predicted to be members of the B27 supertype are shown in Table 4. Peptide binding to each of the allele-specific HLA molecules can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the supermotif.

- [00155]      **HLA-B44 supermotif.** The HLA-B44 supermotif is characterized by the presence in peptide ligands of negatively charged (D or E) residues as a primary anchor in position 2, and hydrophobic residues (F, W, Y, L, I, M, V, or A) as a primary anchor at the C-terminal position of the epitope (*see, e.g.*, Sidney et al., *Immunol. Today* 17:261, 1996). Exemplary members of the corresponding family of HLA molecules that bind to the B44 supermotif (*i.e.*, the B44 supertype) include at least: B\*1801, B\*1802, B\*3701, B\*4001, B\*4002, B\*4006, B\*4402, B\*4403, and B\*4006. Peptide binding to each of the allele-specific HLA molecules can be modulated by substitutions at primary and/or secondary anchor positions; preferably choosing respective residues specified for the supermotif.
- [00156]      **HLA-B58 supermotif.** The HLA-B58 supermotif is characterized by the presence in peptide ligands of a small aliphatic residue (A, S, or T) as a primary anchor residue at position 2, and an aromatic or hydrophobic residue (F, W, Y, L, I, V, M, or A) as a primary anchor residue at the C-terminal position of the epitope (*see, e.g.*, Sidney and Sette, *Immunogenetics*, in press, 1999 for reviews of relevant data). Exemplary members of the corresponding family of HLA molecules that bind to the B58 supermotif (*i.e.*, the B58 supertype) include at least: B\*1516, B\*1517, B\*5701, B\*5702, and B\*5801. Other allele-specific HLA molecules predicted to be members of the B58 supertype are shown in Table 4. Peptide binding to each of the allele-specific HLA molecules can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the supermotif.
- [00157]      **HLA-B62 supermotif.** The HLA-B62 supermotif is characterized by the presence in peptide ligands of the polar aliphatic residue Q or a hydrophobic aliphatic residue (L, V, M, I, or P) as a primary anchor in position 2, and a hydrophobic residue (F, W, Y, M, I, V, L, or A) as a primary anchor at the C-terminal position of the epitope (*see, e.g.*, Sidney and Sette, *Immunogenetics*, in press, 1999). Exemplary members of the corresponding family of HLA molecules that bind to the B62 supermotif (*i.e.*, the B62 supertype) include at least: B\*1501, B\*1502, B\*1513, and B5201. Other allele-specific HLA molecules predicted to be members of the B62 supertype are shown in Table 4. Peptide binding to each of the allele-specific HLA molecules can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the supermotif.
- [00158]      **HLA-A1 motif.** The HLA-A1 motif is characterized by the presence in peptide ligands of T, S, or M as a primary anchor residue at position 2 and the presence of Y as a

primary anchor residue at the C-terminal position of the epitope. An alternative allele-specific A1 motif is characterized by a primary anchor residue at position 3 rather than position 2. This motif is characterized by the presence of D, E, A, or S as a primary anchor residue in position 3, and a Y as a primary anchor residue at the C-terminal position of the epitope (*see, e.g.*, DiBrino *et al.*, *J. Immunol.*, 152:620, 1994; Kondo *et al.*, *Immunogenetics* 45:249, 1997; and Kubo *et al.*, *J. Immunol.* 152:3913, 1994 for reviews of relevant data). Peptide binding to HLA A1 can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the motif.

[00159] Those epitopes comprising T, S, or M at position 2 and Y at the C-terminal position are also HLA-A1 supermotif-bearing peptide epitopes, as these residues are a subset of the A1 supermotif primary anchors.

[00160] **HLA-A\*0201 motif.** An HLA-A2\*0201 motif was determined to be characterized by the presence in peptide ligands of L or M as a primary anchor residue in position 2, and L or V as a primary anchor residue at the C-terminal position of a 9-residue peptide (*see, e.g.*, Falk *et al.*, *Nature* 351:290-296, 1991) and was further found to comprise an I at position 2 and I or A at the C-terminal position of a nine amino acid peptide (*see, e.g.*, Hunt *et al.*, *Science* 255:1261-1263, March 6, 1992; Parker *et al.*, *J. Immunol.* 149:3580-3587, 1992). The A\*0201 allele-specific motif has also been defined by the present inventors to additionally comprise V, A, T, or Q as a primary anchor residue at position 2, and M or T as a primary anchor residue at the C-terminal position of the epitope (*see, e.g.*, Kast *et al.*, *J. Immunol.* 152:3904-3912, 1994). Thus, the HLA-A\*0201 motif comprises peptide ligands with L, I, V, M, A, T, or Q as primary anchor residues at position 2 and L, I, V, M, A, or T as a primary anchor residue at the C-terminal position of the epitope. The preferred and tolerated residues that characterize the primary anchor positions of the HLA-A\*0201 motif are identical to the residues describing the A2 supermotif. (For reviews of relevant data, *see, e.g.*, Del Guercio *et al.*, *J. Immunol.* 154:685-693, 1995; Ruppert *et al.*, *Cell* 74:929-937, 1993; Sidney *et al.*, *Immunol. Today* 17:261-266, 1996; Sette and Sidney, *Curr. Opin. in Immunol.* 10:478-482, 1998). Secondary anchor residues that characterize the A\*0201 motif have additionally been defined (*see, e.g.*, Ruppert *et al.*, *Cell* 74:929-937, 1993). These are shown in Table 3. Peptide binding to HLA-A\*0201 molecules can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the motif.

- [00161]      **HLA-A3 motif.** The HLA-A3 motif is characterized by the presence in peptide ligands of L, M, V, I, S, A, T, F, C, G, or D as a primary anchor residue at position 2, and the presence of K, Y, R, H, F, or A as a primary anchor residue at the C-terminal position of the epitope (*see, e.g., DiBrino et al., Proc. Natl. Acad. Sci USA 90:1508, 1993; and Kubo et al., J. Immunol. 152:3913-3924, 1994*). Peptide binding to HLA-A3 can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the motif.
- [00162]      The A3 supermotif primary anchor residues comprise a subset of the A3- and A11-allele specific motif primary anchor residues.
- [00163]      **HLA-A11 motif.** The HLA-A11 motif is characterized by the presence in peptide ligands of V, T, M, L, I, S, A, G, N, C, D, or F as a primary anchor residue in position 2, and K, R, Y, or H as a primary anchor residue at the C-terminal position of the epitope (*see, e.g., Zhang et al., Proc. Natl. Acad. Sci USA 90:2217-2221, 1993; and Kubo et al., J. Immunol. 152:3913-3924, 1994*). Peptide binding to HLA-A11 can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the motif.
- [00164]      There is extensive overlap between the A3 and A11 motif primary anchor specificities.
- [00165]      **HLA-A24 motif.** The HLA-A24 motif is characterized by the presence in peptide ligands of Y, F, W, or M as a primary anchor residue in position 2, and F, L, I, or W as a primary anchor residue at the C-terminal position of the epitope (*see, e.g., Kondo et al., J. Immunol. 155:4307-4312, 1995; and Kubo et al., J. Immunol. 152:3913-3924, 1994*). Peptide binding to HLA-A24 molecules can be modulated by substitutions at primary and/or secondary anchor positions; preferably choosing respective residues specified for the motif.
- [00166]      The primary anchor residues characterizing the A24 allele-specific motif comprise a subset of the A24 supermotif primary anchor residues.
- [00167]      **Computer or Manual Screening.** Peptides bearing HLA Class I or Class II supermotifs or motifs may be identified by computer searches or manually, e.g., as follows. In utilizing computer screening to identify peptide epitopes, a protein sequence or translated sequence may be analyzed using software developed to search for motifs, for example the "FINDPATTERNS" program (Devereux, *et al. Nucl. Acids Res. 12:387-395,*

1984) or MotifSearch 1.4 software program (D. Brown, San Diego, CA) to identify potential peptide sequences containing appropriate HLA binding motifs. The identified peptides can be scored using customized polynomial algorithms to predict their capacity to bind specific HLA class I or class II alleles. As appreciated by one of ordinary skill in the art, a large array of computer programming software and hardware options are available in the relevant art which can be employed to implement the motifs in order to evaluate (*e.g.*, without limitation, to identify epitopes, identify epitope concentration per peptide length, or to generate analogs) known or unknown peptide sequences.

[00168] Translated antigen protein sequences may be analyzed using a text string search software program, *e.g.*, MotifSearch 1.4 (D. Brown, San Diego) to identify potential peptide sequences containing appropriate HLA binding motifs; alternative programs are readily produced in accordance with information in the art in view of the motif/supermotif disclosure herein. Furthermore, such calculations can be made mentally.

[00169] Identified supermotif or motif sequences may be scored using polynomial algorithms to predict their capacity to bind to specific HLA-Class I or Class II molecules. These polynomial algorithms take into account both extended and refined motifs (that is, to account for the impact of different amino acids at different positions), and are essentially based on the premise that the overall affinity (or  $\Delta G$ ) of peptide-HLA molecule interactions can be approximated as a linear polynomial function of the type:

$$“\Delta G” = a_{1i} \times a_{2i} \times a_{3i} \dots \times a_{ni}$$

where  $a_{ji}$  is a coefficient which represents the effect of the presence of a given amino acid ( $j$ ) at a given position ( $i$ ) along the sequence of a peptide of  $n$  amino acids. The crucial assumption of this method is that the effects at each position are essentially independent of each other (*i.e.*, independent binding of individual side-chains). When residue  $j$  occurs at position  $i$  in the peptide, it is assumed to contribute a constant amount  $j_i$  to the free energy of binding of the peptide irrespective of the sequence of the rest of the peptide. This assumption is justified by studies from our laboratories that demonstrated that peptides are bound to MHC and recognized by T cells in essentially an extended conformation (data omitted herein).

[00170] The method of derivation of specific algorithm coefficients has been described in Gulukota *et al.*, *J. Mol. Biol.* 267:1258-126, 1997; (see also Sidney *et al.*, *Human Immunol.* 45:79-93, 1996; and Southwood *et al.*, *J. Immunol.* 160:3363-3373, 1998). Briefly, for all  $i$  positions, anchor and non-anchor alike, the geometric mean of the average

relative binding (ARB) of all peptides carrying  $j$  is calculated relative to the remainder of the group, and used as the estimate of  $j_i$ . For Class II peptides, if multiple alignments are possible, only the highest scoring alignment is utilized, following an iterative procedure. To calculate an algorithm score of a given peptide in a test set, the ARB values corresponding to the sequence of the peptide are multiplied. If this product exceeds a chosen threshold, the peptide is predicted to bind. Appropriate thresholds are chosen as a function of the degree of stringency of prediction desired.

[00171] Additional methods to identify preferred peptide sequences, which also make use of specific motifs, include the use of neural networks and molecular modeling programs (see, e.g., Milik *et al.*, *Nature Biotechnology* 16:753, 1998; Altuvia *et al.*, *Hum. Immunol.* 58:1, 1997; Altuvia *et al.*, *J. Mol. Biol.* 249:244, 1995; Buus, S. *Curr. Opin. Immunol.* 11:209-213, 1999; Brusic, V. *et al.*, *Bioinformatics* 14:121-130, 1998; Parker *et al.*, *J. Immunol.* 152:163, 1993; Meister *et al.*, *Vaccine* 13:581, 1995; Hammer *et al.*, *J. Exp. Med.* 180:2353, 1994; Sturniolo *et al.*, *Nature Biotechnol.* 17:555 1999).

[00172] **Conserved, Semi-conserved, and Non-conserved Non-anchor Residues.** The determination of non-anchor residues as being conserved (conservative) or semi-conserved (semi-conservative) or non-conserved (non-conservative) in comparison to the non-anchor positions of from one to all of the remaining variant(s) is defined by as follows, the results of which are summarized in Table 5.

[00173] Table 5 shows the similarity assignments between any given amino acid pair so that a given amino acid substitution could be characterized as being a (conservative) or semi-conserved (semi-conservative) or non-conserved (non-conservative) residue.

[00174] The degree of similarity between amino acid pairs was quantified by averaging, for each amino acid pair, the rank coefficient scores for PAM250, hydrophobicity, and side chain volume as described below. Based on the average values of these composite rankings, Table 5 shows each pair to be conserved, semi-conserved or non-conserved.

[00175] The Dayhoff PAM250 score (Dayhoff, M.O., *et al.*, *Atlas of Protein Sequence and Structure*, Vol. 5, suppl.3. (1978) M.O. Dayhoff, ed. National Biomedical Research Foundation, Washington DC, p. 345; Creighton, T.E., *Proteins: structures and molecular properties* (1993) (2nd edition) W.H. Freeman and Company, NY; is a commonly utilized protein alignment scoring matrix which measures the percentage of acceptable point

mutations (PAM) within a defined time frame. The frequencies of these mutations are different from what would be expected from the probability of random mutations, and presumably reflect a bias due to the degree of physical and chemical similarity of the amino acid pair involved in the substitution. To obtain a score of amino acid similarity that could be standardized with other measures of similarity, the PAM250 scores were converted to a rank value, where 1 indicates the highest probability of being an accepted mutation.

[00176] The most commonly utilized scales to represent the relative hydrophobicity of the 20 naturally occurring amino acids (Cornette, J., *et al.*, *J. Mol. Biol.* (1987) 195:659) are those developed on the basis of experimental data by Kyte and Doolittle (Kyte, J. and R.F. Doolittle, *J. Mol. Biol.* (1982) 157:105), and by Fauchere and Pliska (Fauchere, J. and V. Pliska, *Eur. J. Med. Chem.* (1983) 18:369). The Kyte/Doolittle scale measures the H<sub>2</sub>O/organic solvent partition of individual amino acids. Because it considers the position of amino acids in folded proteins, it may most accurately reflect native hydrophobicity in the context of proteins. The Fauchere/Pliska scale measures the octanol/H<sub>2</sub>O partitioning of N-acetyl amino acid amides, and most accurately reflects hydrophobicity in the context of denatured proteins and/or small synthetic peptides. To obtain scores for hydrophobicity, each amino acid residue was ranked on both the Kyte/Doolittle and Fauchere/Pliska hydrophobicity scales. An average rank between the two scales was calculated and the average difference in hydrophobicity for each pair was calculated.

[00177] Finally, for calculating amino acid side-chain volume, the partial volume in solution obtained by noting the increase in volume of water after adding either one molecule or one gram of amino acid residue was considered (Zamyatnin, A.A., *Ann. Rev. Biophys. Bioeng.* (1984) 13:145; Zamyatnin, A.A., *Prog. Biophys. Mol. Biol.* (1972) 24:107). The absolute difference in the partial volume of each possible pairing of the 20 naturally occurring amino acids was calculated and ranked, where 1 indicated residues with the most similar volumes, and 20 the most dissimilar.

[00178] Thus, by consulting Table 5, one can determine whether a residue in a variant is considered to be conserved, semi-conserved, or non-conserved in comparison to a residue in another variant(s). The residue of the parent variant (randomly or otherwise chosen variant) is shown across the top of Table 5, and the residue of the variant(s) it is compared with is shown below the parent residue.

[00179] As shown in Table 5, each of the amino acids shown across the top of the table bears a numerically defined relationship to the remaining 19 genetically encoded amino acids. The lower the index, the higher the conservation; the same amino acid will have a similarity assignment of 1.0; maximally different amino acids will have similarity assignments approaching 20. Using the method set forth above, amino acids which are not gene-encoded can also be assigned similarity indices and can be classified with respect to any natively occurring amino acid as conserved (conservative) or semi-conserved (semi-conservative) or non-conserved (non-conservative).

#### Variant Peptide Epitopes

[00180] In some embodiments, the invention is directed to an isolated peptide comprising or consisting of a variant. In some embodiments, the invention is directed to an isolated polynucleotide encoding such a peptide.

[00181] The isolated variants of the invention are all class I binding peptides, i.e., CTL peptides. In particular, the variants of the invention comprise a motif or supermotif, as described above. Variants of the invention are those set forth in Tables 6-9 and Figures 1A-4 (SEQ ID Nos: 1,2, 9-13, 15,16,18-26, 56-60, 69, 71, 72, 74,77-89, 91-96,99-101, 103, 105, 108, 109, 112-117, 119, 120, 123-127, 129, 130, 132, 133, 136-142, 145-152, 154-158, 160-165, 167, 168, 172-175, 177-179, 181, 182, 184-186, 188, 189, 191-212, 222-237, 262-277). Variants of the invention may be referred to herein as “variants” and “variant peptide epitopes” or referred to by Table or referred to by SEQ ID NO. Other peptide epitopes are referred to herein as CTL epitopes or CTL peptides and HTL epitopes or HTL peptides.

[00182] **Peptides and Polynucleotides.** In some embodiments, the invention is directed to an isolated peptide comprising or consisting of a variant, wherein the variant consists of a sequence selected from those in Tables 6-9 and Figures 1A-4 (SEQ ID Nos:[    ] 1,2, 9-13, 15,16,18-26, 56-60, 69, 71, 72, 74,77-89, 91-96,99-101, 103, 105, 108, 109, 112-117, 119, 120, 123-127, 129, 130, 132, 133, 136-142, 145-152, 154-158, 160-165, 167, 168, 172-175, 177-179, 181, 182, 184-186, 188, 189, 191-212, 222-237, 262-277).

[00183] Peptides of the invention may be fusion proteins of variant(s) to CTL epitope(s), and/or HTL epitope(s), and/or linker(s), and/or spacer(s), and/or carrier(s), and/or additional amino acid(s), and/or may comprise or consist of homopolymers of a variant or heteropolymers of more than one variant, as is described in detail below.

[00184] Peptides which comprise a variant of the invention may comprise or consist of a fragment of an antigen (“fragment” or “antigenic fragment”), wherein the fragment comprises a variant. The fragment may be a portion of any antigen of an infectious agent, e.g., the sequences in Tables 11-



22 (SEQ ID Nos:[    ] 302-1755, respectively). The variant of the invention may be within the fragment or may be linked, directly or indirectly, to the fragment.

**[00185]** The fragment may comprise or consist of a region of a native antigen that contains a high concentration of class I and/or class II epitopes, preferably it contains the greatest number of epitopes per amino acid length. Such epitopes can be present in a frame-shifted manner, *e.g.* a 10 amino acid long peptide could contain two 9 amino acid long epitopes and one 10 amino acid long epitope.

**[00186]** The fragment may be less than or equal to 600 amino acids, less than or equal to 500 amino acids, less than or equal to 400 amino acids, less than or equal to 250 amino acids, less than or equal to 100 amino acids, less than or equal to 85 amino acids, less than or equal to 75 amino acids, less than or equal to 65 amino acids, or less than or equal to 50 amino acids in length. In certain embodiments, a fragment is less than 101 amino acids in length, in any increment down to 5 amino acids in length. For example, the fragment may be 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, or 100 amino acids in length. Fragments of full length antigens may be fragments from about residue 1-20, 21-40, 41-60, 61-80, 81-100, 101-120, 121-140, 141-160, 161-180, 181-200, 201-220, 221-240, 241-260, 261-280, 281-300, 301-320, 321-340, 341-360, 361-380, 381-400, 401-420, 421-440, 441-460, 461-480, 481-500, 501-520, 521-540, 541-560, 561-580, 581-600, 601-620, 621-680, 681-700, 701-720, 721-740, 741-780, 781-800, 801-820, 821-840, 841-860, 861-880, 881-900, 901-920, 921-940, 941-960, 961-980, 981 to the C-terminus of the antigen.

**[00187]** Peptides which comprise a variant of the invention may be a fusion protein comprising one or more amino acid residues in addition to the variant or fragment. Fusion proteins include homopolymers and heteropolymers, as described below.

**[00188]** In some embodiments, the peptide comprises or consists of multiple variants, *e.g.*, 2, 3, 4, 5, 6, 7, 8, or 9 variants of the invention. In some embodiments, the peptide comprises at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, or at least 8 variants of the invention.

**[00189]** The peptide may also be a homopolymer of one variant or the peptide may be a heteropolymer which contains at least two different variants. Polymers have the advantage of increased probability for immunological reaction and, where different variants are used to make up the polymer, the ability to induce antibodies and/or T cells that react with different antigenic determinants of the antigen(s) targeted for an immune response.

**[00190]** A homopolymer may comprise 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 45, 50, 55, 60, 65,

70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135, 140, 145, or 150 copies of the same variant.

[00191] A heteropolymer may comprise one or more copies of an individual variant and one or more copies of one or more different variants of the invention. The variants that form a heteropolymer may all be from the same antigen, e.g., may be from any of those in Tables 11-22 (SEQ ID NOS:[    ] 302-1755) or other antigens herein or known in the art, or may be from different antigens, preferably from infectious agents. Combinations of variants that may form a heteropolymer include, for example, Gag 545 variants EPLTSLKSLF (SEQ ID NO:[    ] 1) and YPLASLKSLF (SEQ ID NO:[    ] 2), or combinations of peptides from different tables in Tables 6-9 (SEQ ID NOS: 1,2, 9-13, 15,16,18-26, 56-60, 69, 71, 72, 74,77-89, 91-96,99-101, 103, 105, 108, 109, 112-117, 119, 120, 123-127, 129, 130, 132, 133, 136-142, 145-152, 154-158, 160-165, 167, 168, 172-175, 177-179, 181, 182, 184-186, 188, 189, 191-212, 222-237, 262-277) and/or Figures 1A-4 (Figure 1A, SEQ ID NOS: 1756-1775; Figure 1B, SEQ ID NOS: 1776-1796; Figure 1C, SEQ ID NOS: 1797-1820; Figure 1D, SEQ ID NOS: 1821-1851; Figure 1E, SEQ ID NOS: 1852-1861; and Figure 4, SEQ ID NOS: 1919-1933) or those combinations in Tables 23-28 (SEQ ID NOS: 1934 - 1946). Heteropolymers may contain multiple copies of one or more variants.

[00192] Thus, peptides of the invention such as heteropolymers may comprise a first variant and at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50 other (different) variants.

[00193] In some embodiments, the peptide comprising a variant may also comprise a number of CTL and/or HTL epitopes, e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50 CTL and/or HTL epitopes.

[00194] The CTL and/or HTL epitope and the variant of the invention may be from the same antigen of an infectious agent or from different antigens. Thus, for example, if the variant is from HIV pol, the CTL peptide and/or HTL peptide may also be from HIV pol. Alternatively, if the variant is from HIV pol, the CTL peptide and/or HTL peptide may be from another antigen such as HIV env or HIV vpr. As another example, if the variant is from HBV E6, the CTL peptide and/or HTL peptide may be from HBV E7. The CTL and/or HTL epitope and the variant of the invention may be from the same infectious agent or different infectious agents. Thus, for example, the variant may be from HIV, and the CTL and/or HTL epitope may be from HIV or may be from another infectious agent such as HBV, HCV, HPV, or *Plasmodium falciparum*.

[00195] The CTL peptide and/or HTL peptide may be from other antigens including hepatitis B core and surface antigens (HBVc, HBVs), hepatitis C antigens, Epstein-Barr virus antigens, human immunodeficiency virus (HIV) antigens and human papilloma virus (HPV) antigens (in particular

antigens from HPV-16, HPV-18, HPV-31, HPV-33, HPV-45, HPV-52, HPV-56 and HPV-58, *Mycobacterium tuberculosis* and *Chlamydia*. Examples of suitable fungal antigens include those derived from *Candida albicans*, *Cryptococcus neoformans*, *Coccidioides spp.*, *Histoplasma spp.* and *Aspergillus fumigatis*. Examples of suitable protozoan parasitic antigens include those derived from *Plasmodium spp.*, including *P. falciparum*, *Trypanosoma spp.*, *Schistosoma spp.*, *Leishmania spp* and the like.

[00196] Alternatively, the CTL peptide and/or HTL peptide may be from tumor-associated antigens such as but not limited to, melanoma antigens MAGE-1, MAGE-2, MAGE-3, MAGE-11, MAGE-A10, as well as BAGE, GAGE, RAGE, MAGE-C1, LAGE-1, CAG-3, DAM, MUC1, MUC2, MUC18, NY-ESO-1, MUM-1, CDK4, BRCA2, NY-LU-1, NY-LU-7, NY-LU-12, CASP8, RAS, KIAA-2-5, SCCs, p53, p73, CEA, HER2/neu, Melan-A, gp100, tyrosinase, TRP2, gp75/TRP1, kallikrein, prostate-specific membrane antigen (PSM), prostatic acid phosphatase (PAP), prostate-specific antigen (PSA), PT1-1,  $\beta$ -catenin, PRAME, Telomerase, FAK, cyclin D1 protein, NOEY2, EGF-R, SART-1, CAPB, HPVE7, p15, Folate receptor CDC27, PAGE-1, and PAGE-4.

[00197] Examples of CTL peptides and HTL peptides are disclosed in WO 01/42270, published 14 June 2001; WO 01/41788, published 14 June 2001; WO 01/42270, published 14 June 2001; WO 01/45728, published 28 June 2001; and WO 01/41787, published 14 June 2001.

[00198] The HTL peptide may comprise a "loosely HLA-restricted" or "promiscuous" sequence. Examples of amino acid sequences that are promiscuous include sequences from antigens such as tetanus toxoid at positions 830-843 (QYIKANSKFIGITE; SEQ ID NO: [[627]] 3), *Plasmodium falciparum* CS protein at positions 378-398 (DIEKKIAKMEKASSVFNVVNS; SEQ ID NO: [[628]] 5), and Streptococcus 18kD protein at positions 116-131 (GAVDSILGGVATYGAA; SEQ ID NO: [[629]] 5). Other examples include peptides bearing a DR 1-4-7 supermotif, or either of the DR3 motifs.

[00199] The HTL peptide may comprise a synthetic peptide such as a Pan-DR-binding epitope (e.g., a PADRE<sup>®</sup> peptide, Epimmune Inc., San Diego, CA, described, for example, in U.S. Patent Number 5,736,142), for example, having the formula aKXVAAZTLKAAa, where "X" is either cyclohexylalanine, phenylalanine, or tyrosine; "Z" is either tryptophan, tyrosine, histidine or asparagine; and "a" is either D-alanine or L-alanine (SEQ ID NO: 746). Certain pan-DR binding epitopes comprise all "L" natural amino acids; these molecules can be provided as peptides or in the form of nucleic acids that encode the peptide. See also, U.S. Patent Nos. 5,679,640 and 6,413,935.

- [00200]** The peptide comprising a variant may comprise additional amino acid(s). Such additional amino acids may be Ala, Arg, Asn, Asp, Cys, Gln, Gly, Glu, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Tyr, Trp, Val, amino acid mimetics, and other unnatural amino acids such as those described below. Additional amino acids may provide for ease of linking peptides one to another, for linking variants to one another, for linking variants to CTL and/or HTL epitopes, for coupling to a carrier support or larger peptide, for modifying the physical or chemical properties of the peptide or oligopeptide, or the like. Amino acids such as Ala, Arg, Asn, Asp, Cys, Gln, Gly, Glu, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Tyr, Trp, or Val, or the like, can be introduced at the C- and/or N-terminus of the peptide and/or can be introduced internally.
- [00201]** The peptide comprising a variant may comprise an amino acid spacer(s), which may be joined to the variants, CTL epitopes, HTL epitopes, carriers, etc. within a peptide or may be joined to the peptide at the N-and/or C-terminus. Thus, spacers may be at the N-terminus or C-terminus of peptide, or may be internal such that they link or join variants, CTL epitopes, HTL epitopes, carriers, additional amino acids, and/or antigenic fragments one to the other.
- [00202]** The spacer is typically comprised of one or more relatively small, neutral molecules, such as amino acids or amino acid mimetics, which are substantially uncharged under physiological conditions. The spacers are typically selected from, *e.g.*, Ala, Gly, or other neutral spacers of nonpolar amino acids or neutral polar amino acids. It will be understood that the optionally present spacer may be composed of the same residues or may be composed of one or more different residues and thus may be a homo- or hetero-oligomer of spacer residues. Thus, the spacer may contain more than one Ala residue (poly-alanine) or more than one Gly residue (poly-glycine), or may contain both Ala and Gly residues, *e.g.*, Gly, Gly-Gly-, Ser, Ser-Ser-, Gly-Ser-, Ser-Gly-, etc. When present, the spacer will usually be at least one or two residues, more usually three to six residues and sometimes 10 or more residues, *e.g.*, 3, 4, 5, 6, 7, 8, 9, or 10, or even more residues. (Livingston, B.D. *et al. Vaccine* 19:4652-4660 (2000)).
- [00203]** Peptides comprising a variant may comprise carrier(s) such as those well known in the art, *e.g.*, thyroglobulin, albumins such as human serum albumin, tetanus toxoid, polyamino acids such as poly L-lysine, poly L-glutamic acid, influenza virus proteins, hepatitis B virus core protein, and the like. (See Table 29).

- [00204] In addition, the peptide comprising or consisting of a variant may be modified by terminal-NH<sub>2</sub> acylation, *e.g.*, by alkanoyl (C<sub>1</sub>-C<sub>20</sub>) or thioglycolyl acetylation, terminal-carboxyl amidation, *e.g.*, ammonia, methylamine, *etc.* In some instances these modifications may provide sites for linking to a support or other molecule.
- [00205] The peptides in accordance with the invention can contain modifications such as but not limited to glycosylation, side chain oxidation, biotinylation, phosphorylation, addition of a surface active material, *e.g.* a lipid, or can be chemically modified, *e.g.*, acetylation, *etc.* Moreover, bonds in the peptide can be other than peptide bonds, *e.g.*, covalent bonds, ester or ether bonds, disulfide bonds, hydrogen bonds, ionic bonds, *etc.*
- [00206] Peptides of the present invention may contain substitutions to modify a physical property (*e.g.*, stability or solubility) of the resulting peptide. For example, peptides may be modified by the substitution of a cysteine (C) with  $\alpha$ -amino butyric acid ("B"). Due to its chemical nature, cysteine has the propensity to form disulfide bridges and sufficiently alter the peptide structurally so as to reduce binding capacity. Substituting  $\alpha$ -amino butyric acid for C not only alleviates this problem, but actually improves binding and crossbinding capability in certain instances. Substitution of cysteine with  $\alpha$ -amino butyric acid may occur at any residue of a peptide, *e.g.*, at either anchor or non-anchor positions of a variant within a peptide, or at other positions of a peptide.
- [00207] The peptides comprising a variant can comprise amino acid mimetics or unnatural amino acids, *e.g.* D- or L-naphylalanine; D- or L-phenylglycine; D- or L-2-thieneylalanine; D- or L-1, -2, 3, or 4-pyreneylalanine; D- or L-3 thieneylalanine; D- or L-(2-pyridinyl)-alanine; D- or L-(3-pyridinyl)-alanine; D- or L-(2-pyrazinyl)-alanine; D- or L-(4-isopropyl)-phenylglycine; D-(trifluoromethyl)-phenylglycine; D-(trifluoromethyl)-phenylalanine; D-*p*-fluorophenylalanine; D- or L-*p*-biphenylphenylalanine; D- or L-*p*-methoxybiphenylphenylalanine; D- or L-2-indole(alkyl)alanines; and, D- or L-alkylalanines, where the alkyl group can be a substituted or unsubstituted methyl, ethyl, propyl, hexyl, butyl, pentyl, isopropyl, iso-butyl, sec-isotyl, iso-pentyl, or a non-acidic amino acids. Aromatic rings of a non-natural amino acid include, *e.g.*, thiazolyl, thiophenyl, pyrazolyl, benzimidazolyl, naphthyl, furanyl, pyrrolyl, and pyridyl aromatic rings. Modified peptides that have various amino acid mimetics or unnatural amino acids are particularly useful, as they tend to manifest increased stability *in vivo*. Such peptides may also possess improved shelf-life or manufacturing properties.

[00208] Peptide stability can be assayed in a number of ways. For instance, peptidases and various biological media, such as human plasma and serum, have been used to test stability. See, e.g., Verhoef, *et al.*, *Eur. J. Drug Metab. Pharmacokinetics* 11:291 (1986). Half-life of the peptides of the present invention is conveniently determined using a 25% human serum (v/v) assay. The protocol is generally as follows: Pooled human serum (Type AB, non-heat inactivated) is delipidated by centrifugation before use. The serum is then diluted to 25% with RPMI-1640 or another suitable tissue culture medium. At predetermined time intervals, a small amount of reaction solution is removed and added to either 6% aqueous trichloroacetic acid (TCA) or ethanol. The cloudy reaction sample is cooled (4°C) for 15 minutes and then spun to pellet the precipitated serum proteins. The presence of the peptides is then determined by reversed-phase HPLC using stability-specific chromatography conditions.

[00209] As indicated above, the peptides in accordance with the invention can be a variety of lengths, and either in their neutral (uncharged) forms or in forms which are salts. The peptides in accordance with the invention can contain modifications such as glycosylation, side chain oxidation, or phosphorylation, generally subject to the condition that modifications do not destroy the biological activity of the peptides.

[00210] The peptides of the invention may be lyophilized, or may be in crystal form.

[00211] It is generally preferable that the variant peptide epitope be as small as possible while still maintaining substantially all of the immunologic activity of the native protein. When possible, it may be desirable to optimize HLA class I binding epitopes of the invention to a length of about 8 to about 13 amino acid residues, for example, 8, 9, 10, 11, 12 or 13, preferably 8 to 11 or 9 to 10. It is to be appreciated that one or more epitopes in this size range can be comprised by a longer peptide (see the Definition Section for the term "epitope" for further discussion of peptide length). HLA class II binding epitopes are preferably optimized to a length of about 6 to about 30 amino acids in length, e.g., 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29 or 30, preferably to between about 13 and about 20 residues, e.g., 13, 14, 15, 16, 17, 18, 19 or 20. Preferably, the epitopes are commensurate in size with endogenously processed pathogen-derived peptides or tumor cell peptides that are bound to the relevant HLA molecules. The identification and preparation of peptides of various lengths can be carried out using the techniques described herein.

[00212] Peptides in accordance with the invention can be prepared synthetically, by recombinant DNA technology or chemical synthesis, or can be isolated from natural sources such as native tumors or pathogenic organisms. Epitopes may be synthesized individually or joined directly or indirectly in a peptide. Although the peptide will preferably be substantially free of other naturally occurring host cell proteins and fragments thereof, in some embodiments the peptides may be synthetically conjugated to be joined to native fragments or particles.

[00213] The peptides of the invention can be prepared in a wide variety of ways. For relatively short sizes, the peptides can be synthesized in solution or on a solid support in accordance with conventional techniques. Various automatic synthesizers are commercially available and can be used in accordance with known protocols. (See, for example, Stewart & Young, SOLID PHASE PEPTIDE SYNTHESIS, 2D. ED., Pierce Chemical Co., 1984). Further, individual peptides can be joined using chemical ligation to produce larger peptides that are still within the bounds of the invention.

[00214] Alternatively, recombinant DNA technology can be employed wherein a nucleotide sequence which encodes a peptide inserted into an expression vector, transformed or transfected into an appropriate host cell and cultivated under conditions suitable for expression. These procedures are generally known in the art, as described generally in Sambrook *et al.*, MOLECULAR CLONING, A LABORATORY MANUAL, Cold Spring Harbor Press, Cold Spring Harbor, New York (1989). Thus, recombinant peptides, which comprise or consist of one or more epitopes of the invention, can be used to present the appropriate T cell epitope.

[00215] Polynucleotides encoding each of the peptides above are also part of the invention. As appreciated by one of ordinary skill in the art, various nucleic acids will encode the same peptide due to the redundancy of the genetic code. Each of these nucleic acids falls within the scope of the present invention. This embodiment of the invention comprises DNA and RNA, and in certain embodiments a combination of DNA and RNA. It is to be appreciated that any polynucleotide that encodes a peptide in accordance with the invention falls within the scope of this invention.

[00216] The polynucleotides encoding peptides contemplated herein can be synthesized by chemical techniques, for example, the phosphotriester method of Matteucci, *et al.*, *J. Am. Chem. Soc.* 103:3185 (1981). Polynucleotides encoding peptides comprising or consisting

of a variant can be made simply by substituting the appropriate and desired nucleic acid base(s) for those that encode a related (e.g., analogous) epitope.

[00217] The polynucleotide, e.g. minigene (see below), may be produced by assembling oligonucleotides that encode the plus and minus strands of the polynucleotide, e.g. minigene. Overlapping oligonucleotides (15-100 bases long) may be synthesized, phosphorylated, purified and annealed under appropriate conditions using well known techniques. The ends of the oligonucleotides can be joined, for example, using T4 DNA ligase. A polynucleotide, e.g. minigene, encoding the peptide of the invention, can be cloned into a desired vector such as an expression vector. The coding sequence can then be provided with appropriate linkers and ligated into expression vectors commonly available in the art, and the vectors used to transform suitable hosts to produce the desired peptide such as a fusion protein.

[00218] A large number of such vectors and suitable host systems are known to those of skill in the art, and are commercially available. The following vectors are provided by way of example. Bacterial: pQE70, pQE60, pQE-9 (Qiagen), pBS, pD10, phagescript, psiX174, pBluescript SK, pbsks, pNH8A, pNH16a, pNH18A, pNH46A (Stratagene); ptrc99a, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia); pCR (Invitrogen). Eukaryotic: pWLNEO, pSV2CAT, pOG44, pXT1, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia); p75.6 (valentis); pCEP (Invitrogen); pCEI (Epimmune). However, any other plasmid or vector can be used as long as it is replicable and viable in the host.

[00219] As representative examples of appropriate hosts, there can be mentioned: bacterial cells, such as *E. coli*, *Bacillus subtilis*, *Salmonella typhimurium* and various species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*; fungal cells, such as yeast; insect cells such as *Drosophila* and Sf9; animal cells such as COS-7 lines of monkey kidney fibroblasts, described by Gluzman, *Cell* 23:175 (1981), and other cell lines capable of expressing a compatible vector, for example, the C127, 3T3, CHO, HeLa and BHK cell lines or Bowes melanoma; plant cells, etc. The selection of an appropriate host is deemed to be within the scope of those skilled in the art from the teachings herein.

[00220] Thus, the present invention is also directed to vectors, preferably expression vectors useful for the production of the peptides of the present invention, and to host cells comprising such vectors.



- [00221] Host cells are genetically engineered (transduced or transformed or transfected) with the vectors of this invention which can be, for example, a cloning vector or an expression vector. The vector can be, for example, in the form of a plasmid, a viral particle, a phage, etc. The engineered host cells can be cultured in conventional nutrient media modified as appropriate for activating promoters, selecting transformants or amplifying the polynucleotides. The culture conditions, such as temperature, pH and the like, are those previously used with the host cell selected for expression, and will be apparent to the ordinarily skilled artisan.
- [00222] For expression of the peptides, the coding sequence will be provided with operably linked start and stop codons, promoter and terminator regions and usually a replication system to provide an expression vector for expression in the desired cellular host. For example, promoter sequences compatible with bacterial hosts are provided in plasmids containing convenient restriction sites for insertion of the desired coding sequence. The resulting expression vectors are transformed into suitable bacterial hosts.
- [00223] Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, *e.g.*, the ampicillin resistance gene of *E. coli* and *S. cerevisiae* TRP1 gene, and a promoter derived from a highly-expressed gene to direct transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK),  $\nabla$ -factor, acid phosphatase, or heat shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an N-terminal identification peptide imparting desired characteristics, *e.g.*, stabilization or simplified purification of expressed recombinant product.
- [00224] Yeast, insect or mammalian cell hosts may also be used, employing suitable vectors and control sequences. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described by Gluzman, *Cell* 23:175 (1981), and other cell lines capable of expressing a compatible vector, for example, the C127, 3T3, CHO, HeLa and BHK cell lines. Mammalian expression vectors will comprise an origin of replication, a suitable promoter and enhancer, and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional

termination sequences, and 5' flanking nontranscribed sequences. Such promoters may also be derived from viral sources, such as, e.g., human cytomegalovirus (CMV-IE promoter) or herpes simplex virus type-1 (HSV TK promoter). Nucleic acid sequences derived from the SV40 splice, and polyadenylation sites can be used to provide the required nontranscribed genetic elements.

[00225] Polynucleotides encoding peptides of the invention may also comprise a ubiquitination signal sequence, and/or a targeting sequence such as an endoplasmic reticulum (ER) signal sequence to facilitate movement of the resulting peptide into the endoplasmic reticulum.

[00226] Polynucleotides of the invention, e.g., minigenes, may be expressed in human cells. A human codon usage table can be used to guide the codon choice for each amino acid. Such polynucleotides preferably comprise spacer amino acid residues between variants, such as those described above, or may comprise naturally-occurring flanking sequences adjacent to the variants (and/or CTL and HTL epitopes).

[00227] The peptides of the invention can also be expressed by viral or bacterial vectors. Examples of expression vectors include attenuated viral hosts, such as vaccinia or fowlpox. As an example of this approach, vaccinia virus is used as a vector to express nucleotide sequences that encode the peptides of the invention. Vaccinia vectors and methods useful in immunization protocols are described in, e.g., U.S. Patent No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover *et al.*, *Nature* 351:456-460 (1991). A wide variety of other vectors useful for therapeutic administration or immunization of the polypeptides of the invention, e.g. adeno and adeno-associated virus vectors, retroviral vectors, *Salmonella typhi* vectors, detoxified anthrax toxin vectors, and the like, will be apparent to those skilled in the art from the description herein. A preferred vector is Modified Vaccinia Ankara (MVA) (e.g., Bavarian Noridic (MVA-BN)).

[00228] Standard regulatory sequences well known to those of skill in the art are preferably included in the vector to ensure expression in the human target cells. Several vector elements are desirable: a promoter with a downstream cloning site for polynucleotide, e.g., minigene insertion; a polyadenylation signal for efficient transcription termination; an *E. coli* origin of replication; and an *E. coli* selectable marker (e.g. ampicillin or kanamycin resistance). Numerous promoters can be used for this purpose, e.g., the human

cytomegalovirus (hCMV) promoter. See, *e.g.*, U.S. Patent Nos. 5,580,859 and 5,589,466 for other suitable promoter sequences. A preferred promoter is the CMV-IE promoter.

[00229] Polynucleotides, *e.g.* minigenes, may comprise one or more synthetic or naturally-occurring introns in the transcribed region. The inclusion of mRNA stabilization sequences and sequences for replication in mammalian cells may also be considered for increasing polynucleotide, *e.g.* minigene, expression.

[00230] In addition, the polynucleotide, *e.g.* minigene, may comprise immunostimulatory sequences (ISSs or CpGs). These sequences may be included in the vector, outside the polynucleotide (*e.g.* minigene) coding sequence to enhance immunogenicity.

[00231] In some embodiments, a bi-cistronic expression vector which allows production of both the polynucleotide- (*e.g.* minigene-) encoded peptides of the invention and a second protein (*e.g.*, one that modulates immunogenicity) can be used. Examples of proteins or polypeptides that, if co-expressed with peptides of the invention, can enhance an immune response include cytokines (*e.g.*, IL-2, IL-12, GM-CSF), cytokine-inducing molecules (*e.g.*, LeIF), costimulatory molecules, or pan-DR binding proteins (PADRE<sup>®</sup> molecules, Epimmune, San Diego, CA). Helper T cell (HTL) epitopes such as PADRE<sup>®</sup> molecules can be joined to intracellular targeting signals and expressed separately from expressed peptides of the invention. Specifically decreasing the immune response by co-expression of immunosuppressive molecules (*e.g.* TGF- $\beta$ ) may be beneficial in certain diseases.

[00232] Once an expression vector is selected, the polynucleotide, *e.g.* minigene, is cloned into the polylinker region downstream of the promoter. This plasmid is transformed into an appropriate bacterial strain, and DNA is prepared using standard techniques. The orientation and DNA sequence of the polynucleotide, *e.g.* minigene, as well as all other elements included in the vector, are confirmed using restriction mapping, DNA sequence analysis, and/or PCR analysis. Bacterial cells harboring the correct plasmid can be stored as cell banks.

[00233] Therapeutic/prophylactic quantities of DNA can be produced for example, by fermentation in *E. coli*, followed by purification. Aliquots from the working cell bank are used to inoculate growth medium, and are grown to saturation in shaker flasks or a bioreactor according to well known techniques. Plasmid DNA is purified using standard bioseparation technologies such as solid phase anion-exchange resins available, *e.g.*, from QIAGEN, Inc. (Valencia, California). If required, supercoiled DNA can be isolated from the open circular and linear forms using gel electrophoresis or other methods.

[00234] Purified polynucleotides, e.g. minigenes, can be prepared for injection using a variety of formulations. The simplest of these is reconstitution of lyophilized polynucleotide, e.g. DNA, in sterile phosphate-buffer saline (PBS). This approach, known as "naked DNA," is currently being used for intramuscular (IM) administration in clinical trials. To maximize the immunotherapeutic effects of polynucleotide vaccines, alternative methods of formulating purified plasmid DNA may be used. A variety of such methods have been described, and new techniques may become available. Cationic lipids, glycolipids, and fusogenic liposomes can also be used in the formulation (see, *e.g.*, WO 93/24640; Mannino & Gould-Fogerite, *BioTechniques* 6(7): 682 (1988); U.S. Patent No. 5,279,833; WO 91/06309; and Felgner, *et al.*, *Proc. Nat'l Acad. Sci. USA* 84:7413 (1987). In addition, peptides and compounds referred to collectively as protective, interactive, non-condensing compounds (PINC) can also be complexed to purified plasmid DNA to influence variables such as stability, intramuscular dispersion, or trafficking to specific organs or cell types.

[00235] Known methods in the art can be used to enhance delivery and uptake of a polynucleotide *in vivo*. For example, the polynucleotide can be complexed to polyvinylpyrrolidone (PVP), to prolong the localized bioavailability of the polynucleotide, thereby enhancing uptake of the polynucleotide by the organism (*see e.g.*, U.S. Patent No. 6,040,295; EP 0 465 529; WO 98/17814). PVP is a polyamide that is known to form complexes with a wide variety of substances, and is chemically and physiologically inert.

[00236] Target cell sensitization can be used as a functional assay of the expression and HLA class I presentation of polynucleotide- (e.g. minigene-) encoded peptides. For example, the polynucleotide, e.g. plasmid DNA, is introduced into a mammalian cell line that is a suitable target for standard CTL chromium release assays. The transfection method used will be dependent on the final formulation. For example, electroporation can be used for "naked" DNA, whereas cationic lipids or PVP-formulated DNA allow direct *in vitro* transfection. A plasmid expressing green fluorescent protein (GFP) can be co-transfected to allow enrichment of transfected cells using fluorescence activated cell sorting (FACS). The transfected cells are then chromium-51 (<sup>51</sup>Cr) labeled and used as targets for epitope-specific CTLs. Cytolysis of the target cells, detected by <sup>51</sup>Cr release, indicates both production and HLA presentation of, polynucleotide-, e.g. minigene-, encoded variants of the invention, or peptides comprising them. Expression of HTL epitopes may be evaluated in an analogous manner using assays to assess HTL activity.

[00237] *In vivo* immunogenicity is a second approach for functional testing of polynucleotides, e.g. minigenes. Transgenic mice expressing appropriate human HLA proteins are immunized with the polynucleotide, e.g. DNA, product. The dose and route of administration are formulation dependent (e.g., IM for polynucleotide (e.g., naked DNA or PVP-formulated DNA) in PBS, intraperitoneal (IP) for lipid-complexed polynucleotide (e.g., DNA)). Eleven to twenty-one days after immunization, splenocytes are harvested and restimulated for one week in the presence of polynucleotides encoding each peptide being tested. Thereafter, for peptides comprising or consisting of variants, standard assays are conducted to determine if there is cytolysis of peptide-loaded, <sup>51</sup>Cr-labeled target cells. Once again, lysis of target cells that were exposed to variants corresponding to those encoded by the polynucleotide (e.g. minigene) demonstrates polynucleotide (e.g., DNA) vaccine function and induction of CTLs. Immunogenicity of HTL epitopes is evaluated in transgenic mice in an analogous manner.

[00238] Alternatively, the nucleic acids can be administered using ballistic delivery as described, for instance, in U.S. Patent No. 5,204,253. Using this technique, particles comprised solely of a polynucleotide such as DNA are administered. In a further alternative embodiment for ballistic delivery, polynucleotides such as DNA can be adhered to particles, such as gold particles.

[00239] The use of polynucleotides such as multi-epitope minigenes is described herein and in, e.g. co-pending application U.S.S.N. 09/311,784; Ishioka *et al.*, *J. Immunol.* 162:3915-3925, 1999; An, L. and Whitton, J. L., *J. Virol.* 71:2292, 1997; Thomson, S. A. *et al.*, *J. Immunol.* 157:822, 1996; Whitton, J. L. *et al.*, *J. Virol.* 67:348, 1993; Hanke, R. *et al.*, *Vaccine* 16:426, 1998. For example, a polynucleotide such as a multi-epitope DNA plasmid can be engineered which encodes an epitope derived from multiple regions of a infectious agent (e.g., p53, HER2/nev, MAGE-2/3, or CEA), a pan-DR binding peptide such as the PADRE<sup>®</sup> universal helper T cell epitope, and an endoplasmic reticulum-translocating signal sequence. As described in the sections above, a peptide/polynucleotide may also comprise/encode epitopes that are derived from other infectious agents.

[00240] Thus, the invention includes peptides as described herein, polynucleotides encoding each of said peptides, as well as compositions comprising the peptides and polynucleotides, and includes methods for producing and methods of using the peptides, polynucleotides, and compositions, as further described below.

- [00241]       **Compositions.** In other embodiments, the invention is directed to a composition comprising one or more peptides and/or polynucleotides of the invention and optionally another component(s).
- [00242]       In some embodiments, the composition comprises or consists of multiple peptides, *e.g.*, 2, 3, 4, 5, 6, 7, 8, or 9 peptides of the invention. In some embodiments, the composition comprises at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, or at least 8 peptides of the invention. Combinations of peptides include, for example, a peptide comprising or alternatively consisting of the Gag 545 variant EPLTSLKSLF (SEQ ID NO:[ ] 1) and a peptide comprising or alternatively consisting of the Gag 545 variant YPLASLKSLF (SEQ ID NO:[ ] 2), or combinations of peptides from different tables in Tables 6-9 and/or Figures 1A-4.
- [00243]       Compositions of the invention may comprise polynucleotides encoding the above peptides and/or combinations of peptides.
- [00244]       The composition can comprise at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, or at least 8 peptides and/or polynucleotides selected from those described above or below. At least one of the one or more peptides can be a heteropolymer or a homopolymer. Additionally, the composition can comprise a CTL and/or HTL epitope, which can be derived from a tumor-associated antigen. The additional epitope can also be a PanDR binding molecule, (*e.g.*, a PADRE<sup>®</sup> universal helper T cell epitope).
- [00245]       Optional components include excipients, diluents, proteins such as peptides comprising a CTL epitope, and/or an HTL epitope such as a pan-DR binding peptide (*e.g.*, a PADRE<sup>®</sup> universal helper T cell epitope), and/or a carrier, polynucleotides encoding such proteins, lipids, or liposomes, as well as other components described herein. There are numerous embodiments of compositions in accordance with the invention, such as a cocktail of one or more peptides and/or polynucleotides (*e.g.*, minigenes); a cocktail of one or more peptides and/or polynucleotides (*e.g.*, minigenes) and one or more CTL and/or HTL epitopes.
- [00246]       Compositions may comprise one or more peptides (and/or polynucleotides such as minigenes) of the invention, along with one or more other components as described above and herein. "One or more" refers to any whole unit integer from 1-150, *e.g.*, at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100,

105, 110, 115, 120, 125, 130, 135, 140, 145, or 150 peptides, polynucleotides, or other components.

[00247] Compositions of the invention may be, for example, polynucleotides or polypeptides of the invention combined with or complexed to cationic lipid formulations; lipopeptides (e.g., Vitiello, A. *et al.*, *J. Clin. Invest.* 95:341, 1995), encapsulated e.g., in poly(DL-lactide-co-glycolide) ("PLG") microspheres (see, e.g., Eldridge, *et al.*, *Molec. Immunol.* 28:287-294, 1991; Alonso *et al.*, *Vaccine* 12:299-306, 1994; Jones *et al.*, *Vaccine* 13:675-681, 1995); peptide compositions contained in immune stimulating complexes (ISCOMS) (see, e.g., Takahashi *et al.*, *Nature* 344:873-875, 1990; Hu *et al.*, *Clin Exp Immunol.* 113:235-243, 1998); multiple antigen peptide systems (MAPs) (see e.g., Tam, J. P., *Proc. Natl. Acad. Sci. U.S.A.* 85:5409-5413, 1988; Tam, J.P., *J. Immunol. Methods* 196:17-32, 1996); viral, bacterial, or, fungal delivery vectors (Perkus, M. E. *et al.*, In: *Concepts in vaccine development*, Kaufmann, S. H. E., ed., p. 379, 1996; Chakrabarti, S. *et al.*, *Nature* 320:535, 1986; Hu, S. L. *et al.*, *Nature* 320:537, 1986; Kieny, M.-P. *et al.*, *AIDS Bio/Technology* 4:790, 1986; Top, F. H. *et al.*, *J. Infect. Dis.* 124:148, 1971; Chanda, P. K. *et al.*, *Virology* 175:535, 1990); particles of viral or synthetic origin (e.g., Kofler, N. *et al.*, *J. Immunol. Methods* 192:25, 1996; Eldridge, J. H. *et al.*, *Sem. Hematol.* 30:16, 1993; Falo, L. D., Jr. *et al.*, *Nature Med.* 7:649, 1995); adjuvants (e.g., incomplete Freund's adjuvant) (Warren, H. S., Vogel, F. R., and Chedid, L. A. *Annu. Rev. Immunol.* 4:369, 1986; Gupta, R. K. *et al.*, *Vaccine* 11:293, 1993); liposomes (Reddy, R. *et al.*, *J. Immunol.* 148:1585, 1992; Rock, K. L., *Immunol. Today* 17:131, 1996); or, particle-absorbed cDNA or other polynucleotides of the invention (Ulmer, J. B. *et al.*, *Science* 259:1745, 1993; Robinson, H. L., Hunt, L. A., and Webster, R. G., *Vaccine* 11:957, 1993; Shiver, J. W. *et al.*, In: *Concepts in vaccine development*, Kaufmann, S. H. E., ed., p. 423, 1996; Cease, K. B., and Berzofsky, J. A., *Annu. Rev. Immunol.* 12:923, 1994 and Eldridge, J. H. *et al.*, *Sem. Hematol.* 30:16, 1993), etc. Toxin-targeted delivery technologies, also known as receptor mediated targeting, such as those of Avant Immunotherapeutics, Inc. (Needham, Massachusetts) or attached to a stress protein, e.g., HSP 96 (Stressgen Biotechnologies Corp., Victoria, BC, Canada) can also be used.

[00248] Compositions of the invention comprise polynucleotide-mediated modalities. DNA or RNA encoding one or more of the peptides of the invention can be administered to a patient. This approach is described, for instance, in Wolff *et al.*, *Science* 247:1465 (1990) as well as U.S. Patent Nos. 5,580,859; 5,589,466; 5,804,566; 5,739,118; 5,736,524;

5,679,647; and, WO 98/04720. Examples of DNA-based delivery technologies include “naked DNA”, facilitated (bupivacaine, polymers (*e.g.*, PVP, PINC, etc.), peptide-mediated) delivery, cationic lipid complexes, and particle-mediated (“gene gun”) or pressure-mediated delivery (*see, e.g.*, U.S. Patent No. 5,922,687). Accordingly, peptides of the invention can be expressed by viral or bacterial vectors. Examples of expression vectors include attenuated viral hosts, such as Modified Vaccinia Ankara (MVA) (*e.g.*, Bavarian Noridic), vaccinia or fowlpox. For example, vaccinia virus is used as a vector to express nucleotide sequences that encode the peptides of the invention. Upon introduction into an acutely or chronically infected host or into a non-infected host, the recombinant vaccinia virus expresses the immunogenic peptide, and thereby elicits an immune response. Vaccinia vectors and methods useful in immunization protocols are described in, *e.g.*, U.S. Patent No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover *et al.*, *Nature* 351:456-460 (1991). A wide variety of other vectors useful for therapeutic administration or immunization of the peptides of the invention, *e.g.* adeno and adeno-associated virus vectors, alpha virus vectors, retroviral vectors, *Salmonella typhi* vectors, detoxified anthrax toxin vectors, and the like, are apparent to those skilled in the art from the description herein.

**[00249]** In certain embodiments, components that induce T cell responses are combined with components that induce antibody responses to the target antigen of interest. A preferred embodiment of such a composition comprises class I and class II epitopes in accordance with the invention. Alternatively, a composition comprises a class I and/or class II epitope in accordance with the invention, along with a PADRE<sup>®</sup> molecule (Epimmune, San Diego, CA).

**[00250]** Compositions of the invention can comprise antigen presenting cells, such as dendritic cells. Antigen presenting cells, *e.g.*, dendritic cells, may be transfected, *e.g.*, with a polynucleotide such as a minigene construct in accordance with the invention, in order to elicit immune responses. The peptide can be bound to an HLA molecule on the antigen-presenting cell, whereby when an HLA-restricted cytotoxic T lymphocyte (CTL) is present, a receptor of the CTL binds to a complex of the HLA molecule and the peptide.

**[00251]** The compositions of the invention may also comprise antiviral drugs such as interferon- $\alpha$ , or immune adjuvants such as IL-12, GM-CSF, etc.

**[00252]** Compositions may comprise an HLA heavy chain,  $\beta_2$ -microglobulin, streptavidin, and/or biotin. The streptavidin may be fluorescently labeled. Compositions may comprise



tetramers (*see e.g.*, U.S. Pat. No. 5,635,363; Science 274:94-96 (1996)). A tetramer composition comprising an HLA heavy chain,  $\beta_2$ -microglobulin, streptavidin, and biotin. The streptavidin may be fluorescently labeled. Compositions may also comprise dimers. A dimer composition comprises as MHC molecule and an Ig molecule (*see e.g.*, PNAS 95:7568-73 (1998)).

[00253] In some embodiments it may be desirable to include in the compositions of the invention at least one component which primes cytotoxic T lymphocytes. Lipids have been identified as agents capable of priming CTL *in vivo* against viral antigens. For example, palmitic acid residues can be attached to the  $\epsilon$ - and  $\alpha$ - amino groups of a lysine residue and then linked, *e.g.*, via one or more linking residues such as Gly, Gly-Gly-, Ser, Ser-Ser, or the like, to an immunogenic peptide. The lipidated peptide can then be administered either directly in a micelle or particle, incorporated into a liposome, or emulsified in an adjuvant, *e.g.*, incomplete Freund's adjuvant. A preferred composition comprises palmitic acid attached to  $\epsilon$ - and  $\alpha$ - amino groups of Lys, which is attached via linkage, *e.g.*, Ser-Ser, to the amino terminus of the peptide.

[00254] As another example of lipid priming of CTL responses, *E. coli* lipoproteins, such as tripalmitoyl-S-glycerylcysteinylserine (P<sub>3</sub>CSS) can be used to prime virus specific CTL when covalently attached to an appropriate peptide (*see, e.g.*, Deres, *et al.*, Nature 342:561, 1989). Peptides of the invention can be coupled to P<sub>3</sub>CSS, for example, and the lipopeptide administered to an individual to specifically prime a CTL response to the target antigen. Moreover, because the induction of neutralizing antibodies can also be primed with P<sub>3</sub>CSS-conjugated epitopes, two such compositions can be combined to more effectively elicit both humoral and cell-mediated responses.

[00255] Another preferred embodiment is a composition comprising one or more peptides of the invention emulsified in IFA.

[00256] Compositions of the invention may also comprise CTL and/or HTL peptides. Such CTL and HTL peptides can be modified by the addition of amino acids to the termini of a peptide to provide for ease of linking peptides one to another, for coupling to a carrier support or larger peptide, for modifying the physical or chemical properties of the peptide or oligopeptide, or the like. Amino acids such as tyrosine, cysteine, lysine, glutamic or aspartic acid, or naturally or unnaturally occurring amino acid residues, can be introduced at the carboxyl- or amino-terminus of the peptide or oligopeptide, particularly class I peptides. However, it is to be noted that modification at the carboxyl terminus of a CTL

epitope may, in some cases, alter binding characteristics of the peptide. In addition, the peptide or oligopeptide sequences can differ from the natural sequence by being modified by terminal-NH<sub>2</sub> acylation, *e.g.*, by alkanoyl (C<sub>1</sub>-C<sub>20</sub>) or thioglycolyl acetylation, terminal-carboxyl amidation, *e.g.*, ammonia, methylamine, *etc.* In some instances these modifications may provide sites for linking to a support or other molecule. CTL and HTL epitopes may comprise additional amino acids, such as those described above including spacers.

[00257] A further embodiment of a composition in accordance with the invention is an antigen presenting cell that comprises one or more peptides in accordance with the invention. The antigen presenting cell can be a “professional” antigen presenting cell, such as a dendritic cell. The antigen presenting cell can comprise the peptide of the invention by any means known or to be determined in the art. Such means include pulsing of dendritic cells with one or more individual peptides, by nucleic acid administration such as ballistic nucleic acid delivery or by other techniques in the art for administration of nucleic acids, including vector-based, *e.g.* viral vector, delivery of nucleic acids.

[00258] Compositions may comprise carriers. Carriers that can be used with compositions of the invention are well known in the art, and include, *e.g.*, thyroglobulin, albumins such as human serum albumin, tetanus toxoid, polyamino acids such as poly L-lysine, poly L-glutamic acid, influenza virus proteins, hepatitis B virus core protein, and the like.

[00259] The compositions (*e.g.* pharmaceutical compositions) can contain a physiologically tolerable diluent such as water, or a saline solution, preferably phosphate buffered saline. Additionally, as disclosed herein, CTL responses can be primed by conjugating peptides of the invention to lipids, such as tripalmitoyl-S-glyceryl-cysteinyl-seryl-serine (P<sub>3</sub>CSS).

[00260] Compositions of the invention may be pharmaceutically acceptable compositions. Pharmaceutical compositions preferably contain an immunologically effective amount of one or more peptides and/or polynucleotides of the invention, and optionally one or more other components which are pharmaceutically acceptable. A preferred composition comprises one or more peptides of the invention and IFA. A more preferred composition of the invention comprises one or more peptides of the invention, one or more peptides, and IFA.

[00261] Upon immunization with a peptide and/or polynucleotide and/or composition in accordance with the invention, via injection (*e.g.*, SC, ID, IM), aerosol, oral, transdermal, transmucosal, intrapleural, intrathecal, or other suitable routes, the immune system of the

host responds to the vaccine by an immune response comprising the production of antibodies, CTLs and/or HTLs specific for the desired antigen(s). Consequently, the host becomes at least partially immune to subsequent exposure to the infectious agent(s), or at least partially resistant to further development of infectious agent-bearing cells and thereby derives a prophylactic or therapeutic benefit.

[00262] Furthermore, the peptides, primers, and epitopes of the invention can be used in any desired immunization or administration regimen; e.g., as part of periodic vaccinations such as annual vaccinations as in the veterinary arts or as in periodic vaccinations as in the human medical arts, or as in a prime-boost regime wherein an inventive vector or recombinant is administered either before or after the administration of the same or of a different epitope of interest or recombinant or vector expressing such as a same or different epitope of interest (including an inventive recombinant or vector expressing such as a same or different epitope of interest), see, e.g., U.S. Pat. Nos. 5,997,878; 6,130,066; 6,180,398; 6,267,965; and 6,348,450. An useful viral vector of the present invention is Modified Vaccinia Ankara (MVA) (e.g., Bavarian Noridic (MVA-BN)).

[00263] Recent studies have indicated that a prime-boost protocol, whereby immunization with a poxvirus recombinant expressing a foreign gene product is followed by a boost using a purified subunit preparation form of that gene product, elicits an enhanced immune response relative to the response elicited with either product alone. Human volunteers immunized with a vaccinia recombinant expressing the HIV-1 envelope glycoprotein and boosted with purified HIV-1 envelope glycoprotein subunit preparation exhibit higher HIV-1 neutralizing antibody titers than individuals immunized with just the vaccinia recombinant or purified envelope glycoprotein alone (Graham *et al.*, *J. Infect. Dis.*, 167:533-537 (1993); Cooney *et al.*, *Proc. Natl. Acad. Sci. USA*, 90:1882-1886 (1993)). Humans immunized with two injections of an ALVAC-HIV-1 env recombinant (vCP125) failed to develop HIV specific antibodies. Boosting with purified rgp160 from a vaccinia virus recombinant resulted in detectable HIV-1 neutralizing antibodies. Furthermore, specific lymphocyte T cell proliferation to rgp160 was clearly increased by the boost with rgp160. Envelope specific cytotoxic lymphocyte activity was also detected with this vaccination regimen (Pialoux *et al.*, *AIDS Res. and Hum. Retroviruses*, 11:272-381 (1995)). Macaques immunized with a vaccinia recombinant expressing the simian immunodeficiency virus (SIV) envelope glycoprotein and boosted with SIV envelope glycoprotein from a baculovirus recombinant are protected against SIV challenge (Hu *et*

*al.*, *AID Res. and Hum. Retroviruses*, 3:615-620 (1991); Hu *et al.*, *Science* 255:456-459 (1992)). In the same fashion, purified HCMVgB protein can be used in prime-boost protocols with NYVAC or ALVAC-gB recombinants.

[00264] In certain embodiments, the polynucleotides are complexed in a liposome preparation. Liposomal preparations for use in the instant invention include cationic (positively charged), anionic (negatively charged) and neutral preparations. However, cationic liposomes are particularly preferred because a tight charge complex can be formed between the cationic liposome and the polyanionic nucleic acid. Cationic liposomes have been shown to mediate intracellular delivery of plasmid DNA (Felgner *et al.*, *Proc. Natl. Acad. Sci. USA* 84:74137416 (1987), which is herein incorporated by reference); mRNA (Malone *et al.*, *Proc. Natl. Acad. Sci. USA* 86:60776081 (1989), which is herein incorporated by reference); and purified transcription factors (Debs *et al.*, *J. Biol. Chem.* 265:1018910192 (1990), which is herein incorporated by reference), in functional form.

[00265] Cationic liposomes are readily available. For example, N-[12,3-dioleoyloxy)-propyl]-N,N,N-triethylammonium (DOTMA) liposomes are particularly useful and are available under the trademark Lipofectin, from GIBCO BRL, Grand Island, N.Y. (See, also, Felgner *et al.*, *Proc. Natl. Acad. Sci. USA* 84:74137416 (1987)). Other commercially available liposomes include transfectace (DDAB/DOPE) and DOTAP/DOPE (Boehringer).

[00266] Other cationic liposomes can be prepared from readily available materials using techniques well known in the art. See, e.g. PCT Publication No. WO 90/11092 for a description of the synthesis of DOTAP (1,2-bis(oleoyloxy)-3-(trimethylammonio)propane) liposomes. Preparation of DOTMA liposomes is explained in the literature, see, e.g., P. Felgner *et al.*, *Proc. Natl. Acad. Sci. USA* 84:74137417. Similar methods can be used to prepare liposomes from other cationic lipid materials.

[00267] Similarly, anionic and neutral liposomes are readily available, such as from Avanti Polar Lipids (Birmingham, Ala.), or can be easily prepared using readily available materials. Such materials include phosphatidyl, choline, cholesterol, phosphatidyl ethanolamine, dioleoylphosphatidyl choline (DOPC), dioleoylphosphatidyl glycerol (DOPG), dioleoylphosphatidyl ethanolamine (DOPE), among others. These materials can also be mixed with the DOTMA and DOTAP starting materials in appropriate ratios. Methods for making liposomes using these materials are well known in the art.

[00268] For example, commercially available dioleoylphosphatidyl choline (DOPC), dioleoylphosphatidyl glycerol (DOPG), and dioleoylphosphatidyl ethanolamine (DOPE) can be used in various combinations to make conventional liposomes, with or without the addition of cholesterol. Thus, for example, DOPG/DOPC vesicles can be prepared by drying 50 mg each of DOPG and DOPC under a stream of nitrogen gas into a sonication vial. The sample is placed under a vacuum pump overnight and is hydrated the following day with deionized water. The sample is then sonicated for 2 hours in a capped vial, using a Heat Systems model 350 sonicator equipped with an inverted cup (bath type) probe at the maximum setting while the bath is circulated at 15EC. Alternatively, negatively charged vesicles can be prepared without sonication to produce multilamellar vesicles or by extrusion through nucleopore membranes to produce unilamellar vesicles of discrete size. Other methods are known and available to those of skill in the art.

[00269] The liposomes can comprise multilamellar vesicles (MLVs), small unilamellar vesicles (SUVs), or large unilamellar vesicles (LUVs), with SUVs being preferred. The various liposome nucleic acid complexes are prepared using methods well known in the art. See, e.g., Straubinger *et al.*, *Methods of Immunology* 101:512527 (1983). For example, MLVs containing nucleic acid can be prepared by depositing a thin film of phospholipid on the walls of a glass tube and subsequently hydrating with a solution of the material to be encapsulated. SUVs are prepared by extended sonication of MLVs to produce a homogeneous population of unilamellar liposomes. The material to be entrapped is added to a suspension of preformed MLVs and then sonicated. When using liposomes containing cationic lipids, the dried lipid film is resuspended in an appropriate solution such as sterile water or an isotonic buffer solution such as 10 mM Tris/NaCl, sonicated, and then the preformed liposomes are mixed directly with the DNA. The liposome and DNA form a very stable complex due to binding of the positively charged liposomes to the cationic DNA. SUVs find use with small nucleic acid fragments. LUVs are prepared by a number of methods, well known in the art. Commonly used methods include  $\text{Ca}^{2+}$ -EDTA chelation (Papahadjopoulos *et al.*, *Biochim. Biophys. Acta* 394:483 (1975); Wilson *et al.*, *Cell* 17:77 (1979)); ether injection (Deamer, D. and Bangham, A., *Biochim. Biophys. Acta* 443:629 (1976); Ostro *et al.*, *Biochem. Biophys. Res. Commun.* 76:836 (1977); Fraley *et al.*, *Proc. Natl. Acad. Sci. USA* 76:3348 (1979)); detergent dialysis (Enoch, H. and Strittmatter, P., *Proc. Natl. Acad. Sci. USA* 76:145 (1979)); and reversephase evaporation (REV) (Fraley *et al.*, *J. Biol. Chem.* 255:10431 (1980); Szoka, F.

and Papahadjopoulos, D., *Proc. Natl. Acad. Sci. USA* 75:145 (1978); SchaeferRidder *et al.*, *Science* 215:166 (1982)).

[00270] Generally, the ratio of DNA to liposomes will be from about 10:1 to about 1:10. Preferably, the ration will be from about 5:1 to about 1:5. More preferably, the ration will be about 3:1 to about 1:3. Still more preferably, the ratio will be about 1:1.

[00271] U.S. Patent No. 5,676,954 reports on the injection of genetic material, complexed with cationic liposome carriers, into mice. U.S. Patent Nos. 4,897,355, 4,946,787, 5,049,386, 5,459,127, 5,589,466, 5,693,622, 5,580,859, 5,703,055, and international publication no. WO 94/9469 provide cationic lipids for use in transfecting DNA into cells and mammals. U.S. Patent Nos. 5,589,466, 5,693,622, 5,580,859, 5,703,055, and international publication no. WO 94/9469 provide methods for delivering DNA-cationic lipid complexes to mammals.

#### Binding Affinity of Variants for HLA Molecules

[00272] As indicated herein, the large degree of HLA polymorphism is an important factor to be taken into account with the epitope-based approach to developing therapeutics and diagnostics. To address this factor, epitope selection encompassing identification of peptides capable of binding at high or intermediate affinity to multiple HLA molecules is preferably utilized, most preferably these epitopes bind at high or intermediate affinity to two or more allele-specific HLA molecules. However, in some embodiments, it is preferred that all epitopes in a given composition bind to the alleles of a single HLA supertype or a single HLA molecule.

[00273] Variants of the invention preferably include those that have an IC<sub>50</sub> or binding affinity value for a class I HLA molecule(s) of 500 nM or better (*i.e.*, the value is  $\leq$  500 nM). In certain embodiments of the invention, peptides of interest have an IC<sub>50</sub> or binding affinity value for a class I HLA molecule(s) of 200 nM or better. In certain embodiments of the invention, peptides of interest, such as A1 and A24 peptides, have an IC<sub>50</sub> or binding affinity value for a class I HLA molecule(s) of 100 nM or better. If HTL epitopes are included, they preferably are HTL epitopes that have an IC<sub>50</sub> or binding affinity value for class II HLA molecules of 1000 nM or better, (*i.e.*, the value is  $\leq$  1,000 nM). For example, peptide binding is assessed by testing the capacity of a candidate peptide to bind to a purified HLA molecule *in vitro*. Peptides exhibiting high or intermediate affinity are

then considered for further analysis. Selected peptides are generally tested on other members of the supertype family. In preferred embodiments, peptides that exhibit cross-reactive binding are then used in cellular screening analyses or vaccines.

[00274] The relationship between binding affinity for HLA class I molecules and immunogenicity of discrete peptide epitopes on bound antigens was determined for the first time by inventors at Epimmune. As disclosed in greater detail herein, higher HLA binding affinity is correlated with greater immunogenicity.

[00275] Greater immunogenicity can be manifested in several different ways. Immunogenicity corresponds to whether an immune response is elicited at all, and to the vigor of any particular response, as well as to the extent of a population in which a response is elicited. For example, a peptide might elicit an immune response in a diverse array of the population, yet in no instance produce a vigorous response. In accordance with these principles, close to 90% of high binding peptides have been found to elicit a response and thus be "immunogenic," as contrasted with about 50% of the peptides that bind with intermediate affinity. (See, e.g., Schaeffer *et al.* PNAS (1988)) High affinity-binding class I peptides generally have an affinity of less than or equal to 100 nM. Moreover, not only did peptides with higher binding affinity have an enhanced probability of generating an immune response, the generated response tended to be more vigorous than the response seen with weaker binding peptides. As a result, less peptide is required to elicit a similar biological effect if a high affinity binding peptide is used rather than a lower affinity one. Thus, in some preferred embodiments of the invention, high affinity binding epitopes are used.

[00276] The correlation between binding affinity and immunogenicity was analyzed by the present inventors by two different experimental approaches (*see, e.g., Sette, et al., J. Immunol.* 153:5586-5592 (1994)). In the first approach, the immunogenicity of potential epitopes ranging in HLA binding affinity over a 10,000-fold range was analyzed in HLA-A\*0201 transgenic mice. In the second approach, the antigenicity of approximately 100 different hepatitis B virus (HBV)-derived potential epitopes, all carrying A\*0201 binding motifs, was assessed by using PBL from acute hepatitis patients. Pursuant to these approaches, it was determined that an affinity threshold value of approximately 500 nM (preferably 50 nM or less) determines the capacity of a peptide epitope to elicit a CTL response. These data are true for class I binding affinity measurements for naturally processed peptides and for synthesized T cell epitopes. These data also indicate the

important role of determinant selection in the shaping of T cell responses (*see, e.g., Schaeffer et al. Proc. Natl. Acad. Sci. USA 86:4649-4653 (1989)*).

[00277] An affinity threshold associated with immunogenicity in the context of HLA class II (*i.e.*, HLA DR) molecules has also been delineated (*see, e.g., Southwood et al. J. Immunology 160:3363-3373 (1998)*, and U.S. Patent No. 6,413,527, issued July 2, 2002). In order to define a biologically significant threshold of HLA class II binding affinity, a database of the binding affinities of 32 DR-restricted epitopes for their restricting element (*i.e.*, the HLA molecule that binds the epitope) was compiled. In approximately half of the cases (15 of 32 epitopes), DR restriction was associated with high binding affinities, *i.e.* binding affinity values of 100 nM or less. In the other half of the cases (16 of 32), DR restriction was associated with intermediate affinity (binding affinity values in the 100-1000 nM range). In only one of 32 cases was DR restriction associated with an IC<sub>50</sub> of 1000 nM or greater. Thus, 1000 nM is defined as an affinity threshold associated with immunogenicity in the context of DR molecules.

[00278] The binding affinity of peptides for HLA molecules can be determined as described in Example 1, below.

#### Enhancing Population Coverage of the Vaccine

[00279] The primary anchor residues of the HLA class I peptide epitope supermotifs and motifs are summarized in Tables 1-2. Allele-specific HLA molecules that are comprised by the various HLA class I supertypes are listed in Table 4. In some cases, patterns of amino acid residues are present in both a motif and a supermotif. The relationship of a particular motif and any related supermotif is indicated in the description of the individual motifs.

[00280] By inclusion of one or more epitopes from several motifs or supermotifs in a vaccine composition, enhanced population coverage for major global ethnicities can be obtained.

#### Assays to Detect T-Cell Responses

[00281] Once HLA binding peptides are identified, they can be tested for the ability to elicit a T-cell response. The preparation and evaluation of motif-bearing peptides are described, *e.g.*, in PCT publications WO 94/20127 and WO 94/03205. Briefly, peptides



comprising epitopes from a particular antigen are synthesized and tested for their ability to bind to relevant HLA proteins. These assays may involve evaluation of peptide binding to purified HLA class I molecules in relation to the binding of a radioiodinated reference peptide. Alternatively, cells expressing empty class I molecules (*i.e.* cell surface HLA molecules that lack any bound peptide) may be evaluated for peptide binding by immunofluorescent staining and flow microfluorimetry. Other assays that may be used to evaluate peptide binding include peptide-dependent class I assembly assays and/or the inhibition of CTL recognition by peptide competition. Those peptides that bind to an HLA class I molecule, typically with an affinity of 500 nM or less, are further evaluated for their ability to serve as targets for CTLs derived from infected or immunized individuals, as well as for their capacity to induce primary *in vitro* or *in vivo* CTL responses that can give rise to CTL populations capable of reacting with selected target cells associated with pathology.

**[00282]** Analogous assays are used for evaluation of HLA class II binding peptides. HLA class II motif-bearing peptides that are shown to bind, typically at an affinity of 1000 nM or less, are further evaluated for the ability to stimulate HTL responses.

**[00283]** Conventional assays utilized to detect T cell responses include proliferation assays, lymphokine secretion assays, direct cytotoxicity assays, and limiting dilution assays. For example, antigen-presenting cells that have been incubated with a peptide can be assayed for the ability to induce CTL responses in responder cell populations. Antigen-presenting cells can be normal cells such as peripheral blood mononuclear cells or dendritic cells. Alternatively, mutant, non-human mammalian cell lines that have been transfected with a human class I MHC gene, and that are deficient in their ability to load class I molecules with internally processed peptides, are used to evaluate the capacity of the peptide to induce *in vitro* primary CTL responses. Peripheral blood mononuclear cells (PBMCs) can be used as the source of CTL precursors. Antigen presenting cells are incubated with peptide, after which the peptide-loaded antigen-presenting cells are then incubated with the responder cell population under optimized culture conditions. Positive CTL activation can be determined by assaying the culture for the presence of CTLs that lyse radio-labeled target cells, either specific peptide-pulsed targets or target cells that express endogenously processed antigen from which the specific peptide was derived. Alternatively, the presence of epitope-specific CTLs can be determined by IFN $\gamma$  *in situ* ELISA.

**[00284]** In an embodiment of the invention, directed to diagnostics, a method has been devised which allows direct quantification of antigen-specific T cells by staining with fluorescein-labelled HLA tetrameric complexes (Altman, J. D. *et al.*, *Proc. Natl. Acad. Sci. USA* 90:10330, 1993; Altman, J. D. *et al.*, *Science* 274:94, 1996). Other options include staining for intracellular lymphokines, and interferon release assays or ELISPOT assays. Tetramer staining, intracellular lymphokine staining and ELISPOT assays all appear to be at least 10-fold more sensitive than more conventional assays (Lalvani, A. *et al.*, *J. Exp. Med.* 186:859, 1997; Dunbar, P. R. *et al.*, *Curr. Biol.* 8:413, 1998; Murali-Krishna, K. *et al.*, *Immunity* 8:177, 1998). Additionally, DimerX technology can be used as a means of quantitation (*see, e.g.*, *Science* 274:94-99 (1996) and *Proc. Natl. Acad. Sci.* 95:7568-73 (1998)).

**[00285]** HTL activation may also be assessed using techniques known to those in the art, such as T cell proliferation or lymphokine secretion (*see, e.g.* Alexander *et al.*, *Immunity* 1:751-761, 1994).

**[00286]** Alternatively, immunization of HLA transgenic mice can be used to determine immunogenicity of peptide epitopes. Several transgenic mouse strains, *e.g.*, mice with human A2.1, A11 (which can additionally be used to analyze HLA-A3 epitopes), and B7 alleles have been characterized. Other transgenic mice strains (*e.g.*, transgenic mice for HLA-A1 and A24) are being developed. Moreover, HLA-DR1 and HLA-DR3 mouse models have been developed. In accordance with principles in the art, additional transgenic mouse models with other HLA alleles are generated as necessary.

**[00287]** Such mice can be immunized with peptides emulsified in Incomplete Freund's Adjuvant; thereafter any resulting T cells can be tested for their capacity to recognize target cells that have been peptide-pulsed or transfected with genes encoding the peptide of interest. CTL responses can be analyzed using cytotoxicity assays described above. Similarly, HTL responses can be analyzed using, *e.g.*, T cell proliferation or lymphokine secretion assays.

#### Minigenes

**[00288]** A number of different approaches are available which allow simultaneous delivery of multiple epitopes. Nucleic acids encoding multiple epitopes are a useful embodiment of the invention; discrete peptide epitopes or polyepitopic peptides can be encoded. The

epitopes to be included in a minigene are preferably selected according to the guidelines set forth in the previous section. Examples of amino acid sequences that can be included in a minigene include: HLA class I epitopes, HLA class II epitopes, a ubiquitination signal sequence, and/or a targeting sequence such as an endoplasmic reticulum (ER) signal sequence to facilitate movement of the resulting peptide into the endoplasmic reticulum. Examples of minigene constructs are shown in Tables 23-28.

**[00289]** The use of multi-epitope minigenes is also described in, *e.g.*, co-pending applications U.S.S.N. 09/311,784, 09/894,018, 60/419,973, 60/415,463; Ishioka *et al.*, *J. Immunol.* 162:3915-3925, 1999; An, L. and Whitton, J. L., *J. Virol.* 71:2292, 1997; Thomson, S. A. *et al.*, *J. Immunol.* 157:822, 1996; Whitton, J. L. *et al.*, *J. Virol.* 67:348, 1993; Hanke, R. *et al.*, *Vaccine* 16:426, 1998. For example, a multi-epitope DNA plasmid encoding nine dominant HLA-A\*0201- and A11-restricted CTL epitopes derived from the polymerase, envelope, and core proteins of HBV and human immunodeficiency virus (HIV), a PADRE® universal helper T cell (HTL) epitope, and an endoplasmic reticulum-translocating signal sequence has been engineered. Immunization of HLA transgenic mice with this plasmid construct resulted in strong CTL induction responses against the nine CTL epitopes tested. This CTL response was similar to that observed with a lipopeptide of known immunogenicity in humans, and significantly greater than immunization using peptides in oil-based adjuvants. Moreover, the immunogenicity of DNA-encoded epitopes *in vitro* was also correlated with the *in vitro* responses of specific CTL lines against target cells transfected with the DNA plasmid. These data show that the minigene served: 1.) to generate a CTL response and 2.) to generate CTLs that recognized cells expressing the encoded epitopes. A similar approach can be used to develop minigenes encoding epitopes of an infectious agent.

**[00290]** For example, to create a DNA sequence encoding the selected epitopes (minigene) for expression in human cells, the amino acid sequences of the epitopes may be reverse translated. A human codon usage table can be used to guide the codon choice for each amino acid. These epitope-encoding DNA sequences may be directly adjoined, so that when translated, a continuous peptide sequence is created. However, to optimize expression and/or immunogenicity, additional elements can be incorporated into the minigene design such as spacer amino acid residues between epitopes. HLA presentation of CTL and HTL epitopes may be improved by including synthetic (*e.g.* poly-alanine) or naturally-occurring flanking sequences adjacent to the CTL or HTL epitopes; these larger

peptides comprising the epitope(s) are within the scope of the invention. In one embodiment, spacer amino acid residues between one or more CTL and/or HTL epitopes are designed so as to minimize junctional epitopes that may result from the juxtaposition of 2 CTL and/or HTL epitopes.

[00291] The minigene sequence may be converted to DNA by assembling oligonucleotides that encode the plus and minus strands of the minigene. Overlapping oligonucleotides (30-100 bases long) may be synthesized, phosphorylated, purified and annealed under appropriate conditions using well known techniques. The ends of the oligonucleotides can be joined, for example, using T4 DNA ligase. This synthetic minigene, encoding the epitope peptide, can then be cloned into a desired expression vector.

[00292] Standard regulatory sequences well known to those of skill in the art are preferably included in the vector to ensure expression in the target cells. Several vector elements are desirable: a promoter with a downstream cloning site for minigene insertion; a polyadenylation signal for efficient transcription termination; an *E. coli* origin of replication; and an *E. coli* selectable marker (*e.g.* ampicillin or kanamycin resistance). Numerous promoters can be used for this purpose, *e.g.*, the human cytomegalovirus (hCMV) CMV-IE promoter. See, *e.g.*, U.S. Patent Nos. 5,580,859 and 5,589,466 for other suitable promoter sequences.

[00293] Optimized peptide expression and immunogenicity can be achieved by certain modifications to a minigene construct. For example, in some cases introns facilitate efficient gene expression, thus one or more synthetic or naturally-occurring introns can be incorporated into the transcribed region of the minigene. The inclusion of mRNA stabilization sequences and sequences for replication in mammalian cells may also be considered for increasing minigene expression.

[00294] Once an expression vector is selected, the minigene is cloned into the polylinker region downstream of the promoter. This plasmid is transformed into an appropriate bacterial strain, and DNA is prepared using standard techniques. The orientation and DNA sequence of the minigene, as well as all other elements included in the vector, are confirmed using restriction mapping, PCR and/or DNA sequence analysis. Bacterial cells harboring the correct plasmid can be stored as cell banks.

[00295] In addition, immunostimulatory sequences (ISSs or CpGs) appear to play a role in the immunogenicity of DNA vaccines. These sequences may be included in the vector, outside the minigene coding sequence to enhance immunogenicity.

[00296] In some embodiments, a bi-cistronic expression vector which allows production of both the minigene-encoded epitopes and a second protein (*e.g.*, one that modulates immunogenicity) can be used. Examples of proteins or polypeptides that, if co-expressed with epitopes, can enhance an immune response include cytokines (*e.g.*, IL-2, IL-12, GM-CSF), cytokine-inducing molecules (*e.g.*, LeIF), costimulatory molecules, or pan-DR binding proteins (PADRE<sup>®</sup>, Epimmune, San Diego, CA). Helper T cell (HTL) epitopes such as PADRE<sup>®</sup> molecules can be joined to intracellular targeting signals and expressed separately from expressed CTL epitopes. This can be done in order to direct HTL epitopes to a cell compartment different than that of the CTL epitopes, one that provides for more efficient entry of HTL epitopes into the HLA class II pathway, thereby improving HTL induction. In contrast to HTL or CTL induction, specifically decreasing the immune response by co-expression of immunosuppressive molecules (*e.g.* TGF- $\beta$ ) may be beneficial in certain diseases.

[00297] Therapeutic quantities of plasmid DNA can be produced for example, by fermentation in *E. coli*, followed by purification. Aliquots from the working cell bank are used to inoculate growth medium, and are grown to saturation in shaker flasks or a bioreactor according to well known techniques. Plasmid DNA is purified using standard bioseparation technologies such as solid phase anion-exchange resins available, *e.g.*, from QIAGEN, Inc. (Valencia, California). If required, supercoiled DNA can be isolated from the open circular and linear forms using gel electrophoresis or other methods.

[00298] Purified plasmid DNA can be prepared for injection using a variety of formulations. The simplest of these is reconstitution of lyophilized DNA in sterile phosphate-buffer saline (PBS). This approach, known as "naked DNA," is currently being used for intramuscular (IM) administration in clinical trials. To maximize the immunotherapeutic effects of minigene vaccines, alternative methods of formulating purified plasmid DNA may be used. A variety of such methods have been described, and new techniques may become available. Cationic lipids, glycolipids, and fusogenic liposomes can also be used in the formulation (see, *e.g.*, WO 93/24640; Mannino & Gould-Fogerite, *BioTechniques* 6(7): 682 (1988); U.S. Patent No. 5,279,833; WO 91/06309; and Felgner, *et al.*, *Proc. Nat'l Acad. Sci. USA* 84:7413 (1987). In addition, peptides and compounds referred to collectively as protective, interactive, non-condensing compounds (PINC) can also be complexed to purified plasmid DNA to influence variables such as stability, intramuscular dispersion, or trafficking to specific organs or cell types.

- [00299] Known methods in the art can be used to enhance delivery and uptake of a polynucleotide *in vivo*. For example, the polynucleotide can be complexed to polyvinylpyrrolidone (PVP), to prolong the localized bioavailability of the polynucleotide, thereby enhancing uptake of the polynucleotide by the organism (*see e.g.*, U.S. Patent No. 6,040,295; EP 0 465 529; WO 98/17814). PVP is a polyamide that is known to form complexes with a wide variety of substances, and is chemically and physiologically inert.
- [00300] Target cell sensitization can be used as a functional assay of the expression and HLA class I presentation of minigene-encoded epitopes. For example, the plasmid DNA is introduced into a mammalian cell line that is a suitable target for standard CTL chromium release assays. The transfection method used will be dependent on the final formulation, electroporation can be used for "naked" DNA, whereas cationic lipids or DNA:PVP compositions allow direct *in vitro* transfection. A plasmid expressing green fluorescent protein (GFP) can be co-transfected to allow enrichment of transfected cells using fluorescence activated cell sorting (FACS). The transfected cells are then chromium-51 ( $^{51}\text{Cr}$ ) labeled and used as targets for epitope-specific CTLs. Cytolysis of the target cells, detected by  $^{51}\text{Cr}$  release, indicates both the production and HLA presentation of, minigene-encoded CTL epitopes. Expression of HTL epitopes may be evaluated in an analogous manner using assays to assess HTL activity.
- [00301] *In vivo* immunogenicity is a second approach for functional testing of minigene DNA formulations. Transgenic mice expressing appropriate human HLA proteins are immunized with the DNA product. The dose and route of administration are formulation dependent (*e.g.*, IM for DNA in PBS, intraperitoneal (IP) for lipid-complexed DNA). Eleven to twenty-one days after immunization, splenocytes are harvested and restimulated for one week in the presence of peptides encoding each epitope being tested. Thereafter, for CTLs, standard assays are conducted to determine if there is cytolysis of peptide-loaded,  $^{51}\text{Cr}$ -labeled target cells. Once again, lysis of target cells that were exposed to epitopes corresponding to those in the minigene, demonstrates DNA vaccine function and induction of CTLs. Immunogenicity of HTL epitopes is evaluated in transgenic mice in an analogous manner.
- [00302] Alternatively, the nucleic acids can be administered using ballistic delivery as described, for instance, in U.S. Patent No. 5,204,253. Using this technique, particles comprised solely of DNA are administered. In a further alternative embodiment for ballistic delivery, DNA can be adhered to particles, such as gold particles.

## Vaccine Compositions

[00303] Vaccines that contain an immunologically effective amount of one or more peptides or polynucleotides of the invention are a further embodiment of the invention. The peptides can be delivered by various means or formulations, all collectively referred to as “vaccine” compositions. Such vaccine compositions, and/or modes of administration, can include, for example, naked DNA, DNA formulated with PVP, DNA in cationic lipid formulations; lipopeptides (e.g., Vitiello, A. *et al.*, *J. Clin. Invest.* 95:341, 1995), DNA or peptides, encapsulated e.g., in poly(DL-lactide-co-glycolide) (“PLG”) microspheres (see, e.g., Eldridge, *et al.*, *Molec. Immunol.* 28:287-294, 1991; Alonso *et al.*, *Vaccine* 12:299-306, 1994; Jones *et al.*, *Vaccine* 13:675-681, 1995); peptide compositions contained in immune stimulating complexes (ISCOMS) (see, e.g., Takahashi *et al.*, *Nature* 344:873-875, 1990; Hu *et al.*, *Clin Exp Immunol.* 113:235-243, 1998); multiple antigen peptide systems (MAPs) (see e.g., Tam, J. P., *Proc. Natl. Acad. Sci. U.S.A.* 85:5409-5413, 1988; Tam, J.P., *J. Immunol. Methods* 196:17-32, 1996); viral, bacterial, or, fungal delivery vectors (Perkus, M. E. *et al.*, In: *Concepts in vaccine development*, Kaufmann, S. H. E., ed., p. 379, 1996; Chakrabarti, S. *et al.*, *Nature* 320:535, 1986; Hu, S. L. *et al.*, *Nature* 320:537, 1986; Kieny, M.-P. *et al.*, *AIDS Bio/Technology* 4:790, 1986; Top, F. H. *et al.*, *J. Infect. Dis.* 124:148, 1971; Chanda, P. K. *et al.*, *Virology* 175:535, 1990); particles of viral or synthetic origin (e.g., Kofler, N. *et al.*, *J. Immunol. Methods* 192:25, 1996; Eldridge, J. H. *et al.*, *Sem. Hematol.* 30:16, 1993; Falo, L. D., Jr. *et al.*, *Nature Med.* 7:649, 1995); adjuvants (e.g., incomplete freund’s adjuvant) (Warren, H. S., Vogel, F. R., and Chedid, L. A. *Annu. Rev. Immunol.* 4:369, 1986; Gupta, R. K. *et al.*, *Vaccine* 11:293, 1993); liposomes (Reddy, R. *et al.*, *J. Immunol.* 148:1585, 1992; Rock, K. L., *Immunol. Today* 17:131, 1996); or, particle-absorbed DNA (Ulmer, J. B. *et al.*, *Science* 259:1745, 1993; Robinson, H. L., Hunt, L. A., and Webster, R. G., *Vaccine* 11:957, 1993; Shiver, J. W. *et al.*, In: *Concepts in vaccine development*, Kaufmann, S. H. E., ed., p. 423, 1996; Cease, K. B., and Berzofsky, J. A., *Annu. Rev. Immunol.* 12:923, 1994 and Eldridge, J. H. *et al.*, *Sem. Hematol.* 30:16, 1993), etc. Toxin-targeted delivery technologies, also known as receptor mediated targeting, such as those of Avant Immunotherapeutics, Inc. (Needham, Massachusetts) or attached to a stress protein, e.g., HSP 96 (Stressgen Biotechnologies Corp., Victoria, BC, Canada) can also be used.

[00304] Vaccines of the invention comprise nucleic acid mediated modalities. DNA or RNA encoding one or more of the peptides of the invention can be administered to a patient. This approach is described, for instance, in Wolff *et. al.*, *Science* 247:1465 (1990) as well as U.S. Patent Nos. 5,580,859; 5,589,466; 5,804,566; 5,739,118; 5,736,524; 5,679,647; and, WO 98/04720. Examples of DNA-based delivery technologies include “naked DNA”, facilitated (bupivacaine, polymers (*e.g.*, PVP), peptide-mediated) delivery, cationic lipid complexes, and particle-mediated (“gene gun”) or pressure-mediated delivery (*see, e.g.*, U.S. Patent No. 5,922,687). Accordingly, peptide vaccines of the invention can be expressed by viral or bacterial vectors. Examples of expression vectors include attenuated viral hosts, such as vaccinia or fowlpox. For example, vaccinia virus is used as a vector to express nucleotide sequences that encode the peptides of the invention (*e.g.*, MVA). Upon introduction into an acutely or chronically infected host or into a non-infected host, the recombinant vaccinia virus expresses the immunogenic peptide, and thereby elicits an immune response. Vaccinia vectors and methods useful in immunization protocols are described in, *e.g.*, U.S. Patent No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover *et al.*, *Nature* 351:456-460 (1991). A wide variety of other vectors useful for therapeutic administration or immunization of the peptides of the invention, *e.g.* adeno and adeno-associated virus vectors, alpha virus vectors, retroviral vectors, *Salmonella typhi* vectors, detoxified anthrax toxin vectors, and the like, are apparent to those skilled in the art from the description herein.

[00305] Furthermore, vaccines in accordance with the invention can comprise one or more peptides of the invention. Accordingly, a peptide can be present in a vaccine individually; alternatively, the peptide can exist as a homopolymer comprising multiple copies of the same peptide, or as a heteropolymer of various peptides. Polymers have the advantage of increased probability for immunological reaction and, where different peptide epitopes are used to make up the polymer, the ability to induce antibodies and/or T cells that react with different antigenic determinants of the antigen targeted for an immune response. The composition may be a naturally occurring region of an antigen or can be prepared, *e.g.*, recombinantly or by chemical synthesis.

[00306] Carriers that can be used with vaccines of the invention are well known in the art, and include, *e.g.*, thyroglobulin, albumins such as human serum albumin, tetanus toxoid, polyamino acids such as poly L-lysine, poly L-glutamic acid, influenza virus proteins,



hepatitis B virus core protein, and the like. The vaccines can contain a physiologically tolerable diluent such as water, or a saline solution, preferably phosphate buffered saline. Generally, the vaccines also include an adjuvant. Adjuvants such as incomplete Freund's adjuvant, aluminum phosphate, aluminum hydroxide, or alum are examples of materials well known in the art. Additionally, as disclosed herein, CTL responses can be primed by conjugating peptides of the invention to lipids, such as tripalmitoyl-S-glyceryl-cysteinyl-serine (P<sub>3</sub>CSS).

[00307] Upon immunization with a peptide composition in accordance with the invention, via injection (*e.g.*, SC, ID, IM), aerosol, oral, transdermal, transmucosal, intrapleural, intrathecal, or other suitable routes, the immune system of the host responds to the vaccine by producing antibodies, CTLs and/or HTLs specific for the desired antigen. Consequently, the host becomes at least partially immune to subsequent exposure to the infectious agent, and thereby derives a prophylactic or therapeutic benefit.

[00308] In certain embodiments, components that induce T cell responses are combined with components that induce antibody responses to the target antigen of interest. A preferred embodiment of such a composition comprises class I and class II epitopes in accordance with the invention. Alternatively, a composition comprises a class I and/or class II epitope in accordance with the invention, along with a PADRE<sup>®</sup> molecule (Epimmune, San Diego, CA).

[00309] Vaccines of the invention can comprise antigen presenting cells, such as dendritic cells, as a vehicle to present peptides of the invention. For example, dendritic cells are transfected, *e.g.*, with a minigene construct in accordance with the invention, in order to elicit immune responses. Minigenes are discussed in greater detail in a following section. Vaccine compositions can be created *in vitro*, following dendritic cell mobilization and harvesting, whereby loading of dendritic cells occurs *in vitro*.

[00310] The vaccine compositions of the invention may also be used in combination with antiviral drugs such as interferon- $\alpha$ , or immune adjuvants such as IL-12, GM-CSF, etc.

[00311] Preferably, the following principles are utilized when selecting epitope(s) and/or analogs for inclusion in a vaccine, either peptide-based or nucleic acid-based formulations. Exemplary variants that may be utilized in a vaccine to treat or prevent infectious agent-mediated disease are set out in Tables 6-9 and Figures 1A-4. Each of the following principles can be balanced in order to make the selection. When multiple epitopes are to be used in a vaccine, the epitopes may be, but need not be, contiguous in sequence in the

native antigen from which the epitopes are derived. Such multiple epitopes can refer to the order of epitopes within a peptide, or to the selection of epitopes that come from the same region, for use in either individual peptides, or in a multi-epitopic peptide.

1.) Variants are selected which, upon administration, mimic immune responses that have been observed to be correlated with prevention or clearance of infectious disease. For HLA Class I, this generally includes 3-7 variants from at least one infectious agent or antigen thereof.

2.) Variants are selected that have the requisite binding affinity established to be correlated with immunogenicity: for HLA Class I an  $IC_{50}$  of 500 nM or less, or for Class II an  $IC_{50}$  of 1000 nM or less. For HLA Class I it is presently preferred to select a peptide having an  $IC_{50}$  of 200 nM or less, as this is believed to better correlate not only to induction of an immune response, but to *in vitro* tumor cell killing as well. For HLA A1 and A24, it is especially preferred to select a peptide having an  $IC_{50}$  of 100 nM or less.

3.) Supermotif bearing-variants, or a sufficient array of allele-specific motif-bearing variants, are selected to give broad population coverage. In general, it is preferable to have at least 80% population coverage. A Monte Carlo analysis, a statistical evaluation known in the art, can be employed to assess the breadth of population coverage.

4.) Of particular relevance are "nested epitopes." Nested epitopes occur where at least two epitopes overlap in a given peptide sequence. For example, a nested epitope can be a fragment of an antigen from a region that contains multiple epitopes that are overleaping, or one epitope that is completely encompassed by another, *e.g.*, A2 peptides MAGE3.159 and MAGE3.160 are nested epitopes. A peptide comprising "transcendent nested epitopes" is a peptide that has both HLA class I and HLA class II epitopes in it. When providing nested epitopes, it is preferable to provide a sequence that has the greatest number of epitopes per provided sequence. Preferably, one avoids providing a peptide that is any longer than the amino terminus of the amino terminal epitope and the carboxyl terminus of the carboxyl terminal epitope in the peptide. When providing a sequence comprising nested epitopes, it is important to evaluate the sequence in order to insure that it does not have pathological or other deleterious biological properties; this is particularly relevant for vaccines directed to infectious organisms.

5.) If a protein with multiple epitopes or a polynucleotide (*e.g.*, minigene) is created, an objective is to generate the smallest peptide that encompasses the epitopes of interest. This principle is similar, if not the same as that employed when selecting a peptide comprising nested epitopes. However, with an artificial peptide comprising multiple epitopes, the size minimization objective is balanced against the need to integrate any spacer sequences between epitopes in the polyepitopic protein. Spacer amino acid residues can be introduced to avoid junctional epitopes (an epitope recognized by the immune system, not present in the target antigen, and only created by the man-made juxtaposition of epitopes), or to facilitate cleavage between epitopes and thereby

enhance epitope presentation. Junctional epitopes are generally to be avoided because the recipient may generate an immune response to that non-native epitope. Of particular concern is a junctional epitope that is a "dominant epitope." A dominant epitope may lead to such a zealous response that immune responses to other epitopes are diminished or suppressed.

[00312] The principles are the same, except junctional epitopes applies to the sequences surrounding the epitope. One must also take care with other sequences in construct to avoid immune response.

### **T CELL PRIMING MATERIALS**

[00313] In some embodiments it may be desirable to include in the pharmaceutical compositions of the invention at least one component which primes cytotoxic T lymphocytes. Lipids have been identified as agents capable of facilitating the priming *in vitro* CTL response against viral antigens. For example, palmitic acid residues can be attached to the  $\epsilon$ - and  $\alpha$ - amino groups of a lysine residue and then linked to an immunogenic peptide. One or more linking moieties can be used such as Gly, Gly-Gly-, Ser, Ser-Ser, or the like. The lipidated peptide can then be administered directly in a micelle or particle, incorporated into a liposome, or emulsified in an adjuvant, *e.g.*, incomplete Freund's adjuvant. A preferred immunogenic composition comprises palmitic acid attached to  $\epsilon$ - and  $\alpha$ - amino groups of Lys via a linking moiety, *e.g.*, Ser-Ser, added to the amino terminus of an immunogenic peptide.

[00314] In another embodiment of lipid-facilitated priming of CTL responses, *E. coli* lipoproteins, such as tripalmitoyl-S-glycerol-cysteinyl-serine (P<sub>3</sub>CSS) can be used to prime CTL when covalently attached to an appropriate peptide. (See, *e.g.*, Deres, *et al.*, *Nature* 342:561, 1989). Thus, peptides of the invention can be coupled to P<sub>3</sub>CSS, and the lipopeptide administered to an individual to specifically prime a CTL response to the target antigen. Moreover, because the induction of neutralizing antibodies can also be primed with P<sub>3</sub>CSS-conjugated epitopes, two such compositions can be combined to elicit both humoral and cell-mediated responses.

### **DENDRITIC CELLS PULSED WITH CTL AND/OR HTL PEPTIDES**

[00315] An embodiment of a vaccine composition in accordance with the invention comprises *ex vivo* administration of a cocktail of epitope-bearing peptides to PBMC, or

isolated DC therefrom, from the patient's blood. A pharmaceutical to facilitate harvesting of DC can be used, such as Progenipoietin™ (Monsanto, St. Louis, MO) or GM-CSF/IL-4. After pulsing the DC with peptides and prior to reinfusion into patients, the DC are washed to remove unbound peptides. In this embodiment, a vaccine comprises peptide-pulsed DCs which present the pulsed peptide epitopes in HLA molecules on their surfaces.

[00316] The DC can be pulsed *ex vivo* with a cocktail of peptides, some of which stimulate CTL responses to one or more antigens of interest, *e.g.*, antigens from infectious agents such as HIV env, HIV pol, HIV gag, HIV vpu, HBV and/or the antigens in Tables 11-22, or otherwise described herein or known in the art. Optionally, a helper T cell (HTL) peptide such as PADRE®, can be included to facilitate the CTL response. Thus, a vaccine in accordance with the invention comprising epitopes from an infectious agent is used to treat or prevent disease mediated by these agents in patients. A vaccine can be used prior to, during, or following other therapies including, for example, antibiotic therapy, antiviral therapy (*e.g.*, highly active antiretroviral therapy (HAART) in the case of HIV-AIDS), antibody therapy, cancer therapy, and adjunct therapy, whereupon the vaccine provides decreased morbidity, increased disease free survival and overall survival in recipients.

#### DIAGNOSTIC AND PROGNOSTIC USES

[00317] In one embodiment of the invention, HLA class I and class II binding peptides can be used as reagents to evaluate an immune response. Preferably, the following principles are utilized when selecting a variant(s) for diagnostic, prognostic and similar uses. Potential principles include having the binding affinities described earlier, and/or matching the HLA-motif/supermotif of a peptide with the HLA-type of a patient.

[00318] The evaluated immune response can be induced by any immunogen. For example, the immunogen may result in the production of antigen-specific CTLs or HTLs that recognize the peptide epitope(s) employed as the reagent. Thus, a peptide of the invention may or may not be used as the immunogen. Assay systems that can be used for such analyses include tetramer-based protocols (*e.g.*, DimerX technology (*see, e.g., Science* 274:94-99 (1996) and *Proc. Natl. Acad. Sci.* 95:7568-73 (1998)), staining for intracellular lymphokines, interferon release assays, or ELISPOT assays.

- [00319] For example, following exposure to a putative immunogen, a peptide of the invention can be used in a tetramer staining assay to assess peripheral blood mononuclear cells for the presence of any antigen-specific CTLs. The HLA-tetrameric complex is used to directly visualize antigen-specific CTLs and thereby determine the frequency of such antigen-specific CTLs in a sample of peripheral blood mononuclear cells (*see, e.g., Ogg et al., Science* 279:2103-2106, 1998; and Altman *et al., Science* 174:94-96, 1996).
- [00320] A tetramer reagent comprising a peptide of the invention is generated as follows: A peptide that binds to an HLA molecule is refolded in the presence of the corresponding HLA heavy chain and  $\beta_2$ -microglobulin to generate a trimolecular complex. The complex is biotinylated at the carboxyl terminal end of the HLA heavy chain, at a site that was previously engineered into the protein. Tetramer formation is then induced by adding streptavidin. When fluorescently labeled streptavidin is used, the tetrameric complex is used to stain antigen-specific cells. The labeled cells are then readily identified, *e.g.*, by flow cytometry. Such procedures are used for diagnostic or prognostic purposes; the cells identified by the procedure can be used for therapeutic purposes.
- [00321] Peptides of the invention are also used as reagents to evaluate immune recall responses. (*see, e.g., Bertoni et al., J. Clin. Invest.* 100:503-513, 1997 and Penna *et al., J. Exp. Med.* 174:1565-1570, 1991.) For example, a PBMC sample from an individual expressing a disease-associated antigen (*e.g.* an antigen from an infectious agent) can be analyzed for the presence of antigen-specific CTLs or HTLs using specific peptides. A blood sample containing mononuclear cells may be evaluated by cultivating the PBMCs and stimulating the cells with a peptide of the invention. After an appropriate cultivation period, the expanded cell population may be analyzed, for example, for CTL or for HTL activity.
- [00322] Thus, the peptides can be used to evaluate the efficacy of a vaccine. PBMCs obtained from a patient vaccinated with an immunogen may be analyzed by methods such as those described herein. The patient is HLA typed, and peptide epitopes that are bound by the HLA molecule(s) present in that patient are selected for analysis. The immunogenicity of the vaccine is indicated by the presence of CTLs and/or HTLs directed to epitopes present in the vaccine.
- [00323] The peptides of the invention may also be used to make antibodies, using techniques well known in the art (*see, e.g. CURRENT PROTOCOLS IN IMMUNOLOGY*, Wiley/Greene, NY; and *Antibodies A Laboratory Manual Harlow*, Harlow and Lane, Cold

Spring Harbor Laboratory Press, 1989). Such antibodies are useful as reagents to determine the presence of disease-associated antigens. Antibodies in this category include those that recognize a peptide when bound by an HLA molecule, *i.e.*, antibodies that bind to a peptide-MHC complex.

#### **ADMINISTRATION FOR THERAPEUTIC OR PROPHYLACTIC PURPOSES**

[00324] The peptides and polynucleotides of the present invention, including cells and compositions comprising them, are useful for administration to mammals, particularly humans, to treat and/or prevent infection by an infectious agent such as HIV, HBV, HCV, HPV, *Plasmodium falciparum* and other agents described herein or known in the art. Vaccine compositions containing the peptides of the invention are administered to a patient infected with a particular infectious agent or to an individual susceptible to, or otherwise at risk for, infection with such an agent to elicit an immune response against antigens of that agent and thus enhance the patient's own immune response capabilities. Where susceptible individuals are identified prior to infection, the composition can be targeted to them, thus minimizing the need for administration to a larger population.

[00325] In therapeutic applications, peptide and/or nucleic acid compositions are administered to a patient in an amount sufficient to elicit an effective immune response to the infectious agent antigen and to thereby cure, arrest or slow symptoms and/or complications. An amount adequate to accomplish this is defined as "therapeutically effective dose." Amounts effective for this use will depend on, *e.g.*, the particular composition administered, the manner of administration, the stage and severity of the disease being treated, the weight and general state of health of the patient, and the judgment of the prescribing physician.

[00326] The vaccine compositions of the invention can be used purely as prophylactic agents. Generally the dosage for an initial prophylactic immunization generally occurs in a unit dosage range where the lower value is about 1, 5, 50, 500, or 1000 µg of peptide and the higher value is about 10,000; 20,000; 30,000; or 50,000 µg of peptide. Dosage values for a human typically range from about 500 µg to about 50,000 µg of peptide per 70 kilogram patient. This is followed by boosting dosages of between about 1.0 µg to about 50,000 µg of peptide, administered at defined intervals from about four weeks to six months after the initial administration of vaccine. The immunogenicity of the vaccine may be assessed by measuring the specific activity of CTL and HTL obtained from a sample of the patient's blood.

[00327] As noted above, peptides comprising CTL and/or HTL epitopes of the invention induce immune responses when presented by HLA molecules and contacted with a CTL or HTL specific

for an epitope comprised by the peptide. The manner in which the peptide is contacted with the CTL or HTL is not critical to the invention. For instance, the peptide can be contacted with the CTL or HTL either *in vitro* or *in vivo*. If the contacting occurs *in vivo*, peptide can be administered directly, or in other forms/vehicles, *e.g.*, DNA vectors encoding one or more peptides, viral vectors encoding the peptide(s), liposomes, antigen presenting cells such as dendritic cells, and the like.

[00328] Accordingly, for pharmaceutical compositions of the invention in the form of peptides or polypeptides, the peptides or polypeptides can be administered directly. Alternatively, the peptide/polypeptides can be administered indirectly presented on APCs, or as DNA encoding them. Furthermore, the peptides or DNA encoding them can be administered individually or as fusions of one or more peptide sequences.

[00329] For therapeutic use, administration should generally begin at the first diagnosis of infectious agent-related disease. This is followed by boosting doses at least until symptoms are substantially abated and for a period thereafter. In chronic disease states, loading doses followed by boosting doses may be required.

[00330] The dosage for an initial therapeutic immunization generally occurs in a unit dosage range where the lower value is about 1, 5, 50, 500, or 1,000  $\mu\text{g}$  of peptide and the higher value is about 10,000; 20,000; 30,000; or 50,000  $\mu\text{g}$  of peptide. Dosage values for a human typically range from about 500  $\mu\text{g}$  to about 50,000  $\mu\text{g}$  of peptide per 70 kilogram patient. Boosting dosages of between about 1.0  $\mu\text{g}$  to about 50,000  $\mu\text{g}$  of peptide, administered pursuant to a boosting regimen over weeks to months, can be administered depending upon the patient's response and condition. Patient response can be determined by measuring the specific activity of CTL and HTL obtained from the patient's blood.

[00331] In certain embodiments, peptides and compositions of the present invention are used in serious disease states. In such cases, as a result of the minimal amounts of extraneous substances and the relative nontoxic nature of the peptides, it is possible and may be desirable to administer substantial excesses of these peptide compositions relative to these stated dosage amounts.

[00332] For treatment of chronic disease, a representative dose is in the range disclosed above, namely where the lower value is about 1, 5, 50, 500, or 1,000  $\mu\text{g}$  of peptide and the higher value is about 10,000; 20,000; 30,000; or 50,000  $\mu\text{g}$  of peptide, preferably from about 500  $\mu\text{g}$  to about 50,000  $\mu\text{g}$  of peptide per 70 kilogram patient. Initial doses followed by boosting doses at established intervals, *e.g.*, from four weeks to six months, may be required, possibly for a prolonged period of time to effectively immunize an individual. In the case of chronic disease, administration should continue until at least clinical symptoms or laboratory tests indicate that the disease has been eliminated or substantially abated, and for a follow-up period thereafter. The dosages, routes of administration, and dose schedules are adjusted in accordance with methodologies known in the art.

[00333] The pharmaceutical compositions for therapeutic treatment are intended for parenteral, topical, oral, intrathecal, or local administration. Preferably, the pharmaceutical compositions are administered parentally, *e.g.*, intravenously, subcutaneously, intradermally, or intramuscularly.

[00334] Thus, in a preferred embodiment the invention provides compositions for parenteral administration which comprise a solution of the immunogenic peptides dissolved or suspended in an acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers may be used, *e.g.*, water, buffered water, 0.8% saline, 0.3% glycine, hyaluronic acid and the like. These compositions may be sterilized by conventional, well known sterilization techniques, or may be sterile filtered. The resulting aqueous solutions may be packaged for use as is, or lyophilized, the lyophilized preparation being combined with a sterile solution prior to administration. The compositions may contain pharmaceutically acceptable auxiliary substances or pharmaceutical excipients as may be required to approximate physiological conditions, such as pH-adjusting and buffering agents, tonicity adjusting agents, wetting agents, preservatives, and the like, for example, sodium acetate, sodium lactate, sodium chloride, potassium chloride, calcium chloride, sorbitan monolaurate, triethanolamine oleate, *etc.*

[00335] The concentration of peptides of the invention in the pharmaceutical formulations can vary widely, *i.e.*, from less than about 0.1%, usually at or at least about 2% to as much as 20% to 50% or more by weight, and will be selected primarily by fluid volumes, viscosities, *etc.*, in accordance with the particular mode of administration selected.

[00336] A human unit dose form of the peptide composition is typically included in a pharmaceutical composition that also comprises a human unit dose of an acceptable carrier, preferably an aqueous carrier, and is administered in a volume of fluid that is known by those of skill in the art to be used for administration of such compositions to humans (*see, e.g., Remington's Pharmaceutical Sciences*, 17<sup>th</sup> Edition, A. Gennaro, Editor, Mack Publishing Co., Easton, Pennsylvania, 1985).

[00337] The peptides of the invention can also be administered via liposomes, which serve to target the peptides to a particular tissue, such as lymphoid tissue, or to target selectively to infected cells, as well as to increase the half-life of the peptide composition. Liposomes include emulsions, foams, micelles, insoluble monolayers, liquid crystals, phospholipid dispersions, lamellar layers and the like. In these preparations, the peptide to be delivered is incorporated as part of a liposome, alone or in conjunction with a molecule which binds to a receptor prevalent among lymphoid cells (such as monoclonal antibodies which bind to the CD45 antigen) or with other therapeutic or immunogenic compositions. Thus, liposomes either filled or decorated with a desired peptide of the invention can be directed to the site of lymphoid cells, where the liposomes then deliver the peptide compositions. Liposomes for use in accordance with the invention are formed from standard vesicle-forming lipids, which generally include neutral and negatively



charged phospholipids and a sterol, such as cholesterol. The selection of lipids is generally guided by consideration of, *e.g.*, liposome size, acid lability and stability of the liposomes in the blood stream. A variety of methods are available for preparing liposomes, as described in, *e.g.*, Szoka, *et al.*, *Ann. Rev. Biophys. Bioeng.* 9:467 (1980), and U.S. Patent Nos. 4,235,871, 4,501,728, 4,837,028, and 5,019,369.

[00338] For targeting compositions of the invention to cells of the immune system, a ligand can be incorporated into the liposome, *e.g.*, antibodies or fragments thereof specific for cell surface determinants of the desired immune system cells. A liposome suspension containing a peptide may be administered intravenously, locally, topically, *etc.* in a dose which varies according to, *inter alia*, the manner of administration, the peptide being delivered, and the stage of the disease being treated.

[00339] For solid compositions, conventional nontoxic solid carriers may be used which include, for example, pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharin, talcum, cellulose, glucose, sucrose, magnesium carbonate, and the like. For oral administration, a pharmaceutically acceptable nontoxic composition is formed by incorporating any of the normally employed excipients, such as those carriers previously listed, and generally 10-95% of active ingredient, that is, one or more peptides of the invention, often at a concentration of 25%-75%.

[00340] For aerosol administration, the immunogenic peptides are preferably supplied in finely divided form, along with a surfactant and propellant. Typical percentages of peptides are 0.01%-20% by weight, often 1%-10%. The surfactant must, of course, be pharmaceutically acceptable, and preferably soluble in the propellant. Representative of such agents are the esters or partial esters of fatty acids containing from 6 to 22 carbon atoms, such as caproic, octanoic, lauric, palmitic, stearic, linoleic, linolenic, olesteric and oleic acids with an aliphatic polyhydric alcohol or its cyclic anhydride. Mixed esters, such as mixed or natural glycerides may be employed. The surfactant may constitute 0.1%-20% by weight of the composition, preferably 0.25-5%. The balance of the composition is ordinarily propellant, although an atomizer may be used in which no propellant is necessary and other percentages are adjusted accordingly. A carrier can also be included, *e.g.*, lecithin for intranasal delivery.

[00341] Antigenic peptides of the invention have been used to elicit a CTL and/or HTL response *ex vivo*, as well. The resulting CTLs or HTLs can be used to treat chronic infections, or tumors in patients that do not respond to other conventional forms of therapy, or who do not respond to a therapeutic peptide or nucleic acid vaccine in accordance with the invention. *Ex vivo* CTL or HTL responses to a particular antigen (infectious or tumor-associated) are induced by incubating in tissue culture the patient's, or genetically compatible, CTL or HTL precursor cells together with a source of antigen-presenting cells (APC), such as dendritic cells, and the appropriate immunogenic

peptide. After an appropriate incubation time (typically about 7-28 days), in which the precursor cells are activated and expanded into effector cells, the cells are infused back into the patient, where they will destroy (CTL) or facilitate destruction (HTL) of their specific target cell (an infected cell or a tumor cell).

## KITS

[00342] The peptide and nucleic acid compositions of this invention can be provided in kit form together with instructions for vaccine administration. Typically the kit would include desired composition(s) of the invention in a container, preferably in unit dosage form and instructions for administration. For example, a kit would include an APC, such as a dendritic cell, previously exposed to and now presenting peptides of the invention in a container, preferably in unit dosage form together with instructions for administration. An alternative kit would include a minigene construct with desired nucleic acids of the invention in a container, preferably in unit dosage form together with instructions for administration. Lymphokines such as IL-2 or IL-12 may also be included in the kit. Other kit components that may also be desirable include, for example, a sterile syringe, booster dosages, and other desired excipients.

[00343] The invention will be described in greater detail by way of specific examples. The following examples are offered for illustrative purposes, and are not intended to limit the invention in any manner. Those of skill in the art will readily recognize a variety of non-critical parameters that can be changed or modified to yield alternative embodiments in accordance with the invention.

## EXAMPLES

### EXAMPLE 1. HLA CLASS I AND CLASS II BINDING ASSAYS

[00344] The following example of peptide binding to HLA molecules demonstrates quantification of binding affinities of HLA class I and class II peptides. Binding assays can be performed with peptides that are either motif-bearing or not motif-bearing.

[00345] Cell lysates were prepared and HLA molecules purified in accordance with disclosed protocols (Sidney *et al.*, *Current Protocols in Immunology* 18.3.1 (1998); Sidney, *et al.*, *J. Immunol.* 154:247 (1995); Sette, *et al.*, *Mol. Immunol.* 31:813 (1994)).

The cell lines used as sources of HLA molecules and the antibodies used for the extraction of the HLA molecules from the cell lysates are also described in these publications and are well known in the art.

[00346] Epstein-Barr virus (EBV)-transformed homozygous cell lines, fibroblasts, CIR, or 721.221-transfectants were used as sources of HLA class I molecules. These cells were cultured in RPMI 1640 medium supplemented with 2mM L-glutamine (GIBCO, Grand Island, NY), 50µM 2-ME, 100µg/ml of streptomycin, 100U/ml of penicillin (Irvine Scientific) and 10% heat-inactivated FCS (Irvine Scientific, Santa Ana, CA).

[00347] Cell lysates were prepared as follows. Briefly, cells were lysed at a concentration of  $10^8$  cells/ml in 50 mM Tris-HCl, pH 8.5, containing 1% Nonidet P-40 (Fluka Biochemika, Buchs, Switzerland), 150 mM NaCl, 5 mM EDTA, and 2 mM PMSF. Lysates were cleared of debris and nuclei by centrifugation at 15,000 x g for 30min.

[00348] HLA molecules were purified from lysates by affinity chromatography. Lysates were passed twice through two pre-columns of inactivated Sepharose CL4-B and protein A-Sepharose. Next, the lysate was passed over a column of Sepharose CL-4B beads coupled to an appropriate antibody. The anti-HLA column was then washed with 10-column volumes of 10mM Tris-HCL, pH 8.0, in 1% NP-40, PBS, 2-column volumes of PBS, and 2-column volumes of PBS containing 0.4% n-octylglucoside. Finally, MHC molecules were eluted with 50mM diethylamine in 0.15M NaCl containing 0.4% n-octylglucoside, pH 11.5. A 1/25 volume of 2.0M Tris, pH 6.8, was added to the eluate to reduce the pH to ~8.0. Eluates were then concentrated by centrifugation in Centriprep 30 concentrators at 2000 rpm (Amicon, Beverly, MA). Protein content was evaluated by a BCA protein assay (Pierce Chemical Co., Rockford, IL) and confirmed by SDS-PAGE.

[00349] A detailed description of the protocol utilized to measure the binding of peptides to Class I and Class II MHC has been published (Sette *et al.*, *Mol. Immunol.* 31:813, 1994; Sidney *et al.*, in *Current Protocols in Immunology*, Margulies, Ed., John Wiley & Sons, New York, Section 18.3, 1998). Briefly, purified MHC molecules (5 to 500nM) were incubated with various unlabeled peptide inhibitors and 1-10nM  $^{125}$ I-radiolabeled probe peptides for 48h in PBS containing 0.05% Nonidet P-40 (NP40) (or 20% w/v digitonin for H-2 IA assays) in the presence of a protease inhibitor cocktail. The final concentrations of protease inhibitors (each from CalBioChem, La Jolla, CA) were 1 mM PMSF, 1.3 nM 1.10 phenanthroline, 73 µM pepstatin A, 8mM EDTA, 6mM N-ethylmaleimide (for Class II assays), and 200 µM N alpha-p-tosyl-L-lysine chloromethyl ketone (TLCK). All assays

were performed at pH 7.0 with the exception of DRB1\*0301, which was performed at pH 4.5, and DRB1\*1601 (DR2w21 $\beta$ <sub>1</sub>) and DRB4\*0101 (DRw53), which were performed at pH 5.0. pH was adjusted as described elsewhere (*see* Sidney *et al.*, in *Current Protocols in Immunology*, Margulies, Ed., John Wiley & Sons, New York, Section 18.3, 1998).

**[00350]** Following incubation, MHC-peptide complexes were separated from free peptide by gel filtration on 7.8 mm x 15 cm TSK200 columns (TosoHaas 16215, Montgomeryville, PA), eluted at 1.2 mls/min with PBS pH 6.5 containing 0.5% NP40 and 0.1% NaN<sub>3</sub>. Because the large size of the radiolabeled peptide used for the DRB1\*1501 (DR2w2 $\beta$ <sub>1</sub>) assay makes separation of bound from unbound peaks more difficult under these conditions, all DRB1\*1501 (DR2w2 $\beta$ <sub>1</sub>) assays were performed using a 7.8mm x 30cm TSK2000 column eluted at 0.6 mls/min. The eluate from the TSK columns was passed through a Beckman 170 radioisotope detector, and radioactivity was plotted and integrated using a Hewlett-Packard 3396A integrator, and the fraction of peptide bound was determined.

**[00351]** Radiolabeled peptides were iodinated using the chloramine-T method. Representative radiolabeled probe peptides utilized in each assay, and its assay specific IC<sub>50</sub> nM, are known in the art. Typically, in preliminary experiments, each MHC preparation was titrated in the presence of fixed amounts of radiolabeled peptides to determine the concentration of HLA molecules necessary to bind 10-20% of the total radioactivity. All subsequent inhibition and direct binding assays were performed using these HLA concentrations.

**[00352]** Since under these conditions [label]<[HLA] and IC<sub>50</sub>≥[HLA], the measured IC<sub>50</sub> values are reasonable approximations of the true K<sub>D</sub> values. Peptide inhibitors are typically tested at concentrations ranging from 120  $\mu$ g/ml to 1.2 ng/ml, and are tested in two to four completely independent experiments. To allow comparison of the data obtained in different experiments, a relative binding figure is calculated for each peptide by dividing the IC<sub>50</sub> of a positive control for inhibition by the IC<sub>50</sub> for each tested peptide (typically unlabeled versions of the radiolabeled probe peptide). For inter-experiment comparisons, relative binding values are compiled. These values can subsequently be converted back into IC<sub>50</sub> nM values by dividing the IC<sub>50</sub> nM of the positive controls for inhibition by the relative binding of the peptide of interest. This method of data compilation has proven to be the most accurate and consistent for comparing peptides that have been tested on different days, or with different lots of purified MHC.

- [00353] Because the antibody used for HLA-DR purification (LB3.1) is  $\alpha$ -chain specific,  $\beta_1$  molecules are not separated from  $\beta_3$  (and/or  $\beta_4$  and  $\beta_5$ ) molecules. The  $\beta_1$  specificity of the binding assay is obvious in the cases of DRB1\*0101 (DR1), DRB1\*0802 (DR8w2), and DRB1\*0803 (DR8w3), where no  $\beta_3$  is expressed. It has also been demonstrated for DRB1\*0301 (DR3) and DRB3\*0101 (DR52a), DRB1\*0401 (DR4w4), DRB1\*0404 (DR4w14), DRB1\*0405 (DR4w15), DRB1\*1101 (DR5), DRB1\*1201 (DR5w12), DRB1\*1302 (DR6w19) and DRB1\*0701 (DR7). The problem of  $\beta$  chain specificity for DRB1\*1501 (DR2w2 $\beta_1$ ), DRB5\*0101 (DR2w2 $\beta_2$ ), DRB1\*1601 (DR2w21 $\beta_1$ ), DRB5\*0201 (DR51Dw21), and DRB4\*0101 (DRw53) assays is circumvented by the use of fibroblasts. Development and validation of assays with regard to DR $\beta$  molecule specificity have been described previously (*see, e.g., Southwood et al., J. Immunol.* 160:3363-3373, 1998).
- [00354] Binding assays as outlined above may be used to analyze supermotif and/or motif-bearing epitopes.

## EXAMPLE 2. RECOGNITION OF VARIANT PEPTIDES BY CTL DERIVED FROM DNA IMMUNIZATION

- [00355] Variants corresponding to five HLA-A2 and -A3 restricted epitopes from 167 HIV variantst were identified and synthesized. These represented all the complete sequences in the Los Alamos database at the time (116 strains), as well as 51 complete clade C sequences from Botswana, and included 22 subtype B and 62 subtype C sequences. These peptides were then characterized with regard to MHC binding, variant distribution, and immunogenicity. To measure immunogenicity, HLA-A2/K<sup>b</sup> or HLA-A11/K<sup>b</sup> transgenic mice were immunized with the epitopes encoded in a DNA based format (). Eleven days after immunization, splenocytes were restimulated with either the epitope corresponding to the epitope encoded by the DNA (parent) or each of the variant peptides. After 6 days in culture, IFN- $\gamma$  secretion was measured in response to the peptide used to stimulate each culture.
- [00356] The data for these epitopes are shown in Figure 1. The HLA-A2-restricted epitope corresponding to the Env 134 epitope (KLTPLCVTL, SEQ ID NO: 9; Figure 1A) used as the immunogen was the form observed most often (134/167). All single anchor variants

were recognized to approximately the same extent as the parent peptide. Many of the single non-anchor variants (9/13) were also recognized within 10-fold of the parent peptide. Conservative substitutions (R and Q for K; see Table 4) at position 1 (P1) were tolerated, while the non-conservative substitution (E for K; see Table 4) lowered binding and eliminated recognition. Three P4 variants were observed. Two of these (F or S for P) were recognized within 10-fold of the recognition of the parent peptide, while one substitution (Q for P) completely eliminated recognition. The binding for these peptides was not significantly different from the parent peptide, indicating that this residue may be involved in TCR recognition. Both the conservative (F for L) and non-conservative (R for L) substitutions seen at P5 completely abrogated recognition, indicating that this residue is important in TCR recognition. Finally, one substitution at P8 (I for V), and four substitutions at P9 show little effect on recognition. None of the variants with multiple substitutions were recognized, although this may be due to the poor binding of these peptides.

**[00357]** The Gag 386 sequence utilized as the immunogen was the second most common form (VLAEAMSQV, SEQ ID NO: 10), present in 54 strains (Figure 1B). The most prevalent variant, differing by a single tolerated C terminal anchor residue (V to A; 67 strains), was recognized equally to the parent epitope by CTL raised against the parent, as were the remaining single-anchor variants. Single substitutions were also tolerated at the non-anchor positions, P1 (I for V) and P8 (R, K, or H for Q). Only the P7 variant (G for S), probably a TCR contact residue, was not recognized.

**[00358]** Many of the multiple variants for Gag 386 were also recognized by CTL raised against the parent peptide. All the variants with multiple changes combined a change of V to A or T at the C terminus with 1-3 additional substitutions. Two variants with N terminal changes (V to A or I) were observed. The non-conservative A substitution was not recognized, while the conservative I substitution was. A double variant with a conservative substitution at P3 (A to G) was not recognized, implicating P3 in TCR recognition. Double variants with conservative changes at position 8 (Q to R, K, or H) were not well recognized, although the variants with single changes at the same positions were recognized. The variant combining a non-conservative A residue at position 8 with A at the C terminus was recognized as well as the parent. Equally surprising was the observation that all the variants with 3 or 4 substitutions were recognized within 10-fold of the parent peptide.

[00359] The parent form of the HLA-A2-restricted epitope, Vpr 62 (RILQQLLFI, SEQ ID NO: 11; Figure 1C) was the most common form observed (86/167). Seven well-tolerated single anchor substitutions, 4 P2 and 3 C terminal, were also observed, accounting for most of the remaining variants (47/167). Single substitutions were, in general, also well tolerated. The single exception was the non-conservative substitution (P for L) at P6, while an M for L substitution at the same site was well tolerated. Binding was not affected for either variant, indicating that the reduction in activity is due to a change in a contact residue. Most variants with multiple changes also showed recognition to approximately the same extent as the parent. Several variants however did show reduced recognition. The variant with changes at both anchors (I to T at P2 and I to T at P9) had reduced binding ( $IC_{50}$  of 9700), and recognition of the peptide was reduced, although not lost completely. Two variants with Q to H changes at P5, in combination with anchor residue changes (I to M at P2 and I to A at P9), exhibited greatly reduced recognition although binding was not affected. Other changes at P5 (Q to R or L at P5) reduced recognition only slightly.

[00360] The HLA-A3/11-restricted epitope, Pol 98 (Figure 1D), represented the most diverse epitope in terms of the number of variant epitopes identified. The peptide encoded in the DNA was represented in only 18 out of 167 strains. Approximately a third of the peptides identified at that position (49 out of 167) did not have recognizable A3/A11 motifs. The most common variant (30 strains) differed from the parent peptide at 3 residues (VSIKVGGQIK, SEQ ID NO: 12), but was recognized within 10-fold of the parent peptide. Two variants with conservative changes at anchor residues were both recognized, although the T to A substitution at P2 resulted in a 10-fold reduction in recognition of the variant peptide. All peptides with single changes in non-anchor positions were also recognized, although the P5 variant (G to E) exhibited a decrease in recognition. As the binding was not affected, this probably indicates involvement in T cell recognition.

[00361] Peptides with two changes showed mixed results. In general, peptides with a V substitution at position 3, in combination with another substitution were recognized to the same extent as the corresponding single substitution, indicating the V substitution was tolerated well and is not a TCR contact residue. Combinations including the P2 anchor residue (T to A or N) were not recognized, although the binding of these peptides was also low. Variants with 3 substitutions were generally not recognized well. Two exceptions

with very conservative substitutions were noted (Figure 1D). CTL were unable to recognize peptides with four or more substitutions.

[00362] The HLA-A3/11- restricted Env 47 epitope (Figure 1E; VTVYYGVPVWK, SEQ ID NO: 13) was highly conserved, with only 9 variants identified. The most common form observed was the parent peptide (99 strains), while the second most common form, a single anchor substitution observed in 40 strains, was recognized to the same extent as the parent. All the variants were recognized within 10-fold of the parent epitope.

[00363] Taken together, these data show trends towards promiscuous recognition of variant peptides by CTL generated from immunization with a single peptide. In general, changes that disrupted binding also decreased recognition. Recognition was also affected by the position of the change, with potential TCR contact residues (P3-7) exerting a greater effect on recognition than other residues. In general, conservative residue changes were more widely tolerated than were non-conservative changes. Recognition was also dependent on the number of changes, with progressively lower recognition with a greater number of changes.

[00364] **Recognition after multiple restimulations** The observed recognition of variant peptides by CTL raised against the parent peptide might be due to either promiscuous recognition at the level of a single TCR or simply a mixture of TCRs against the immunizing peptide which are each able to recognize subtly different peptides. To distinguish between these two possibilities, Env 134- or Gag 386-specific T cell lines were generated by stimulating five times with the immunizing peptide, and then tested for recognition of a partial panel of variant peptides. These T cell lines were also characterized for V $\beta$  TCR usage against a panel of antibodies predicted to react with the TCR of the mouse strains utilized for these experiments.

[00365] The data for these peptide-specific lines are shown in Table 5. Because the SU is a measure of the number of cells needed to secrete a defined amount of IFN- $\gamma$ , a higher SU value would correspond to an enrichment of IFN- $\gamma$  producing cells. A comparison of one and five peptide stimulations indeed shows an enrichment of CTL specific for the immunizing peptide for both of the peptide lines generated (Table 5A and 5B, first line). The Gag 386 line (Table 5A) also demonstrated increased recognition of all the variant peptides measured except one peptide (ILAEAMSKA, SEQ ID NO: 14) that was never



recognized. The Env 134 line also demonstrated enrichment for CTL able to recognize several of the variant peptides (Table 5B).

[00366] To further characterize these lines, we examined them for V $\beta$  usage, utilizing a panel of commercially available antibodies available for mouse TCR V $\beta$  2-14. To determine background levels for the various TCR V $\beta$  molecules, primary splenocytes from mice that had been immunized with EP HIV-1090 were also examined. The results for the Gag 386 line are shown in Figure 2A. After a single stimulation with the parent peptide, the Gag 386 line showed a mixture of TCR positive populations, including V $\beta$  3, 5, and 14. After 5 stimulations, those populations had been reduced to background levels, and approximately 50% of the CD8<sup>+</sup> cells expressed the V $\beta$  6 TCR. The Env 134 line showed a similar pattern of multiple TCR positive populations after a single round of stimulation with reduction to background levels after 5 stimulations (data not shown). However, no single V $\beta$  usage significantly above background could be demonstrated, probably due to lack of the relevant TCR V $\beta$  antibody.

[00367] Both lines were also characterized with regard to the affinity of certain of the variant peptides by titrating the variant peptides examined above (Table 5A and 5B). The data for both the Gag 386 and Env 134 lines are shown in Figure 2B. For the Gag 386 line, the parent peptide along with two single anchor variants (VLA E A M S Q I, SEQ ID NO: 15, and VLA E A M S Q A, SEQ ID NO: 16) showed the highest affinity. Four other peptides demonstrated lower affinity, but still produced IFN- $\gamma$  in response to higher peptide concentrations. A single peptide (I L A E A M S K A, SEQ ID NO: 14) was not recognized.

[00368] As expected, the parent peptide, which was used to generate the Env 134 line, showed the highest affinity for the TCR. The other 2 variant peptides, K I T P L C V T L (SEQ ID NO: 18) and Q L T P L C V T L (SEQ ID NO: 19), also demonstrated higher affinity, but reduced from the parent peptide by approximately 10-fold and 100-fold, respectively. It was notable that only at the highest peptide concentration examined (1  $\mu$ g/ml) was any IFN- $\gamma$  secretion detected for five of the peptides (Q I T P L C V T L, SEQ ID NO: 20, E L T P L C V T L, SEQ ID NO: 21, K L T P F C V T L, SEQ ID NO: 22, K L T P L C V I L, SEQ ID NO: 23, and K L T P L C V P L, SEQ ID NO: 24). These five peptides showed little or no enrichment of CTL able to recognize them, and exhibited the lowest activity as measured by SU after five restimulations (see Table 5B).

[00369] In summary, these cell lines seem to consist of a narrow, possibly single, TCR population. This TCR population recognizes the parent peptide with the highest affinity,

but is also able to recognize a number of other variant peptides with equal or lesser affinity.

**[00370] Recognition of variant peptides by CTL derived from an HIV infected patient.**

**[00371]** To determine if the same immunological conservation was observed in natural infections, we identified an HIV-infected individual expressing the HLA-A3 allele. The HIV strain and subtype with which this patient was infected is unknown. We had previously shown that T cells from this individual responded to the HLA-A3 restricted epitopes Pol 98 and Env 47. PBL from this patient were examined in an ELISPOT assay to determine if they also showed the capacity for broad cross-reactivity. The data are shown in Figure 3. Although the actual peptide represented in the HIV strain with which this individual is infected is unknown, we observed recognition of a large number of the variant peptides for both Pol 98 (Figure 3A) and Env 47 (Figure 3B). The recognition patterns were remarkably similar for the mouse and patient data (compare Figure 1 and Figure 3), although the mouse expressed a transgene for HLA-A11 and the patient was HLA-A3.

**[00372] Prediction of Immunological Conservation.** We had observed that the variant peptides that were recognized by CTL raised against the parent epitope had amino acid substitutions that followed previous observations. For example, the anchor residue changes that were tolerated in the variant peptides were also described as anchors that to define the respective HLA supertypes (). In general, conservative substitutions were tolerated at non-anchor residues, while non-conservative substitutions were less well tolerated. These followed closely the prediction model used to identify heteroclitic analogs (Tangri et al).

**[00373]** Based on these observations, we designed a computer program to predict immunological conservation. For anchor positions, this program utilized the conserved anchor residues described for the A2, A3, and B7 supertypes. For non-anchor positions only conservative substitutions, as defined in Tangri et.al. (), were allowed. All substitutions at non-anchor positions were analyzed independently and all conservative substitutions were allowed regardless of the number of substitutions. Finally, the position of the substitution was not factored into analysis. Each variant was compared with the parent epitope, and its ability to be recognized was predicted as either positive or negative.

[00374] The first sets of epitopes to be evaluated by this program were the five HIV epitopes and variants previously described. For the Env 134 epitope, the program predicted that 13 of the variant peptides should be immunologically conserved, while 6 should not be recognized. Comparison of the observed immunological data with the prediction showed that the program predicted correctly for 14 of the peptides and incorrectly for 5. Of the incorrect predictions, in two cases the program predicted negative results for peptides that were recognized, while in 3 cases the program predicted positive results for peptides that were not recognized. A similar analysis was performed for all five peptides. Of 101 total variant peptides, 68 were correctly identified (67%). The discordant data were fairly evenly split between peptides incorrectly predicted negative (15) and those incorrectly predicted positive (18).

[00375] As noted previously, the more substitutions present in a variant peptide, the lower the likelihood of its immunogenicity. Since the prediction program treated all substitutions independently, and did not take into account the number of substitutions, we hypothesized that prediction of single substitutions would be more accurate. Indeed, the immunogenicity of 38 of 47 single substitution variants (80%) was correctly predicted.

[00376] With the limitations of the program in mind, it is useful to predict the recognition of the variants for a package of HLA-A2, -A3, and -B7 supertype epitopes. These epitopes had been identified as being well conserved in Clade B variants. When comparing the conservation of this group of epitopes based on sequence identity versus immunological conservation, it is interesting to note that the predicted recognition gains taking into account immunological conservation are significant (Table 6).

[00377] This particular group of 21 epitopes was selected based on their identity conservation in Clade B HIV sequences, with conservation across HIV clades as a secondary consideration. Because of this criteria, the form of epitope chosen as the parent peptide was not the most common variant (e.g. Gag 386, Gag 271, Pol 98). In some cases (e.g., see Gag 386 data), the “parent” epitope and the most common variant were recognized to the same extent. However, in some cases the selection of epitope to include as the “parent” epitope was predicted to make a difference in the immunological conservation. An example of this was the Gag 271 epitope (Figure 4). The variant most commonly seen in clade B sequences was the MTNNPPIPV form (SEQ ID NO: 25), while the most common form of the epitope was MTSNPPIPV (SEQ ID NO: 26). Not all amino acids are considered equal to each other in their ability to substitute (Tangri). For example,

asparagine (N) is considered a conservative substitution for serine (S), while the opposite substitution is only considered semi-conserved. When the program calculated immunological conservation using the MTNNPPIPV peptide (SEQ ID NO: 25) as the parent peptide, only two variants were predicted to be immunogenic. However, when the immunological conservation was predicted using the MTSNPPIPV peptide (SEQ ID NO: 26), most of the variants were predicted to be recognized (Figure 4). This prediction was tested using HLA-A2 transgenic mice. The results show that if the MTSNPPIPV form (SEQ ID NO: 26) of the peptide was utilized in vaccines, approximately 152 of 167 variants would be recognized, while if the MTNNPPIPV form (SEQ ID NO: 25) of the epitope was utilized, only 39 of 167 variants would be recognized. This has important implications in epitope selection for vaccine development, and epitope performance can be predicted.

### EXAMPLE 3. A PADRE® MOLECULE AS A HELPER EPITOPE FOR ENHANCEMENT OF CTL INDUCTION

[00378] There is increasing evidence that HTL activity is critical for the induction of long-lasting CTL responses (Livingston *et al. J. Immunol* 162:3088-3095 (1999); Walter *et al., New Engl. J. Med.* 333:1038-1044 (1995); Hu *et al., J. Exp. Med.* 177:1681-1690 (1993)). Therefore, one or more peptides that bind to HLA class II molecules and stimulate HTLs can be used in accordance with the invention. Accordingly, a preferred embodiment of a vaccine includes a molecule from the PADRE® family of universal T helper cell epitopes (HTL) that target most DR molecules in a manner designed to stimulate helper T cells. For instance, a pan-DR-binding epitope peptide having the formula: aKXVAAZTLKAAa, where "X" is either cyclohexylalanine, phenylalanine, or tyrosine; "Z" is either tryptophan, tyrosine, histidine or asparagine; and "a" is either D-alanine or L-alanine (SEQ ID NO:29), has been found to bind to most HLA-DR alleles, and to stimulate the response of T helper lymphocytes from most individuals, regardless of their HLA type.

[00379] A particularly preferred PADRE® molecule is a synthetic peptide, aKXVAAWTLKAAa SEQ ID NO: 28 (a = D-alanine, X = cyclohexylalanine), containing non-natural amino acids, specifically engineered to maximize both HLA-DR binding capacity and induction of T cell immune responses.

[00380] Alternative preferred PADRE<sup>®</sup> molecules are the peptides, aKFVAAWTLKAAa (SEQ ID NO: 29), aKYVAAWTLKAAa (SEQ ID NO: 30), aKFVAAWTLKAAa (SEQ ID NO: 31), aKXVAAWTLKAAa (SEQ ID NO: 32), aKYVAAWTLKAAa (SEQ ID NO: 33), aKFVAAHTLKAAa (SEQ ID NO: 34), aKXVAAHTLKAAa (SEQ ID NO: 35), aKYVAAHTLKAAa (SEQ ID NO: 36), aKFVAAANTLKAAa (SEQ ID NO: 37), aKXVAAANTLKAAa (SEQ ID NO: 38), aKYVAAANTLKAAa (SEQ ID NO: 39), AKXVAAWTLKAAA (SEQ ID NO: [[30]] 40), AKFVAAWTLKAAA (SEQ ID NO: [[31]] 41), AKYVAAWTLKAAA (SEQ ID NO: [[32]] 42), AKFVAAWTLKAAA (SEQ ID NO: [[33]] 43), AKXVAAWTLKAAA (SEQ ID NO: [[34]] 44), AKYVAAWTLKAAA (SEQ ID NO: [[35]] 45), AKFVAAHTLKAAA (SEQ ID NO: [[36]] 46), AKXVAAHTLKAAA (SEQ ID NO: [[37]] 47), AKYVAAHTLKAAA (SEQ ID NO: [[38]] 48), AKFVAAANTLKAAA (SEQ ID NO: [[39]] 49), AKXVAAANTLKAAA (SEQ ID NO: [[40]] 50), AKYVAAANTLKAAA (SEQ ID NO: [[41]] 51) (a = D-alanine, X = cyclohexylalanine).

[00381] In a preferred embodiment, the PADRE<sup>®</sup> peptide is amidated. For example, a particularly preferred amidated embodiment of a PADRE<sup>®</sup> molecule is conventionally written aKXVAAWTLKAAa-NH<sub>2</sub>.

[00382] Competitive inhibition assays with purified HLA-DR molecules demonstrated that the PADRE<sup>®</sup> molecule aKXVAAWTLKAAa-NH<sub>2</sub> binds with high or intermediate affinity (IC<sub>50</sub> ≤ 1,000 nM) to 15 out of 16 of the most prevalent HLA-DR molecules ((Kawashima *et al.*, *Human Immunology* 59:1-14 (1998); Alexander *et al.*, *Immunity* 1:751-761 (1994)). A comparison of the DR binding capacity of PADRE<sup>®</sup> and tetanus toxoid (TT) peptide 830-843, a "universal" epitope has been published (Panina-Bordignon *et al.*, *Eur. J. Immunology* 19:2237-2242 (1989)). The TT 830-843 peptide bound to only seven of 16 DR molecules tested, while PADRE<sup>®</sup> bound 15 of 16. At least 1 of the 15 DR molecules that bind PADRE<sup>®</sup> is predicted to be present in >95% of all humans. Therefore, this PADRE<sup>®</sup> molecule is anticipated to induce an HTL response in virtually all patients, despite the extensive polymorphism of HLA-DR molecules in the human population.

[00383] PADRE<sup>®</sup> has been specifically engineered for optimal immunogenicity for human T cells. Representative data from *in vitro* primary immunizations of normal human T cells with TT 830-843 antigen and the PADRE<sup>®</sup> molecule aKXVAAWTLKAAa-NH<sub>2</sub> are shown in Figure 1. Peripheral blood mononuclear cells (PBMC) from three normal donors

were stimulated with the peptides *in vitro*. Following the third round of stimulation, it was observed that PADRE<sup>®</sup> generated significant primary T cell responses for all three donors as measured in a standard T cell proliferation assay. With the PADRE<sup>®</sup> peptide, the 10,000 cpm proliferation level was generally reached with 10 to 100 ng/ml of antigen. In contrast, TT 830-843 antigen generated responses for only 2 out of 3 of the individuals tested. Responses approaching the 10,000 cpm range were reached with about 10,000 ng/ml of antigen. In this respect, it was noted that PADRE<sup>®</sup> was, on a molar basis, about 100-fold more potent than TT 830-843 antigen for activation of T cell responses.

[00384] Early data from a phase I/II investigator-sponsored trial, conducted at the University of Leiden (C.J.M. Melief), support the principle that the PADRE<sup>®</sup> molecule aKXVAAWTLKAAa (SEQ ID NO: 28), possibly the amidated aKXVAAWTLKAAa - NH<sub>2</sub>, is highly immunogenic in humans (Ressing *et al.*, J. Immunother. 23(2):255-66 (2000)). In this trial, a PADRE<sup>®</sup> molecule was co-emulsified with various human papilloma virus (HPV)-derived CTL epitopes and was injected into patients with recurrent or residual cervical carcinoma. However, because of the late stage of carcinoma with the study patients, it was expected that these patients were immunocompromised. The patients' immunocompromised status was demonstrated by their low frequency of influenza virus-specific CTL, reduced levels of CD3 expression, and low incidence of proliferative recall responses after *in vitro* stimulation with conventional antigens. Thus, no efficacy was anticipated in the University of Leiden trial, rather the goal of that trial was essentially to evaluate safety. Safety was, in fact, demonstrated. In addition to a favorable safety profile, PADRE<sup>®</sup> T cell reactivity was detected in four of 12 patients (Figure 2) in spite of the reduced immune competence of these patients.

[00385] Thus, the PADRE<sup>®</sup> peptide component(s) of the vaccine bind with broad specificity to multiple allelic forms of HLA-DR molecules. Moreover, PADRE<sup>®</sup> peptide component(s) bind with high affinity (IC<sub>50</sub> ≤ 1000 nM), i.e., at a level of affinity correlated with being immunogenic for HLA Class II restricted T cells. The *in vivo* administration of PADRE<sup>®</sup> peptide(s) stimulates the proliferation of HTL in normal humans as well as patient populations.

[00386] One or more PADRE<sup>®</sup> peptide(s) may be included in a composition, e.g., a vaccine, comprising one or more peptides, either as an individual peptide(s), fused to one or more variant peptides, or both.

#### EXAMPLE 4. CTL RECOGNITION OF ENDOGENOUS PROCESSED ANTIGENS AFTER PRIMING

- [00387] This example determines that CTL induced by native or analoged peptide epitopes recognize endogenously synthesized, *i.e.*, native antigens.
- [00388] Effector cells isolated from transgenic mice that are immunized with peptide epitopes are re-stimulated *in vitro* using peptide-coated stimulator cells. Six days later, effector cells are assayed for cytotoxicity and the cell lines that contain peptide-specific cytotoxic activity are further re-stimulated. An additional six days later, these cell lines are tested for cytotoxic activity on  $^{51}\text{Cr}$  labeled Jurkat-A2.1/K<sup>b</sup> target cells in the absence or presence of peptide, and also tested on  $^{51}\text{Cr}$  labeled target cells bearing the endogenously synthesized antigen, *i.e.* cells that are stably transfected with HIV expression vectors.
- [00389] The result will demonstrate that CTL lines obtained from animals primed with peptide epitope recognize endogenously synthesized HIV antigen. The choice of transgenic mouse model to be used for such an analysis depends upon the epitope(s) that is being evaluated. In addition to HLA-A\*0201/K<sup>b</sup> transgenic mice, several other transgenic mouse models including mice with human A11, which may also be used to evaluate A3 epitopes, and B7 alleles have been characterized and others (*e.g.*, transgenic mice for HLA-A1 and A24) are being developed. HLA-DR1 and HLA-DR3 mouse models have also been developed, which may be used to evaluate HTL epitopes.

#### EXAMPLE 5. ACTIVITY OF CTL-HTL CONJUGATED EPITOPES IN TRANSGENIC MICE

- [00390] This example illustrates the induction of CTLs and HTLs in transgenic mice by use of a HIV CTL/HTL peptide conjugate whereby the vaccine composition comprises peptides administered to an HIV-infected patient or an individual at risk for HIV. The peptide composition can comprise multiple CTL and/or HTL epitopes. This analysis demonstrates enhanced immunogenicity that can be achieved by inclusion of one or more HTL epitopes in a vaccine composition. Such a peptide composition can comprise an HTL epitope conjugated to a preferred CTL epitope containing, for example, at least one CTL epitope, or an analog of that epitope. The peptides may be lipidated, if desired.

- [00391] Immunization procedures: Immunization of transgenic mice is performed as described (Alexander *et al.*, *J. Immunol.* 159:4753-4761, 1997). For example, A2/K<sup>b</sup> mice, which are transgenic for the human HLA A2.1 allele and are useful for the assessment of the immunogenicity of HLA-A\*0201 motif- or HLA-A2 supermotif-bearing epitopes, are primed subcutaneously (base of the tail) with a 0.1 ml of peptide in Incomplete Freund's Adjuvant, or if the peptide composition is a lipidated CTL/HTL conjugate, in DMSO/saline or if the peptide composition is a polypeptide, in PBS or Incomplete Freund's Adjuvant. Seven days after priming, splenocytes obtained from these animals are restimulated with syngenic irradiated LPS-activated lymphoblasts coated with peptide.
- [00392] Cell lines: Target cells for peptide-specific cytotoxicity assays are Jurkat cells transfected with the HLA-A2.1/K<sup>b</sup> chimeric gene (e.g., Vitiello *et al.*, *J. Exp. Med.* 173:1007, 1991).
- [00393] *In vitro* CTL activation: One week after priming, spleen cells ( $30 \times 10^6$  cells/flask) are co-cultured at 37°C with syngeneic, irradiated (3000 rads), peptide coated lymphoblasts ( $10 \times 10^6$  cells/flask) in 10 ml of culture medium/T25 flask. After six days, effector cells are harvested and assayed for cytotoxic activity.
- [00394] Assay for cytotoxic activity: Target cells ( $1.0$  to  $1.5 \times 10^6$ ) are incubated at 37°C in the presence of 200  $\mu$ l of  $^{51}\text{Cr}$ . After 60 minutes, cells are washed three times and resuspended in R10 medium. Peptide is added where required at a concentration of 1  $\mu\text{g/ml}$ . For the assay,  $10^4$   $^{51}\text{Cr}$ -labeled target cells are added to different concentrations of effector cells (final volume of 200  $\mu$ l) in U-bottom 96-well plates. After a 6 hour incubation period at 37°C, a 0.1 ml aliquot of supernatant is removed from each well and radioactivity is determined in a Micromedic automatic gamma counter. The percent specific lysis is determined by the formula: percent specific release =  $100 \times (\text{experimental release} - \text{spontaneous release}) / (\text{maximum release} - \text{spontaneous release})$ . To facilitate comparison between separate CTL assays run under the same conditions, %  $^{51}\text{Cr}$  release data is expressed as lytic units/ $10^6$  cells. One lytic unit is arbitrarily defined as the number of effector cells required to achieve 30% lysis of 10,000 target cells in a 6 hour  $^{51}\text{Cr}$  release assay. To obtain specific lytic units/ $10^6$ , the lytic units/ $10^6$  obtained in the absence of peptide is subtracted from the lytic units/ $10^6$  obtained in the presence of peptide. For example, if 30%  $^{51}\text{Cr}$  release is obtained at the effector (E): target (T) ratio of 50:1 (i.e.,  $5 \times 10^5$  effector cells for 10,000 targets) in the absence of peptide and 5:1 (i.e.,  $5 \times 10^4$



effector cells for 10,000 targets) in the presence of peptide, the specific lytic units would be:  $[(1/50,000)-(1/500,000)] \times 10^6 = 18 \text{ LU}$ .

[00395] The results are analyzed to assess the magnitude of the CTL responses of animals injected with the immunogenic CTL/HTL conjugate vaccine preparation and are compared to the magnitude of the CTL response achieved using the CTL epitope as outlined in above. Analyses similar to this may be performed to evaluate the immunogenicity of peptide conjugates containing multiple CTL epitopes and/or multiple HTL epitopes. In accordance with these procedures it is found that a CTL response is induced, and concomitantly that an HTL response is induced upon administration of such compositions.

#### EXAMPLE 6. SELECTION OF CTL AND HTL EPITOPES FOR INCLUSION IN AN HIV-SPECIFIC VACCINE.

[00396] This example illustrates the procedure for the selection of peptide epitopes for vaccine compositions of the invention. The peptides in the composition can be in the form of a nucleic acid sequence, either single or one or more sequences (*i.e.*, minigene) that encodes peptide(s), or can be single and/or polypeptidic peptides.

[00397] The following principles are utilized when selecting an array of epitopes for inclusion in a vaccine composition. Each of the following principles is balanced in order to make the selection.

[00398] Epitopes are selected which, upon administration, mimic immune responses that correlate with virus clearance. For example, if it has been observed that patients who clear HIV generate an immune response to at least 3 epitopes on at least one HIV antigen, then 3-4 epitopes should be included for HLA class I. A similar rationale is used to determine HLA class II epitopes.

[00399] When selecting an array of HIV epitopes, it is preferred that at least some of the epitopes are derived from early and late proteins. The early proteins of HIV are expressed when the virus is replicating, either following acute or dormant infection. Therefore, it is particularly preferred to use epitopes from early stage proteins to alleviate disease manifestations at the earliest stage possible.

[00400] Epitopes are often selected that have a binding affinity of an  $IC_{50}$  of 500 nM or less for an HLA class I molecule, or for class II, an  $IC_{50}$  of 1000 nM or less.

- [00401] Sufficient supermotif bearing peptides, or a sufficient array of allele-specific motif bearing peptides, are selected to give broad population coverage. For example, epitopes are selected to provide at least 80% population coverage. A Monte Carlo analysis, a statistical evaluation known in the art, can be employed to assess breadth, or redundancy, of population coverage.
- [00402] When creating a polyepitopic compositions, *e.g.* a minigene, it is typically desirable to generate the smallest peptide possible that encompasses the epitopes of interest. The principles employed are similar, if not the same, as those employed when selecting a peptide comprising nested epitopes.
- [00403] In cases where the sequences of multiple variants of the same target protein are available, potential peptide epitopes can also be selected on the basis of their conservancy. For example, a criterion for conservancy may define that the entire sequence of an HLA class I binding peptide or the entire 9-mer core of a class II binding peptide be conserved in a designated percentage of the sequences evaluated for a specific protein antigen.
- [00404] Peptide epitopes for inclusion in vaccine compositions are, for example, selected from those listed in Tables 6-9 or Figures 1A-4. A vaccine composition comprised of selected peptides, when administered, is safe, efficacious, and elicits an immune response similar in magnitude of an immune response that clears an acute HIV infection.

#### EXAMPLE 7. CONSTRUCTION OF MINIGENE MULTI-EPITOPE DNA PLASMIDS

- [00405] This example provides general guidance for the construction of a minigene expression plasmid. Minigene plasmids may, of course, contain various configurations of CTL and/or HTL epitopes or epitope analogs as described herein. Expression plasmids have been constructed and evaluated as described, for example, in co-pending U.S.S.N. 09/311,784 filed 5/13/99 and in Ishioka *et al.*, *J. Immunol.* 162:3915-3925, 1999. An example of such a plasmid for the expression of HIV epitopes is shown in Figure 2, which illustrates the orientation of HIV peptide epitopes in a minigene construct.
- [00406] A minigene expression plasmid typically includes multiple CTL and HTL peptide epitopes. In the present example, HLA-A2, -A3, -B7 supermotif-bearing peptide epitopes and HLA-A1 and -A24 motif-bearing peptide epitopes are used in conjunction with DR supermotif-bearing epitopes and/or DR3 epitopes (Figure 2). Preferred epitopes are

identified, for example, in Tables 6-9 and Figures 1A-4. HLA class I supermotif or motif-bearing peptide epitopes derived from multiple HIV antigens, are selected such that multiple supermotifs/motifs are represented to ensure broad population coverage. Similarly, HLA class II epitopes are selected from multiple HIV antigens to provide broad population coverage, *i.e.* both HLA DR-1-4-7 supermotif-bearing epitopes and HLA DR-3 motif-bearing epitopes are selected for inclusion in the minigene construct. The selected CTL and HTL epitopes are then incorporated into a minigene for expression in an expression vector.

[00407] Such a construct may additionally include sequences that direct the HTL epitopes to the endoplasmic reticulum. For example, the Ii protein may be fused to one or more HTL epitopes as described in co-pending application U.S.S.N. 09/311,784 filed 5/13/99, wherein the CLIP sequence of the Ii protein is removed and replaced with an HLA class II epitope sequence so that HLA class II epitope is directed to the endoplasmic reticulum, where the epitope binds to an HLA class II molecules.

[00408] This example illustrates the methods to be used for construction of a minigene-bearing expression plasmid. Other expression vectors that may be used for minigene compositions are available and known to those of skill in the art.

[00409] The minigene DNA plasmid contains a consensus Kozak sequence and a consensus murine kappa Ig-light chain signal sequence followed by CTL and/or HTL epitopes selected in accordance with principles disclosed herein. The construct can also include, for example, The sequence encodes an open reading frame fused to the Myc and His antibody epitope tag coded for by the pcDNA 3.1 Myc-His vector.

[00410] Overlapping oligonucleotides, for example eight oligonucleotides, averaging approximately 70 nucleotides in length with 15 nucleotide overlaps, are synthesized and HPLC-purified. The oligonucleotides encode the selected peptide epitopes as well as appropriate linker nucleotides, Kozak sequence, and signal sequence. The final multiepitope minigene is assembled by extending the overlapping oligonucleotides in three sets of reactions using PCR. A Perkin/Elmer 9600 PCR machine is used and a total of 30 cycles are performed using the following conditions: 95°C for 15 sec, annealing temperature (5° below the lowest calculated T<sub>m</sub> of each primer pair) for 30 sec, and 72°C for 1 min.

[00411] For the first PCR reaction, 5 µg of each of two oligonucleotides are annealed and extended: Oligonucleotides 1+2, 3+4, 5+6, and 7+8 are combined in 100 µl reactions

containing *Pfu* polymerase buffer (1x= 10 mM KCL, 10 mM (NH<sub>4</sub>)<sub>2</sub>SO<sub>4</sub>, 20 mM Tris-chloride, pH 8.75, 2 mM MgSO<sub>4</sub>, 0.1% Triton X-100, 100 µg/ml BSA), 0.25 mM each dNTP, and 2.5 U of *Pfu* polymerase. The full-length dimer products are gel-purified, and two reactions containing the product of 1+2 and 3+4, and the product of 5+6 and 7+8 are mixed, annealed, and extended for 10 cycles. Half of the two reactions are then mixed, and 5 cycles of annealing and extension carried out before flanking primers are added to amplify the full length product for 25 additional cycles. The full-length product is gel-purified and cloned into pCR-blunt (Invitrogen) and individual clones are screened by sequencing.

#### EXAMPLE 8. THE PLASMID CONSTRUCT AND THE DEGREE TO WHICH IT INDUCES IMMUNOGENICITY.

[00412] The degree to which a plasmid construct, for example a plasmid constructed in accordance as above is able to induce immunogenicity can be evaluated *in vitro* by testing for epitope presentation by APC following transduction or transfection of the APC with an epitope-expressing nucleic acid construct. Such a study determines “antigenicity” and allows the use of human APC. The assay determines the ability of the epitope to be presented by the APC in a context that is recognized by a T cell by quantifying the density of epitope-HLA class I complexes on the cell surface. Quantitation can be performed by directly measuring the amount of peptide eluted from the APC (*see, e.g.,* Sijts *et al., J. Immunol.* 156:683-692, 1996; Demotz *et al., Nature* 342:682-684, 1989); or the number of peptide-HLA class I complexes can be estimated by measuring the amount of lysis or lymphokine release induced by infected or transfected target cells, and then determining the concentration of peptide necessary to obtained equivalent levels of lysis or lymphokine release (*see, e.g.,* Kageyama *et al., J. Immunol.* 154:567-576, 1995).

[00413] Alternatively, immunogenicity can be evaluated through *in vivo* injections into mice and subsequent *in vitro* assessment of CTL and HTL activity, which are analysed using cytotoxicity and proliferation assays, respectively, as detailed *e.g.,* in copending U.S.S.N. 09/311,784 filed 5/13/99 and Alexander *et al., Immunity* 1:751-761, 1994.

[00414] For example, to assess the capacity of a DNA minigene construct (*e.g.,* a pMin minigene construct generated as described in U.S.S.N. 09/311,784) containing at least one

HLA-A2 supermotif peptide to induce CTLs *in vivo*, HLA-A2.1/K<sup>b</sup> transgenic mice, for example, are immunized intramuscularly with 100 µg of naked cDNA. As a means of comparing the level of CTLs induced by cDNA immunization, a control group of animals is also immunized with an actual peptide composition that comprises multiple epitopes synthesized as a single polypeptide as they would be encoded by the minigene.

[00415] Splenocytes from immunized animals are stimulated twice with each of the respective compositions (peptide epitopes encoded in the minigene or the polyepitopic peptide), then assayed for peptide-specific cytotoxic activity in a <sup>51</sup>Cr release assay. The results indicate the magnitude of the CTL response directed against the A2-restricted epitope, thus indicating the *in vivo* immunogenicity of the minigene vaccine and polyepitopic vaccine. It is, therefore, found that the minigene elicits immune responses directed toward the HLA-A2 supermotif peptide epitopes as does the polyepitopic peptide vaccine. A similar analysis is also performed using other HLA-A3 and HLA-B7 transgenic mouse models to assess CTL induction by HLA-A3 and HLA-B7 motif or supermotif epitopes.

[00416] To assess the capacity of a class II epitope encoding minigene to induce HTLs *in vivo*, DR transgenic mice, or for those epitope that cross react with the appropriate mouse MHC molecule, I-A<sup>b</sup>-restricted mice, for example, are immunized intramuscularly with 100 µg of plasmid DNA. As a means of comparing the level of HTLs induced by DNA immunization, a group of control animals is also immunized with an actual peptide composition emulsified in complete Freund's adjuvant. CD4<sup>+</sup> T cells, *i.e.* HTLs, are purified from splenocytes of immunized animals and stimulated with each of the respective compositions (peptides encoded in the minigene). The HTL response is measured using a <sup>3</sup>H-thymidine incorporation proliferation assay, (*see, e.g.*, Alexander et al. *Immunity* 1:751-761, 1994). The results indicate the magnitude of the HTL response, thus demonstrating the *in vivo* immunogenicity of the minigene.

[00417] DNA minigenes, constructed as described above or below, may also be evaluated as a vaccine in combination with a boosting agent using a prime boost protocol. The boosting agent can consist of recombinant protein (*e.g.*, Barnett *et al.*, *Aids Res. and Human Retroviruses* 14, Supplement 3:S299-S309, 1998) or recombinant vaccinia, for example, expressing a minigene or DNA encoding the complete protein of interest (*see, e.g.*, Hanke *et al.*, *Vaccine* 16:439-445, 1998; Sedegah *et al.*, *Proc. Natl. Acad. Sci USA*

95:7648-53, 1998; Hanke and McMichael, *Immunol. Letters* 66:177-181, 1999; and Robinson *et al.*, *Nature Med.* 5:526-34, 1999).

[00418] For example, the efficacy of the DNA minigene used in a prime boost protocol is initially evaluated in transgenic mice. In this example, A2.1/K<sup>b</sup> transgenic mice are immunized IM with 100 µg of a DNA minigene encoding the immunogenic peptides including at least one HLA-A2 supermotif-bearing peptide. After an incubation period (ranging from 3-9 weeks), the mice are boosted IP with 10<sup>7</sup> pfu/mouse of a recombinant vaccinia virus expressing the same sequence encoded by the DNA minigene. Control mice are immunized with 100 µg of DNA or recombinant vaccinia without the minigene sequence, or with DNA encoding the minigene, but without the vaccinia boost. After an additional incubation period of two weeks, splenocytes from the mice are immediately assayed for peptide-specific activity in an ELISPOT assay. Additionally, splenocytes are stimulated *in vitro* with the A2-restricted peptide epitopes encoded in the minigene and recombinant vaccinia, then assayed for peptide-specific activity in an IFN-γ ELISA.

[00419] It is found that the minigene utilized in a prime-boost protocol elicits greater immune responses toward the HLA-A2 supermotif peptides than with DNA alone. Such an analysis can also be performed using HLA-A11 or HLA-B7 transgenic mouse models to assess CTL induction by HLA-A3 or HLA-B7 motif or supermotif epitopes.

[00420] The use of prime boost protocols in humans is described in below.

#### EXAMPLE 9. PEPTIDE COMPOSITION FOR PROPHYLACTIC USES

[00421] Vaccine compositions of the present invention can be used to prevent HIV infection in persons who are at risk for such infection. For example, a polypeptopic peptide epitope composition (or a nucleic acid comprising the same) containing multiple CTL and HTL epitopes, which are also selected to target greater than 80% of the population, is administered to individuals at risk for HIV infection.

[00422] For example, a peptide-based composition can be provided as a single polypeptide that encompasses multiple epitopes. The vaccine is typically administered in a physiological solution that comprises an adjuvant, such as Incomplete Freund's Adjuvant. The dose of peptide for the initial immunization is from about 1 to about 50,000 µg, generally 100-5,000 µg, for a 70 kg patient. The initial administration of vaccine is

followed by booster dosages at 4 weeks followed by evaluation of the magnitude of the immune response in the patient, by techniques that determine the presence of epitope-specific CTL populations in a PBMC sample. Additional booster doses are administered as required. The composition is found to be both safe and efficacious as a prophylaxis against HIV infection.

[00423] Alternatively, a composition typically comprising transfecting agents can be used for the administration of a nucleic acid-based vaccine in accordance with methodologies known in the art and disclosed herein.

#### EXAMPLE 10. POLYEPITOPIC VACCINE COMPOSITIONS DERIVED FROM NATIVE HIV SEQUENCES

[00424] A native HIV polyprotein sequence is screened, preferably using computer algorithms defined for each class I and/or class II supermotif or motif, to identify “relatively short” regions of the polyprotein that comprise multiple epitopes and is preferably less in length than an entire native antigen. This relatively short sequence that contains multiple distinct, even overlapping, epitopes is selected and used to generate a minigene construct. The construct is engineered to express the peptide, which corresponds to the native protein sequence. The “relatively short” peptide is generally less than 250 amino acids in length, often less than 100 amino acids in length, preferably less than 75 amino acids in length, and more preferably less than 50 amino acids in length. The protein sequence of the vaccine composition is selected because it has maximal number of epitopes contained within the sequence, *i.e.*, it has a high concentration of epitopes. As noted herein, epitope motifs may be nested or overlapping, for example, two 9-mer epitopes and one 10-mer epitope can be present in a 10 amino acid peptide. Such a vaccine composition is administered for therapeutic or prophylactic purposes.

[00425] The vaccine composition will preferably include, for example, three CTL epitopes and at least one HTL epitope from HIV. This polyepitopic native sequence is administered either as a peptide or as a nucleic acid sequence which encodes the peptide. Alternatively, an analog can be made of this native sequence, whereby one or more of the epitopes comprise substitutions that alter the cross-reactivity and/or binding affinity properties of the polyepitopic peptide.

[00426] The embodiment of this example provides for the possibility that an as yet undiscovered aspect of immune system processing will apply to the native nested sequence and thereby facilitate the production of therapeutic or prophylactic immune response-inducing vaccine compositions. Additionally such an embodiment provides for the possibility of motif-bearing epitopes for an HLA makeup that is presently unknown. Furthermore, this embodiment (absent analogs) directs the immune response to multiple peptide sequences that are actually present in native HIV antigens thus avoiding the need to evaluate any junctional epitopes. Lastly, the embodiment provides an economy of scale when producing nucleic acid vaccine compositions.

[00427] Related to this embodiment, computer programs can be derived in accordance with principles in the art, which identify in a target sequence, the greatest number of epitopes per sequence length.

#### EXAMPLE 11. POLYEPITOPIC VACCINE COMPOSITIONS DIRECTED TO MULTIPLE DISEASES

[00428] The HIV peptide epitopes of the present invention are used in conjunction with peptide epitopes from target antigens related to one or more other diseases, to create a vaccine composition that is useful for the prevention or treatment of HIV as well as the one or more other disease(s). Examples of the other diseases include, but are not limited to, HCV and HBV.

[00429] For example, a polyepitopic peptide composition comprising multiple CTL and HTL epitopes that target greater than 98% of the population may be created for administration to individuals at risk for both HBV and HIV infection. The composition can be provided as a single polypeptide that incorporates the multiple epitopes from the various disease-associated sources, or can be administered as a composition comprising one or more discrete epitopes.

#### EXAMPLE 12. USE OF PEPTIDES TO EVALUATE AN IMMUNE RESPONSE

[00430] Peptides of the invention may be used to analyze an immune response for the presence of specific CTL or HTL populations directed to HIV. Such an analysis may be



performed in a manner as that described by Ogg *et al.*, *Science* 279:2103-2106, 1998. In the following example, peptides in accordance with the invention are used as a reagent for diagnostic or prognostic purposes, not as an immunogen.

**[00431]** In this example highly sensitive human leukocyte antigen tetrameric complexes (“tetramers”) are used for a cross-sectional analysis of, for example, HIV HLA-A\*0201-specific CTL frequencies from HLA A\*0201-positive individuals at different stages of infection or following immunization using an HIV peptide containing an A\*0201 motif. Tetrameric complexes are synthesized as described (Musey *et al.*, *N. Engl. J. Med.* 337:1267, 1997). Briefly, purified HLA heavy chain (A\*0201 in this example) and  $\beta$ 2-microglobulin are synthesized by means of a prokaryotic expression system. The heavy chain is modified by deletion of the transmembrane-cytosolic tail and COOH-terminal addition of a sequence containing a BirA enzymatic biotinylation site. The heavy chain,  $\beta$ 2-microglobulin, and peptide are refolded by dilution. The 45-kD refolded product is isolated by fast protein liquid chromatography and then biotinylated by BirA in the presence of biotin (Sigma, St. Louis, Missouri), adenosine 5'triphosphate and magnesium. Streptavidin-phycoerythrin conjugate is added in a 1:4 molar ratio, and the tetrameric product is concentrated to 1 mg/ml. The resulting product is referred to as tetramer-phycoerythrin.

**[00432]** For the analysis of patient blood samples, approximately one million PBMCs are centrifuged at 300 x g for 5 minutes and resuspended in 50  $\mu$ l of cold phosphate-buffered saline. Tri-color analysis is performed with the tetramer-phycoerythrin, along with anti-CD8-Tricolor, and anti-CD38. The PBMCs are incubated with tetramer and antibodies on ice for 30 to 60 min and then washed twice before formaldehyde fixation. Gates are applied to contain >99.98% of control samples. Controls for the tetramers include both A\*0201-negative individuals and A\*0201-positive uninfected donors. The percentage of cells stained with the tetramer is then determined by flow cytometry. The results indicate the number of cells in the PBMC sample that contain epitope-restricted CTLs, thereby readily indicating the extent of immune response to the HIV epitope, and thus the stage of infection with HIV, the status of exposure to HIV, or exposure to a vaccine that elicits a protective or therapeutic response.

### EXAMPLE 13. USE OF PEPTIDE EPITOPES TO EVALUATE RECALL RESPONSES

[00433] The peptide epitopes of the invention are used as reagents to evaluate T cell responses, such as acute or recall responses, in patients. Such an analysis may be performed on patients who have recovered from infection, who are chronically infected with HIV, or who have been vaccinated with an HIV vaccine.

[00434] For example, the class I restricted CTL response of persons who have been vaccinated may be analyzed. The vaccine may be any HIV vaccine. PBMC are collected from vaccinated individuals and HLA typed. Appropriate peptide epitopes of the invention that, optimally, bear supermotifs to provide cross-reactivity with multiple HLA supertype family members, are then used for analysis of samples derived from individuals who bear that HLA type.

[00435] PBMC from vaccinated individuals are separated on Ficoll-Histopaque density gradients (Sigma Chemical Co., St. Louis, MO), washed three times in HBSS (GIBCO Laboratories), resuspended in RPMI-1640 (GIBCO Laboratories) supplemented with L-glutamine (2mM), penicillin (50U/ml), streptomycin (50 µg/ml), and Hepes (10mM) containing 10% heat-inactivated human AB serum (complete RPMI) and plated using microculture formats. A synthetic peptide comprising an epitope of the invention is added at 10 µg/ml to each well and HBV core 128-140 epitope is added at 1 µg/ml to each well as a source of T cell help during the first week of stimulation.

[00436] In the microculture format,  $4 \times 10^5$  PBMC are stimulated with peptide in 8 replicate cultures in 96-well round bottom plate in 100 µl/well of complete RPMI. On days 3 and 10, 100 ml of complete RPMI and 20 U/ml final concentration of rIL-2 are added to each well. On day 7 the cultures are transferred into a 96-well flat-bottom plate and restimulated with peptide, rIL-2 and  $10^5$  irradiated (3,000 rad) autologous feeder cells. The cultures are tested for cytotoxic activity on day 14. A positive CTL response requires two or more of the eight replicate cultures to display greater than 10% specific  $^{51}\text{Cr}$  release, based on comparison with uninfected control subjects as previously described (Rehermann, *et al.*, *Nature Med.* 2:1104,1108, 1996; Rehermann *et al.*, *J. Clin. Invest.* 97:1655-1665, 1996; and Rehermann *et al.* *J. Clin. Invest.* 98:1432-1440, 1996).

[00437] Target cell lines are autologous and allogeneic EBV-transformed B-LCL that are either purchased from the American Society for Histocompatibility and Immunogenetics

(ASHI, Boston, MA) or established from the pool of patients as described (Guilhot, *et al. J. Virol.* 66:2670-2678, 1992).

[00438] Cytotoxicity assays are performed in the following manner. Target cells consist of either allogeneic HLA-matched or autologous EBV-transformed B lymphoblastoid cell line that are incubated overnight with the synthetic peptide epitope of the invention at 10  $\mu$ M, and labeled with 100  $\mu$ Ci of  $^{51}\text{Cr}$  (Amersham Corp., Arlington Heights, IL) for 1 hour after which they are washed four times with HBSS.

[00439] Cytolytic activity is determined in a standard 4-h, split well  $^{51}\text{Cr}$  release assay using U-bottomed 96 well plates containing 3,000 targets/well. Stimulated PBMC are tested at effector/target (E/T) ratios of 20-50:1 on day 14. Percent cytotoxicity is determined from the formula:  $100 \times [(\text{experimental release} - \text{spontaneous release}) / (\text{maximum release} - \text{spontaneous release})]$ . Maximum release is determined by lysis of targets by detergent (2% Triton X-100; Sigma Chemical Co., St. Louis, MO). Spontaneous release is <25% of maximum release for all experiments.

[00440] The results of such an analysis indicate the extent to which HLA-restricted CTL populations have been stimulated by previous exposure to HIV or an HIV vaccine.

[00441] The class II restricted HTL responses may also be analyzed. Purified PBMC are cultured in a 96-well flat bottom plate at a density of  $1.5 \times 10^5$  cells/well and are stimulated with 10  $\mu\text{g/ml}$  synthetic peptide, whole antigen, or PHA. Cells are routinely plated in replicates of 4-6 wells for each condition. After seven days of culture, the medium is removed and replaced with fresh medium containing 10U/ml IL-2. Two days later, 1  $\mu\text{Ci}$   $^3\text{H}$ -thymidine is added to each well and incubation is continued for an additional 18 hours. Cellular DNA is then harvested on glass fiber mats and analyzed for  $^3\text{H}$ -thymidine incorporation. Antigen-specific T cell proliferation is calculated as the ratio of  $^3\text{H}$ -thymidine incorporation in the presence of antigen divided by the  $^3\text{H}$ -thymidine incorporation in the absence of antigen.

#### EXAMPLE 14. INDUCTION OF SPECIFIC CTL RESPONSE IN HUMANS

[00442] A human clinical trial for an immunogenic composition comprising CTL and HTL epitopes of the invention is set up as an IND Phase I, dose escalation study and carried out

as a randomized, double-blind, placebo-controlled trial. Such a trial is designed, for example, as follows:

[00443] A total of about 27 subjects are enrolled and divided into 3 groups:

Group I: 3 subjects are injected with placebo and 6 subjects are injected with 5 µg of peptide composition;

Group II: 3 subjects are injected with placebo and 6 subjects are injected with 50 µg peptide composition;

Group III: 3 subjects are injected with placebo and 6 subjects are injected with 500 µg of peptide composition.

[00444] After 4 weeks following the first injection, all subjects receive a booster inoculation at the same dosage.

[00445] The endpoints measured in this study relate to the safety and tolerability of the peptide composition as well as its immunogenicity. Cellular immune responses to the peptide composition are an index of the intrinsic activity of this the peptide composition, and can therefore be viewed as a measure of biological efficacy. The following summarize the clinical and laboratory data that relate to safety and efficacy endpoints.

[00446] Safety: The incidence of adverse events is monitored in the placebo and drug treatment group and assessed in terms of degree and reversibility.

[00447] Evaluation of Vaccine Efficacy: For evaluation of vaccine efficacy, subjects are bled before and after injection. Peripheral blood mononuclear cells are isolated from fresh heparinized blood by Ficoll-Hypaque density gradient centrifugation, aliquoted in freezing media and stored frozen. Samples are assayed for CTL and HTL activity.

[00448] The vaccine is found to be both safe and efficacious.

#### EXAMPLE 15. PHASE II TRIALS IN PATIENTS INFECTED WITH HIV

[00449] Phase II trials are performed to study the effect of administering the CTL-HTL peptide compositions to HIV-infected patients. The main objectives of the trials are to determine an effective dose and regimen for inducing CTLs in chronically infected HIV patients, to establish the safety of inducing a CTL and HTL response in these patients, and to see to what extent activation of CTLs improves the clinical picture of chronically infected HIV patients, as manifested by a reduction in viral load and an increase in CD4<sup>+</sup> cells counts. Such a study is designed, for example, as follows:

- [00450] The studies are performed in multiple centers. The trial design is an open-label, uncontrolled, dose escalation protocol wherein the peptide composition is administered as a single dose followed six weeks later by a single booster shot of the same dose. The dosages are 50, 500 and 5,000 micrograms per injection. Drug-associated adverse effects (severity and reversibility) are recorded.
- [00451] There are three patient groupings. The first group is injected with 50 micrograms of the peptide composition and the second and third groups with 500 and 5,000 micrograms of peptide composition, respectively. The patients within each group range in age from 21-65, include both males and females, and represent diverse ethnic backgrounds. All of them are infected with HIV for over five years and are HCV, HBV and delta hepatitis virus (HDV) negative, but have positive levels of HIV antigen.
- [00452] The viral load and CD4<sup>+</sup> levels are monitored to assess the effects of administering the peptide compositions. The vaccine composition is found to be both safe and efficacious in the treatment of HIV infection.

#### EXAMPLE 16. INDUCTION OF CTL RESPONSES USING A PRIME BOOST PROTOCOL

- [00453] A prime boost protocol can also be used for the administration of the vaccine to humans. Such a vaccine regimen can include an initial administration of, for example, naked DNA followed by a boost using recombinant virus encoding the vaccine, or recombinant protein/polypeptide or a peptide mixture administered in an adjuvant.
- [00454] For example, the initial immunization is performed using an expression vector, such as that constructed above, in the form of naked nucleic acid administered IM (or SC or ID) in the amounts of 0.5-5 mg at multiple sites. The nucleic acid (0.1 to 1000 µg) can also be administered using a gene gun. Following an incubation period of 3-4 weeks, a booster dose is then administered. The booster is, for example, recombinant fowlpox virus administered at a dose of  $5 \cdot 10^7$  to  $5 \cdot 10^9$  pfu. An alternative recombinant virus, such as an MVA, canarypox, adenovirus, or adeno-associated virus, can also be used for the booster, or the polyepitopic protein or a mixture of the peptides can be administered. For evaluation of vaccine efficacy, patient blood samples are obtained before immunization as well as at intervals following administration of the initial vaccine and booster doses of the

vaccine. Peripheral blood mononuclear cells are isolated from fresh heparinized blood by Ficoll-Hypaque density gradient centrifugation, aliquoted in freezing media and stored frozen. Samples are assayed for CTL and HTL activity.

[00455] Analysis of the results indicates that a magnitude of sufficient response to achieve protective immunity against HIV is generated.

#### EXAMPLE 17. ADMINISTRATION OF VACCINE COMPOSITIONS USING DENDRITIC CELLS

[00456] Vaccines comprising peptide epitopes of the invention can be administered using APCs, or “professional” APCs such as DC. In this example, the peptide-pulsed DC are administered to a patient to stimulate a CTL response *in vivo*. In this method, dendritic cells are isolated, expanded, and pulsed with a vaccine comprising peptide CTL and HTL epitopes of the invention. The dendritic cells are infused back into the patient to elicit CTL and HTL responses *in vivo*. The induced CTL and HTL then destroy or facilitate destruction of the specific target cells that bear the proteins from which the epitopes in the vaccine are derived.

[00457] For example, a cocktail of epitope-bearing peptides is administered *ex vivo* to PBMC, or isolated DC therefrom. A pharmaceutical to facilitate harvesting of DC can be used, such as Progenipoiectin™ (Monsanto, St. Louis, MO) or GM-CSF/IL-4. After pulsing the DC with peptides and prior to reinfusion into patients, the DC are washed to remove unbound peptides.

[00458] As appreciated clinically, and readily determined by one of skill based on clinical outcomes, the number of DC reinfused into the patient can vary (*see, e.g., Nature Med.* 4:328, 1998; *Nature Med.* 2:52, 1996 and *Prostate* 32:272, 1997). Although  $2\text{--}50 \times 10^6$  DC per patient are typically administered, larger number of DC, such as  $10^7$  or  $10^8$  can also be provided. Such cell populations typically contain between 50-90% DC.

[00459] In some embodiments, peptide-loaded PBMC are injected into patients without purification of the DC. For example, PBMC containing DC generated after treatment with an agent such as Progenipoiectin™ are injected into patients without purification of the DC. The total number of PBMC that are administered often ranges from  $10^8$  to  $10^{10}$ . Generally, the cell doses injected into patients is based on the percentage of DC in the

blood of each patient, as determined, for example, by immunofluorescence analysis with specific anti-DC antibodies. Thus, for example, if Progenipoietin™ mobilizes 2% DC in the peripheral blood of a given patient, and that patient is to receive  $5 \times 10^6$  DC, then the patient will be injected with a total of  $2.5 \times 10^8$  peptide-loaded PBMC. The percent DC mobilized by an agent such as Progenipoietin™ is typically estimated to be between 2-10%, but can vary as appreciated by one of skill in the art.

*Ex vivo activation of CTL/HTL responses*

[00460] Alternatively, *ex vivo* CTL or HTL responses to HIV antigens can be induced by incubating in tissue culture the patient's, or genetically compatible, CTL or HTL precursor cells together with a source of APC, such as DC, and the appropriate immunogenic peptides. After an appropriate incubation time (typically about 7-28 days), in which the precursor cells are activated and expanded into effector cells, the cells are infused back into the patient, where they will destroy or facilitate destruction of their specific target cells.

[00461] It is understood that the examples and embodiments described herein are for illustrative purposes only and that various modifications or changes in light thereof will be suggested to persons skilled in the art and are to be included within the spirit and purview of this application and scope of the appended claims. All publications, patents, patent applications and sequence listings cited herein are hereby incorporated by reference in their entirety for all purposes.

TABLE 1

SUPERMOTIFS	POSITION	POSITION	POSITION
	2 (Primary Anchor)	3 (Primary Anchor)	C Terminus (Primary Anchor)
A1	<b>T, I, L, V, M, S</b>		<b>F, W, Y</b>
A2	<b>L, I, V, M, A, T, Q</b>		<b>I, V, M, A, T, L</b>
A3	<b>V, S, M, A, T, L, I</b>		<b>R, K</b>
A24	<b>Y, F, W, I, V, L, M, T</b>		<b>F, I, Y, W, L, M</b>
B7	<b>P</b>		<b>V, I, L, F, M, W, Y, A</b>
B27	<b>R, H, K</b>		<b>F, Y, L, W, M, I, V, A</b>
B44	<b>E, D</b>		<b>F, W, L, I, M, V, A</b>
B58	<b>A, T, S</b>		<b>F, W, Y, L, I, V, M, A</b>
B62	<b>Q, L, I, V, M, P</b>		<b>F, W, Y, M, I, V, L, A</b>
MOTIFS			
A1	<b>T, S, M</b>		<b>Y</b>
A1		<b>D, E, A, S</b>	<b>Y</b>
A2.1	<b>L, M, V, Q, I, A, T</b>		<b>V, L, I, M, A, T</b>
A3	<b>L, M, V, I, S, A, T, F, C, G, D</b>		<b>K, Y, R, H, F, A</b>
A11	<b>V, T, M, L, I, S, A, G, N, C, D, F</b>		<b>K, R, Y, H</b>
A24	<b>Y, F, W, M</b>		<b>F, L, I, W</b>
A*3101	<b>M, V, T, A, L, I, S</b>		<b>R, K</b>
A*3301	<b>M, V, A, L, F, I, S, T</b>		<b>R, K</b>
A*6801	<b>A, V, T, M, S, L, I</b>		<b>R, K</b>
B*0702	<b>P</b>		<b>L, M, F, W, Y, A, I, V</b>
B*3501	<b>P</b>		<b>L, M, F, W, Y, I, V, A</b>
B51	<b>P</b>		<b>L, I, V, F, W, Y, A, M</b>
B*5301	<b>P</b>		<b>I, M, F, W, Y, A, L, V</b>
B*5401	<b>P</b>		<b>A, T, I, V, L, M, F, W, Y</b>

Bolded residues are preferred, italicized residues are tolerated: A peptide is considered motif-bearing if it has primary anchors at each primary anchor position for a motif or supermotif as specified in the above table.



TABLE 2

SUPERMOTIFS	POSITION	POSITION	POSITION
	2 (Primary Anchor)	3 (Primary Anchor)	C Terminus (Primary Anchor)
A1	<b>T, I, L, V, M, S</b>		<b>F, W, Y</b>
A2	<b>V, Q, A, T</b>		<b>I, V, L, M, A, T</b>
A3	<b>V, S, M, A, T, L, I</b>		<b>R, K</b>
A24	<b>Y, F, W, I, V, L, M, T</b>		<b>F, I, Y, W, L, M</b>
B7	<b>P</b>		<b>V, I, L, F, M, W, Y, A</b>
B27	<b>R, H, K</b>		<b>F, Y, L, W, M, I, V, A</b>
B58	<b>A, T, S</b>		<b>F, W, Y, L, I, V, M, A</b>
B62	<b>Q, L, I, V, M, P</b>		<b>F, W, Y, M, I, V, L, A</b>
MOTIFS			
A1	<b>T, S, M</b>		<b>Y</b>
A1		<b>D, E, A, S</b>	<b>Y</b>
A2.1	<b>V, Q, A, T*</b>		<b>V, L, I, M, A, T</b>
A3.2	<b>L, M, V, I, S, A, T, F, C, G, D</b>		<b>K, Y, R, H, F, A</b>
A11	<b>V, T, M, L, I, S, A, G, N, C, D, F</b>		<b>K, R, H, Y</b>
A24	<b>Y, F, W</b>		<b>F, L, I, W</b>

\*If 2 is V, or Q, the C-term is not L

Bolded residues are preferred, italicized residues are tolerated: A peptide is considered motif-bearing if it has primary anchors at each primary anchor position for a motif or supermotif as specified in the above table.













**Table 4**

HLA-supertype	Allele-specific HLA-supertype members	
	Verified <sup>a</sup>	Predicted <sup>b</sup>
A1	A*0101, A*2501, A*2601, A*2602, A*3201	A*0102, A*2604, A*3601, A*4301, A*8001
A2	A*0201, A*0202, A*0203, A*0204, A*0205, A*0206, A*0207, A*0209, A*0214, A*6802, A*6901	A*0208, A*0210, A*0211, A*0212, A*0213
A3	A*0301, A*1101, A*3101, A*3301, A*6801	A*0302, A*1102, A*2603, A*3302, A*3303, A*3401, A*3402, A*6601, A*6602, A*7401
A24	A*2301, A*2402, A*3001	A*2403, A*2404, A*3002, A*3003
B7	B*0702, B*0703, B*0704, B*0705, B*1508, B*3501, B*3502, B*3503, B*3504, B*3505, B*3506, B*3507, B*3508, B*5101, B*5102, B*5103, B*5104, B*5105, B*5301, B*5401, B*5501, B*5502, B*5601, B*5602, B*6701, B*7801	B*1511, B*4201, B*5901
B27	B*1401, B*1402, B*1509, B*2702, B*2703, B*2704, B*2705, B*2706, B*3801, B*3901, B*3902, B*7301	B*2701, B*2707, B*2708, B*3802, B*3903, B*3904, B*3905, B*4801, B*4802, B*1510, B*1518, B*1503
B44	B*1801, B*1802, B*3701, B*4402, B*4403, B*4404, B*4001, B*4002, B*4006	B*4101, B*4501, B*4701, B*4901, B*5001
B58	B*5701, B*5702, B*5801, B*5802, B*1516, B*1517	
B62	B*1501, B*1502, B*1513, B*5201	B*1301, B*1302, B*1504, B*1505, B*1506, B*1507, B*1515, B*1520, B*1521, B*1512, B*1514, B*1510

- a. Verified alleles include alleles whose specificity has been determined by pool sequencing analysis, peptide binding assays, or by analysis of the sequences of CTL epitopes.
- b. Predicted alleles are alleles whose specificity is predicted on the basis of B and F pocket structure to overlap with the supertype specificity.



Table 5. Compiled rankings and similarity assignments.

A	C	D	E	F	G	H	I	K	L
A 1.0	C 1.0	D 1.0	E 1.0	F 1.0	G 1.0	H 1.0	I 1.0	K 1.0	L 1.0
S 4.5	V 5.5	N 3.5	Q 3.3	L 3.8	S 2.8	Q 2.0	L 2.5	R 2.7	I 3.3
T 4.8	T 6.5	E 4.0	N 4.2	Y 4.3	A 4.2	E 5.8	M 4.5	Q 6.0	M 4.0
P 5.3	A 6.7	Q 6.2	D 4.7	I 4.8	T 4.7	N 6.2	F 5.2	H 6.8	F 4.5
G 5.7	S 7.3	T 7.2	H 5.3	M 6.2	D 6.3	R 8.2	V 5.2	N 7.2	V 5.5
C 9.3	P 8.0	S 7.7	T 8.3	V 6.7	P 7.0	K 8.7	Y 8.8	E 7.5	Y 8.2
V 9.5	I 9.0	H 7.8	K 8.7	W 7.2	N 7.3	P 9.0	T 10.3	D 8.5	H 9.7
D 10.0	Y 10.2	G 8.8	P 9.0	H 10.2	E 8.3	D 9.2	H 11.3	M 9.2	Q 10.5
M 10.0	N 10.7	P 9.2	R 10.5	C 11.2	Q 9.3	S 10.5	A 11.5	T 10.5	W 11.0
N 10.2	F 11.0	A 9.3	S 10.5	T 11.5	H 9.8	T 10.5	C 11.7	S 11.3	T 11.3
E 11.3	G 11.0	K 9.5	V 11.0	R 11.8	C 11.5	Y 11.0	K 12.0	P 11.5	A 11.8
Q 11.3	M 11.0	R 11.5	G 12.0	A 13.0	V 12.0	M 11.2	P 12.0	I 12.2	K 12.2
H 12.3	H 11.3	C 12.0	A 12.2	K 13.3	M 13.3	V 12.2	Q 12.2	L 12.7	P 12.2
Y 13.0	D 12.0	V 13.2	M 12.3	P 13.3	K 13.3	L 13.3	R 13.0	Y 12.8	R 13.2
I 14.3	F 13.7	M 14.3	I 15.0	S 13.8	V 14.2	I 13.7	S 13.2	V 13.7	C 13.7
W 14.3	G 13.7	Y 15.8	C 15.2	Q 14.0	R 15.3	A 13.8	E 14.0	A 14.3	E 14.2
P 14.3	W 15.0	I 16.0	L 15.3	N 14.2	I 16.3	C 13.8	N 14.3	G 14.3	N 14.5
K 14.3	K 16.3	I 16.7	V 15.7	E 15.3	L 16.8	F 15.3	W 14.7	F 14.8	S 15.3
R 14.3	K 17.0	W 18.0	F 17.8	G 16.3	W 17.3	C 17.2	D 15.7	W 15.5	G 16.8
		P 18.3	W 18.0	D 18.0	F 18.2	W 17.5	G 17.0	C 17.5	D 17.2

☐ Conserved (1-7)

☐ Semi-conserved (7.1-13)

☐ Non-conserved (13.1-20)

Table 5 (continued)

M	N	P	Q	R	S	T	V	W	Y
M 1.0	N 1.0	P 1.0	Q 1.0	R 1.0	S 1.0	T 1.0	V 1.0	W 1.0	Y 1.0
L 3.8	D 3.2	T 3.5	E 3.2	K 2.0	T 4.0	P 4.7	L 5.3	F 4.2	F 6.2
I 5.0	E 4.5	S 6.0	H 3.3	H 5.8	G 4.2	S 5.0	I 5.5	Y 4.5	W 6.3
V 5.2	Q 5.8	A 6.3	N 6.0	Q 6.7	A 4.7	A 5.7	M 5.5	L 6.3	H 7.3
F 7.0	H 6.8	H 7.2	K 7.0	E 8.7	P 5.3	N 6.5	P 7.8	M 6.5	M 8.0
K 9.7	T 7.2	Q 7.2	D 7.2	N 8.7	N 6.5	D 7.8	T 8.2	R 8.7	L 9.7
Q 10.3	S 7.7	N 7.8	R 8.3	M 9.2	D 8.0	E 8.3	F 8.5	I 9.2	T 10.0
R 10.5	K 8.5	D 9.2	P 8.5	D 10.0	C 9.3	G 8.8	A 10.0	H 10.2	I 10.3
Y 10.8	P 8.7	E 9.5	M 10.5	P 10.2	E 9.3	H 10.5	C 10.7	V 10.3	C 10.7
H 11.0	R 10.5	G 10.2	T 10.8	W 10.3	H 10.2	Q 10.5	H 11.0	K 10.5	V 11.0
A 11.2	A 10.7	V 11.2	V 11.3	S 11.3	Q 10.5	V 10.5	Q 11.0	Q 12.3	P 11.5
T 11.3	G 11.8	C 11.8	S 12.3	T 12.0	K 12.3	C 12.2	E 11.3	S 12.3	A 11.7
P 11.8	V 12.8	M 12.2	A 13.0	I 12.5	V 13.5	K 12.2	N 12.3	A 12.5	N 11.7
W 12.7	S 13.0	R 13.2	G 13.3	L 13.0	R 13.7	M 12.3	S 12.7	P 12.7	Q 12.0
C 13.0	M 13.8	K 13.5	L 13.8	Y 13.0	M 14.5	I 13.7	G 13.2	T 12.7	S 12.2
E 13.2	N 13.2	Y 13.8	I 14.2	V 13.7	Y 14.7	Y 14.3	Y 14.0	N 13.2	K 12.7
N 13.2	F 14.0	H 14.0	Y 15.0	F 14.3	I 16.0	R 15.5	D 14.8	C 13.3	R 13.0
S 13.5	L 13.5	L 14.3	C 16.3	A 15.2	W 16.5	W 16.3	K 15.2	F 15.7	A 14.2
G 14.2	W 14.7	W 16.3	F 17.3	G 15.2	L 17.5	L 16.5	W 15.7	G 16.7	A 14.7
C 14.3	F 14.3	F 14.8	W 17.5	C 17.3	F 18.3	F 17.7	R 16.3	D 17.3	D 18.0

Conserved (1-7)

Semi-conserved (7.1-13)

Non-conserved (13.1-20)

Table 6. Recognition of variant peptides by CTL generated after one and five stimulations with the parent peptide.

<b>A. Gag 386 (VLAEAMSQV)</b>			
<b>Peptide Sequence</b>	<b>Binding IC50 (nM)</b>	<b>1 Stimulation (SU)</b>	<b>5 Stimulations (SU)</b>
VLAEAMSQV	49.9	31.6	222.0
VLAEAMSQA	23.8	17.0	133.5
VLAEAMSQI	70.9	21.2	246.1
VLAEAMSKV	230.5	10.8	130.9
VLAEAMSKA	69.4	NT	36.6
ILAEAMSQA	29.3	4.0	49.7
ILAEAMSKA	72.4	--	--
VLAEAMAAA	17	16.3	90.3
<b>B. Env 134 (KLTPLCVTL)</b>			
KLTPLCVTL	77.0	278.4	683.6
KITPLCVTL	461	231.8	700.8
QLTPLCVTL	63.6	166.2	361.5
QITPLCVTL	975	105.0	166.9
ELTPLCVTL	7190	91.7	100.0
KLTPFCVTL	87.3	36.1	75.4
KLTPLCVIL	356	77.2	29.1
KLTPLCVPL	14.6	9.6	14.8

Table 7. Conservation of EP HIV-1090 epitopes across clades, calculated as identity or immunological conservation

Protein	Sequence	<u>Total</u>		<u>Clade B</u>		<u>Clade C</u>	
		Identity	Imm. Cons.	Identity	Imm. Cons.	Identity	Imm. Cons.
Pol 498	ILKEPVHGV	62%	87%	77%	86%	74%	95%
Gag 386	VLAEMSQV	32%	93%	68%	91%	5%	94%
Pol 448	KLVGKLNWA	95%	96%	95%	95%	95%	98%
Env 134	KLTPLCVTL	80%	93%	90%	95%	89%	98%
Vpr 62	RILQQLLFI	51%	93%	68%	91%	61%	95%
Nef 221	LTFGWCFKL	49%	74%	77%	91%	47%	81%
Gag 271	MTNNPPIPV	20%	25%	91%	95%	8%	19%
Env 47	VTVYYGVPVWK	59%	87%	95%	100%	61%	92%
Pol 929	QMAVFIHNFK	84%	98%	100%	100%	94%	97%
Pol 98	VTIKIGGQLK	11%	71%	59%	91%	2%	89%
Pol 971	KIQNFRVYYR	80%	86%	91%	95%	79%	89%
Pol 347	AIFQSSMTK	53%	75%	77%	82%	44%	79%
Pol 722	KVYLAWVPAHK	14%	97%	82%	95%	3%	97%
Env 61	TTLFCASDAK	72%	89%	90%	100%	69%	92%
Nef 94	FPVRPQVPL	81%	93%	77%	95%	82%	94%
Gag 545	YPLASLRSLF	7%	29%	45%	95%	0%	0%
Rev 75	VPLQLPPL	44%	78%	68%	77%	27%	79%
Env 259	IPIHYCAPA	74%	95%	45%	95%	79%	97%
Gag 237	HPVHAGPIA	27%	54%	68%	95%	44%	94%
Pol 893	IPYNPQSQGVV	92%	96%	82%	95%	240%	97%
Env 250	CPKVSFEPI	45%	91%	77%	100%	45%	97%
Mean		54%	81%	77%	93%	59%	84%
n=		167		22		62	

Table 8. HIV Peptides predicted to be immunologically conserved

Protein	Sequence	Conserved Epitopes*	SEQ ID NO	Sequence Distribution					
				All	Subtype				
					A	B	C	D	G
Pol 498	ILKEPVHGV	<b>ILKEPVHGV</b>	<u>69</u>	104	1	17	46	2	2
		ILREPVHGV	<u>91</u>	12			5		1
		ILKEPVHGA	<u>92</u>	10			2	1	
		ILKDPVHGV	<u>93</u>	8	5				
		KLKEPVHGV	<u>94</u>	3					
		ILKDPVHGA	<u>95</u>	2	2				
		ILKNPVHGV	<u>96</u>	2					
Gag 386	VLAEAMSQV	<b>VLAEAMSQA</b>	<u>16</u>	67	2	1	36	3	3
		<b>VLAEAMSQV</b>	<u>10</u>	54	7	15	3	1	
		VLAEAMSQT	<u>99</u>	11			9		
		VLAEAMSHA	<u>100</u>	6			4		
		ILAEAMSQV	<u>101</u>	5		3			
		ILAEAMSQA	<u>58</u>	3			2		
		VLAEAMSHV	<u>103</u>	2					
Pol 448	KLVGKLNWA	<b>KLVGKLNWA</b>	<u>72</u>	158	9	21	59	3	3
		KLIGKLNWA	<u>105</u>	1					
Env 134	KLTPLCVTL	<b>KLTPLCVTL</b>	<u>9</u>	134	8	19	55		
		QLTPLCVTL	<u>19</u>	5	2	1			
		KLTPLCVAL	<u>108</u>	3					
		RLTPLCVTL	<u>109</u>	3			3		
		KITPLCVTL	<u>18</u>	2					
Vpr 62	RILQQLLFI	<b>RILQQLLFI</b>	<u>11</u>	86	1	15	28	4	3
		RILQQLLFV	<u>112</u>	21	2		2		
		RTLQQLLFI	<u>113</u>	10		2	4		
		RTLQQLLFV	<u>114</u>	10			1		
		RILQQLLFT	<u>115</u>	6			2		
		RMLQQLLFI	<u>116</u>	4		1	3		
		RVLQQLLFI	<u>117</u>	3			3		
Nef 221	LTFGWCFKL	<b>LTFGWCFKL</b>	<u>74</u>	82	8	17	29		3
		LTFGWCYKL	<u>119</u>	31	1	2	17		
		LTLGWCFKL	<u>120</u>	4			1		

Gag 271	MTNNPPIP	<b>MTSNPPIP</b>	<u>26</u>	60	3		24	4	1
		MTNNPPIP	<u>25</u>	33		20	5		
		MTSNPPVP	<u>123</u>	26	1		15		1
		MTGNPPIP	<u>124</u>	15	5		1		
		MTGNPPVP	<u>125</u>	9			5		
		MTNNPPVP	<u>126</u>	6			6		
		MTANPPVP	<u>127</u>	3			2		
Env 47	VTVYGV	<b>VTVYGV</b>	<u>13</u>	99	6	21	30	3	
		VTVYGVWR	<u>129</u>	40	1		18		
		VTIYGV	<u>130</u>	2					
Pol 929	QMAVFIHNF	<b>QMAVFIHNF</b>	<u>77</u>	153	10	22	58	4	3
		QMAVHVHNF	<u>132</u>	3			1		
		QMAVHVHNY	<u>133</u>	2					
Pol 98	VTIKIGGQL	<b>VSIKVGQI</b>	<u>12</u>	30			30		
		<b>VTIKIGGQL</b>	<u>78</u>	18		13	1		
		VTVKIGGQL	<u>136</u>	11	1	1		1	
		VTVRIGGQL	<u>137</u>	6	3				
		VSIKVGQIR	<u>138</u>	6			6		
		VSIRVGQI	<u>139</u>	4			4		
		VTIRIGGQL	<u>140</u>	3		2			
		VTVKIGGQLR	<u>141</u>	3	1				
		VTVKVGQI	<u>142</u>	3					
Pol 971	KIQNFRVYYR	<b>KIQNFRVYYR</b>	<u>79</u>	133	6	20	49	4	3
Pol 347	AIFQSSMT	<b>AIFQSSMT</b>	<u>80</u>	88	5	17	27	3	2
		AIFQCSMT	<u>145</u>	19		2	5		
		AIFQSSMT	<u>146</u>	13		1	11		1
		AIFQASMT	<u>147</u>	9	1		1		
		SIFQSSMT	<u>148</u>	9	3		6		
		AIFQYSMT	<u>149</u>	4					
		AIFQSTMT	<u>150</u>	2			1		
Pol 722	KVYLAWVPAH	<b>KVYLSWVPAH</b>	<u>151</u>	56	8		12	1	3
		<b>RVYLSWVPAH</b>	<u>152</u>	55			41		
		KVYLAWVPAH	<u>81</u>	23	1	18		3	

		KVYLTWVPAHK	<u>154</u>	5		2			
		KIYLSWVPAHK	<u>155</u>	5			3		
		RIYLSWVPAHK	<u>156</u>	5			4		
		KIYLAWVPAHK	<u>157</u>	2		1			
		QVYLTWVPAHK	<u>158</u>	2					
Env 61	TTLFCASDAK	<b>TTLFCASDAK</b>	<u>82</u>	121	9	19	41	4	1
		ATLFCASDAK	<u>160</u>	7			7		
		TILFCASDAK	<u>161</u>	6					
		PTLFCASDAK	<u>162</u>	2			1		
		TTLFCASDAR	<u>163</u>	2		2			
		TTLFCASEAK	<u>164</u>	2		1			
		ATLFCASDAR	<u>165</u>	2			2		
Nef 94	FPVRPQVPL	<b>FPVRPQVPL</b>	<u>83</u>	135	8	17	51	4	3
		FPVKPQVPL	<u>167</u>	9	1	3	2		
		FPVRPQVPV	<u>168</u>	4			2		
Gag 545	YPLASLRSLF	<b>EPLTSLKSLF*</b>	<u>1</u>	22			21		
		<b>YPLASLKSLF*</b>	<u>2</u>	13		5		2	
*These two would not be predicted to XR. Would choose both to get maximal population coverage.									
		YPLASLRSLF	<u>84</u>	11		10			
		YPLTSLKSLF	<u>172</u>	10		1		2	1
		YPPLASLKSL	<u>173</u>	10					
		YPLTSLRSLF	<u>174</u>	6		4			
		YPPLTSLKSL	<u>175</u>	6					
Rev 75	VPLQLPPL	<b>VPLQLPPL</b>	<u>85</u>	64	5	15	7	4	2
		<b>VPLQLPPI</b>	<u>177</u>	34	2	1	19		
		VPFQLPPI	<u>178</u>	26			23		
		VPFQLPPL	<u>179</u>	3		1			1
Env 259	IPIHYCAPA	<b>IPIHYCAPA</b>	<u>86</u>	124	8	10	49	3	2
		IPIHYCTPA	<u>181</u>	25	1	8	8		
		IPIHFCAPA	<u>182</u>	3		1	1	1	
Gag 237	HPVHAGPIA	<b>HPVHAGPIA</b>	<u>87</u>	39		15	21	1	
		<b>HPVHAGPVA</b>	<u>184</u>	34	1	3	27	2	
		HPVQAGPVA	<u>185</u>	12		3	6	1	

		HPIHAGPIA	<u>186</u>	2			2		
Pol 893	IPYNPQSQGVV	<b>IPYNPQSQGVV</b>	<u>88</u>	153	9	18	60	4	3
		IPYNPQSQGVI	<u>188</u>	5		3			
		IPYNPQSQGAV	<u>189</u>	2			1		
Env 250	CPKVSFEPI	<b>CPKVSFEPI</b>	<u>89</u>	50	5	17	3	2	0
		<b>CPKVSFDPI</b>	<u>191</u>	42			33		
		CPKVTFDPI	<u>192</u>	16			13		1
		CPKVTFEPI	<u>193</u>	13	3		1		1
		CPKISFDPI	<u>194</u>	9			5		
		CPKISFEPI	<u>195</u>	7		4		1	
		CPKVSWDPI	<u>196</u>	6					
		CPKVSFQPI	<u>197</u>	4		1			

\* The preferred epitopes are shown in bold



Table 9. Predicted immunological conservation for a panel of HLA-A2 restriction peptides.

Source	Parent Sequence	HPV Strain	Variant Sequences	SEQ ID NO	Predicted Immunogenicity	Measured Immunogenicity (SU) *
HPV16.E7.86	TLGIVCPI	16	TLGIVCPI	<u>198</u>	+	103.7
		18	TLSFVCPW	199	-	
		31	SFGIVCPN	200	-	
		33	TVNIVCPT	201	-	
		45	TLSFVCPW	199	-	
		52	TLQVVC PG	203	-	
		56	ALTVTCPL	204	-	
		58	TCTIVCPS	205	-	
HPV31.E6.11	KLHELSSAL	16	KLPQLCTEL	<u>206</u>	-	
		18	KLPDLCTEL	207	-	
		31	KLHELSSAL	208	+	26.3
		33	TLHDL CQAL	209	-	
		45	KLPDLCTEL	207	-	
		52	TLHELCEVL	211	-	
		56	SLHHLSEVL	212	-	
		58	TLHDL CQAL	209	-	
HPV18/45.E6.13	KLPDLCTEL	16	KLPQLCTEL	<u>206</u>	+	15.7
		18	KLPDLCTEL	210	+	212.7
		31	KLHELSSAL	208	-	
		33	TLHDL CQAL	209	-	
		45	KLPDLCTEL	207	+	205.1
		52	TLHELCEVL	211	-	
		56	SLHHLSEVL	212	-	
		58	TLHDL CQAL	209	-	
HPV52.E6.18	VLEESVHEI	16	ELQTTIHDI	<u>222</u>	-	
		18	ELNTSLQDI	223	-	
		31	ALEIPYDEL	224	-	
		33	ALETTIHNI	225	-	
		45	ELNTSLQDV	226	-	
		52	VLEESVHEI	227	+	64.1
		56	VLEIPLIDL	228	-	
		58	ALETSVHEI	229	-	
HPV18.E6.47	FAFKDLFVV	16	FAFRDLCIV	<u>230</u>	-	
		18	FAFKDLFVV	231	+	350.6
		31	FAFTDLTIV	232	-	
		33	FAFADLTIV	233	-	31.4
		45	FAFKDLCIV	234	-	176.9

		52	FLFTDLRIV	235	-	
		56	FACTELKLV	236	-	
		58	FVFADLRIV	237	-	7.7
HPV31.E6.45	FAFTDLTIV	16	FAFRDLCIV	<u>230</u>	-	
		18	FAFKDLFVV	231	-	
		31	FAFTDLTIV	232	+	20.7
		33	FAFADLTVV	233	+	11.6
		45	FAFKDLCIV	234	-	
		52	FLFTDLRIV	235	-	
		56	FACTELKLV	236	-	
		58	FVFADLRIV	237	-	
HPV52.E6.45	FLFTDLRIV	16	FAFRDLCIV	<u>230</u>	-	
		18	FAFKDLFVV	231	-	
		31	FAFTDLTIV	232	-	
		33	FAFADLTVV	233	-	
		45	FAFKDLCIV	234	-	
		52	FLFTDLRIV	235	+	421.4
		56	FACTELKLV	236	-	57.5
		58	FVFADLRIV	237	+	94.1
HPV58.E6.45	FVFADLRIV	16	FAFRDLCIV	<u>230</u>	-	
		18	FAFKDLFVV	231	-	
		31	FAFTDLTIV	232	-	
		33	FAFADLTVV	233	-	
		45	FAFKDLCIV	234	-	
		52	FLFTDLRIV	235	+	13.3
		56	FACTELKLV	236	-	21.0
		58	FVFADLRIV	237	+	62.8
HPV18.E7.7	TLQDIVLHL	16	TLHEYMLDL	<u>262</u>	-	
		18	TLQDIVLHL	263	+	99.0
		31	TLQDYVLDL	264	-	
		33	TLKEYVLDL	265	-	
		45	TLQEIVLHL	266	+	
		52	TIKDYILDL	267	-	
		56	TLQDVVLEL	268	+	38.0
		58	TLREYILDL	269	-	
HPV16.E7.82	LLMGTLGIV	16	LLMGTLGIV	270	+	518.5
		18	LFLNTLSFV	271	-	
		31	LLMGSGGIV	272	+	90.1
		33	LLMGTVNIV	273	-	
		45	LFLSTLSFV	274	+	
		52	MLLGTQVIV	275	-	
		56	LLMGALTVT	276	+	
		58	LLMGTCIV	277	-	

HPV33.E7.81	LLMGTVNIV	16	LLMGTLGIV	<u>270</u>	-	
		18	LFLNTLSFV	<u>271</u>	-	
		31	LLMGSFGIV	<u>272</u>	-	
		33	LLMGTVNIV	<u>273</u>	+	179.4
		45	LFLSTLSFV	<u>274</u>	-	
		52	MLLGTLQVV	<u>275</u>	+	
		56	LLMGALTVT	<u>276</u>	-	20.8
		58	LLMGCTIV	<u>277</u>	-	
HPV52.E7.84	MLLGTLQVV	16	LLMGTLGIV	<u>270</u>	-	
		18	LFLNTLSFV	<u>271</u>	-	
		31	LLMGSFGIV	<u>272</u>	-	
		33	LLMGTVNIV	<u>273</u>	+	
		45	LFLSTLSFV	<u>274</u>	-	
		52	MLLGTLQVV	<u>275</u>	+	99.8
		56	LLMGALTVT	<u>276</u>	-	
		58	LLMGCTIV	<u>277</u>	-	
HPV56.E7.89	LLMGALTVT	16	LLMGTLGIV	<u>270</u>	-	
		18	LFLNTLSFV	<u>271</u>	-	
		31	LLMGSFGIV	<u>272</u>	-	
		33	LLMGTVNIV	<u>273</u>	+	
		45	LFLSTLSFV	<u>274</u>	-	
		52	MLLGTLQVV	<u>275</u>	-	
		56	LLMGALTVT	<u>276</u>	+	263.5
		58	LLMGCTIV	<u>277</u>	-	43.6

\* Immunogenicity was measured for all variants. Only the positive responses are shown in the table. All other responses were negative.

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**Table 10. 167 HIV-1 Variants**

<b>SEQ ID-NO</b>	<b>Sequence Designation</b>	<b>Name</b>	<b>Accession Number</b>	<b>SubType</b>	<b>Country</b>
A.UG.92UG037_U51190		92UG037	U51190	A	UG
A.BY.97BL006_AF1932		97BL006	AF193275	A	BY
A.KE.Q23_AF004885		Q23	AF004885	A	KE
A.SE.SE6594_AF06967		SE6594	AF069672	A	SE
A.SE.SE7253_AF06967		SE7253	AF069670	A	SE
A.SE.SE7535_AF06967		SE7535	AF069671	A	SE
A.SE.SE8538_AF06966		SE8538	AF069669	A	SE
A.SE.SE8891_AF06967		SE8891	AF069673	A	SE
A.UG.U455_M62320		U455	M62320	A	UG
A.SE.UGSE8131_AF107		UGSE8131	AF107771	A	SE
A2.CY.94CY017.41_AF		94CY017.41	AF286237	A2	CY
A2.CD.97CDKTB48_AF2		97CDKTB48	AF286238	A2	CD
A2D.-.97KR004_AF286		97KR004	AF286239	A2D	KR
A2G.CD.97CDKP58_AF3		97CDKP58	AF316544	A2G	CD
AC.IN.21301_AF06715		21301	AF067156	AC	IN
AC.RW.92RW009_U8882		92RW009	U88823	AC	RW
AC.SE.SE9488_AF0714		SE9488	AF071474	AC	SE
ACD.SE.SE8603_AF075		SE8603	AF075702	ACD	SE
ACG.BE.VI1035_AJ276		VI1035	AJ276595	ACG	BE
AD.SE.SE6954_AF0757		SE6954	AF075701	AD	SE
AD.SE.SE7108_AF0714		SE7108	AF071473	AD	SE
ADHK.NO.97NOGIL3_AJ		97NOGIL3	AJ237565	ADHK	NO
ADK.CD.MAL_X04415		MAL	X04415	ADK	CD
AG.NG.92NG003_U8882		92NG003	U88825	AG	NG
AG.BE.VI1197_AJ2765		VI1197	AJ276596	AG	BE
AGHU.GA.VI354_AF076		VI354	AF076474	AGHU	GA
AGU.CD.Z321_U76035		Z321	U76035	AGU	CD
AJ.BW.BW2117_AF1921		BW2117	AF192135	AJ	BW
B.NL.3202A21_U34604		3202A21	U34604	B	NL
B.US.BC_L02317		BC	L02317	B	US
B.GB.CAM1_D10112		CAM1	D10112	B	GB
B.DE.D31_U43096		D31	U43096	B	DE
B.US.DH123_AF069140		DH123	AF069140	B	US
B.GB.GB8.C1_Y13716		GB8	AJ271445	B	GB
B.DE.HAN_U43141		HAN	U43141	B	DE
B.FR.HXB2_K03455		HXB2	K03455	B	FR
B.US.JRCSF_M38429		JRCSF	M38429	B	US
B.GB.MANC_U23487		MANC	U23487	B	GB
B.US.MNCG_M17449		MNCG	M17449	B	US
B.GA.OYI_M26727		OYI	M26727	B	GA
B.US.P896_U39362		P896	M96155	B	US
B.US.RF_M17451		RF	M17451	B	US
B.CN.RL42_U71182		RL42	U71182	B	CN
B.US.SF2_K02007		SF2	K02007	B	US
B.TW.TWCYS_AF086817		TWCYS	AF086817	B	TW
B.AU.VH_AF146728		VH	AF146728	B	AU
B.US.WEAU160_U21135		WEAU160	U21135	B	US
B.KR.WK_AF224507		WK	AF224507	B	KR

B.US.WR27_U26546	WR27	U26546	B	US
B.US.YU2_M93258	YU2	M93258	B	US
BF1.BR.93BR029.4_AF	93BR029.4	AF005495	BF1	BR
C.BR.92BR025_U52953	92BR025	U52953	C	BR
C.IN.93IN101_AB0238	93IN101	AB023804	C	IN
C.IN.93IN904_AF0671	93IN904	AF067157	C	IN
C.IN.93IN999_AF0671	93IN999	AF067154	C	IN
C.IN.94IN11246_AF06	94IN11246	AF067159	C	IN
C.IN.95IN21068_AF06	95IN21068	AF067155	C	IN
C.BW.96BW0402_AF110	96BW0402	AF110962	C	BW
C.BW.96BW1210_AF110	96BW1210	AF110972	C	BW
C.BW.96BW15B03_AF11	96BW15B03	AF110973	C	BW
C.ET.ETH2220_U46016	ETH2220	U46016	C	ET
C.BW.96BW11B01_AF11	96BW11	AF110969	C	BW
C.BW.00BW0762.1_AF44	00BW0762.1	AF443088	C	BW
C.BW.00BW0768.20_AF44	00BW0768.20	AF443089	C	BW
C.BW.00BW0874.21_AF44	00BW0874.21	AF443090	C	BW
C.BW.00BW1471.27_AF44	00BW1471.27	AF443091	C	BW
C.BW.00BW1616.2_AF44	00BW1616.2	AF443092	C	BW
C.BW.00BW1686.8_AF44	00BW1686.8	AF443093	C	BW
C.BW.00BW1759.3_AF44	00BW1759.3	AF443094	C	BW
C.BW.00BW1773.2_AF44	00BW1773.2	AF443095	C	BW
C.BW.00BW1783.5_AF44	00BW1783.5	AF443096	C	BW
C.BW.00BW1795.6_AF44	00BW1795.6	AF443097	C	BW
C.BW.00BW1811.3_AF44	00BW1811.3	AF443098	C	BW
C.BW.00BW1859.5_AF44	00BW1859.5	AF443099	C	BW
C.BW.00BW1880.2_AF44	00BW1880.2	AF443100	C	BW
C.BW.00BW1921.13_AF44	00BW1921.13	AF443101	C	BW
C.BW.00BW2036.1_AF44	00BW2036.1	AF443102	C	BW
C.BW.00BW2063.6_AF44	00BW2063.6	AF443103	C	BW
C.BW.00BW2087.2_AF44	00BW2087.2	AF443104	C	BW
C.BW.00BW2127.214_AF44	00BW2127.214	AF443105	C	BW
C.BW.00BW2128.3_AF44	00BW2128.3	AF443106	C	BW
C.BW.00BW2276.7_AF44	00BW2276.7	AF443107	C	BW
C.BW.00BW3819.3_AF44	00BW3819.3	AF443108	C	BW
C.BW.00BW3842.8_AF44	00BW3842.8	AF443109	C	BW
C.BW.00BW3871.3_AF44	00BW3871.3	AF443110	C	BW
C.BW.00BW3876.9_AF44	00BW3876.9	AF443111	C	BW
C.BW.00BW3886.8_AF44	00BW3886.8	AF443112	C	BW
C.BW.00BW3891.6_AF44	00BW3891.6	AF443113	C	BW
C.BW.00BW3970.2_AF44	00BW3970.2	AF443114	C	BW
C.BW.00BW5031.1_AF44	00BW5031.1	AF443115	C	BW
C.BW.96BW01B21_AF11	96BW01B21	AF110960	C	BW
C.BW.96BW0407_AF11	96BW0407	AF110963	C	BW
C.BW.96BW0502_AF11	96BW0502	AF110967	C	BW
C.BW.96BW06.J4_AF29	96BW06.J4	AF290028	C	BW
C.BW.96BW11.06_AF11	96BW11.06	AF110970	C	BW
C.BW.96BW1210_AF11	96BW1210	AF110972	C	BW
C.BW.96BW15B03_AF11	96BW15B03	AF110973	C	BW
C.BW.96BW16.26_AF11	96BW16.26	AF110978	C	BW
C.BW.96BW17A09_AF11	96BW17A09	AF110979	C	BW
C.BW.96BWMO1.5_AF44	96BWMO1.5	AF443074	C	BW
C.BW.96BWMO3.2_AF44	96BWMO3.2	AF443075	C	BW
C.BW.98BWMC12.2_AF44	98BWMC12.2	AF443076	C	BW

C.BW.98BWMC13.4_AF44	98BWMC13.4	AF443077	C	BW
C.BW.98BWMC14.a3_AF44	98BWMC14.a3	AF443078	C	BW
C.BW.98BWMO14.10_AF44	98BWMO14.10	AF443079	C	BW
C.BW.98BWMO18.d5_AF44	98BWMO18.d5	AF443080	C	BW
C.BW.98BWMO36.a5_AF44	98BWMO36.a5	AF443081	C	BW
C.BW.98BWMO37.d5_AF44	98BWMO37.d5	AF443082	C	BW
C.BW.99BW3932.12_AF44	99BW3932.12	AF443083	C	BW
C.BW.99BW4642.4_AF44	99BW4642.4	AF443084	C	BW
C.BW.99BW4745.8_AF44	99BW4745.8	AF443085	C	BW
C.BW.99BW4754.7_AF44	99BW4754.7	AF443086	C	BW
C.BW.99BWMC16.8_AF44	99BWMC16.8	AF443087	C	BW
CRF01_AE.CF.90CF11697_	90CF11697	AF197340	CRF01_AE	CF
CRF01_AE.CF.90CF402_U5	90CF402	U51188	CRF01_AE	CF
CRF01_AE.CF.90CF4071_A	90CF4071	AF197341	CRF01_AE	CF
CRF01_AE.TH.93TH057_AF	93TH057	AF197338	CRF01_AE	TH
CRF01_AE.TH.93TH065_AF	93TH065	AF197339	CRF01_AE	TH
CRF01_AE.TH.93TH253_U5	93TH253	U51189	CRF01_AE	TH
CRF01_AE.TH.95TNIH047_	95TNIH047	AB032741	CRF01_AE	TH
CRF01_AE.TH.CM240_U547	CM240	U54771	CRF01_AE	TH
CRF01_AE.TH.TH022_AB03	TH022	AB032740	CRF01_AE	TH
CRF02_AG.SN.98SEMP1211	98SEMP1211	AJ251056	CRF02_AG	SN
CRF02_AG.FR.DJ263_AF06	DJ263	AF063223	CRF02_AG	FR
CRF02_AG.FR.DJ264_AF06	DJ264	AF063224	CRF02_AG	FR
CRF02_AG.GH.G829_AF184	G829	AF184155	CRF02_AG	GH
CRF02_AG.NG.IBNG_L3910	IBNG	L39106	CRF02_AG	NG
CRF02_AG.SE.SE7812_AF1	SE7812	AF107770	CRF02_AG	SE
CRF03_AB.RU.KAL153-2_A	KAL153-2	AF193276	CRF03_AB	RU
CRF03_AB.RU.RU98001_AF	RU98001	AF193277	CRF03_AB	RU
CRF04_cpx.CY.94CY032-3	94CY032-3	AF049337	CRF04_cpx	CY
CRF04_cpx.GR.97PVCH_AF	97PVCH	AF119820	CRF04_cpx	GR
CRF04_cpx.GR.97PVMY_AF	97PVMY	AF119819	CRF04_cpx	GR
CRF05_DF.BE.VI1310_AF1	VI1310	AF193253	CRF05_DF	BE
CRF05_DF.BE.VI961_AF07	VI961	AF076998	CRF05_DF	BE
CRF06_cpx.ML.95ML127_A	95ML127	AJ288982	CRF06_cpx	ML
CRF06_cpx.ML.95ML84_AJ	95ML84	AJ245481	CRF06_cpx	ML
CRF06_cpx.SN.97SE1078_	97SE1078	AJ288981	CRF06_cpx	SN
CRF06_cpx.AU.BFP90_AF0	BFP90	AF064699	CRF06_cpx	AU
CRF11_cpx.CM.97CM-MP81	97CM-MP818	AJ291718	CRF11_cpx	CM
CRF11_cpx.GR.GR17_AF17	GR17	AF179368	CRF11_cpx	GR
D.CD.84ZR085_U88822	84ZR085	U88822	D	CD
D.UG.94UG1141_U8882	94UG1141	U88824	D	UG
D.CD.ELI_K03454	ELI	K03454	D	CD
D.CD.NDK_M27323	NDK	M27323	D	CD
F1.BR.93BR020.1_AF0	93BR020.1	AF005494	F1	BR
F1.FI.FIN9363_AF075	FIN9363	AF075703	F1	FI
F1.FR.MP411_AJ24923	MP411	AJ249238	F1	FR
F1.BE.VI850_AF07733	VI850	AF077336	F1	BE
F2.CM.MP257_AJ24923	MP257	AJ249237	F2	CM
F2KU.BE.VI1126_AF07	VI1126	AF076475	F2KU	BE
G.NG.92NG083_U88826	92NG083	U88826	G	NG
G.BE.DRCBL_AF084936	DRCBL	AF084936	G	BE
G.SE.SE6165_AF06164	SE6165	AF061642	G	SE
H.CF.90CF056_AF0054	90CF056	AF005496	H	CF
H.BE.VI991_AF190127	VI991	AF190127	H	BE

H.BE.VI997_AF190128	VI997	AF190128	H	BE
J.SE.SE7022_AF08239	SE7022	AF082395	J	SE
J.SE.SE7887_AF08239	SE7887	AF082394	J	SE
K.CD.EQTB11C_AJ2492	EQTB11C	AJ249235	K	CD
K.CM.MP535_AJ249239	MP535	AJ249239	K	CM
N.CM.YBF30_AJ006022	YBF30	AJ006022	N	CM
O.SN.99SE-MP1299_ZX	SEMP1299	AJ302646	O	SN
O.SN.99SE-MP1300_ZX	SEMP1300	AJ302647	O	SN
O.CM.ANT70_L20587	ANT70	L20587	O	CM
O.CM.MVP5180_L20571	MVP5180	L20571	O	CM
U.CD.-.83CD0031	83CD0031	AF286236	U	CD

Table 11. HIV Gag Sequence Alignment

GCG Multiple Sequence File.

Written by Omega 1.1

Name: 00BW0762_1	<u>SEQ ID NO: 302</u>	Len: 556	Check: 2513	Weight: 1.00
Name: 00BW0768_2	<u>SEQ ID NO: 303</u>	Len: 556	Check: 8965	Weight: 1.00
Name: 00BW0874_2	<u>SEQ ID NO: 304</u>	Len: 556	Check: 9574	Weight: 1.00
Name: 00BW1471_2	<u>SEQ ID NO: 305</u>	Len: 556	Check: 5395	Weight: 1.00
Name: 00BW1616_2	<u>SEQ ID NO: 306</u>	Len: 556	Check: 4692	Weight: 1.00
Name: 00BW1686_8	<u>SEQ ID NO: 307</u>	Len: 556	Check: 7822	Weight: 1.00
Name: 00BW1759_3	<u>SEQ ID NO: 308</u>	Len: 556	Check: 7777	Weight: 1.00
Name: 00BW1773_2	<u>SEQ ID NO: 309</u>	Len: 556	Check: 9727	Weight: 1.00
Name: 00BW1783_5	<u>SEQ ID NO: 310</u>	Len: 556	Check: 9681	Weight: 1.00
Name: 00BW1795_6	<u>SEQ ID NO: 311</u>	Len: 556	Check: 9667	Weight: 1.00
Name: 00BW1811_3	<u>SEQ ID NO: 312</u>	Len: 556	Check: 4422	Weight: 1.00
Name: 00BW1859_5	<u>SEQ ID NO: 313</u>	Len: 556	Check: 7320	Weight: 1.00
Name: 00BW1880_2	<u>SEQ ID NO: 314</u>	Len: 556	Check: 1603	Weight: 1.00
Name: 00BW1921_1	<u>SEQ ID NO: 315</u>	Len: 556	Check: 883	Weight: 1.00
Name: 00BW2036_1	<u>SEQ ID NO: 316</u>	Len: 556	Check: 2591	Weight: 1.00
Name: 00BW2063_6	<u>SEQ ID NO: 317</u>	Len: 556	Check: 5152	Weight: 1.00
Name: 00BW2087_2	<u>SEQ ID NO: 318</u>	Len: 556	Check: 5183	Weight: 1.00
Name: 00BW2127_2	<u>SEQ ID NO: 319</u>	Len: 556	Check: 5469	Weight: 1.00
Name: 00BW2128_3	<u>SEQ ID NO: 320</u>	Len: 556	Check: 9621	Weight: 1.00
Name: 00BW2276_7	<u>SEQ ID NO: 321</u>	Len: 556	Check: 4153	Weight: 1.00
Name: 00BW3819_3	<u>SEQ ID NO: 322</u>	Len: 556	Check: 4227	Weight: 1.00
Name: 00BW3842_8	<u>SEQ ID NO: 323</u>	Len: 556	Check: 9312	Weight: 1.00
Name: 00BW3871_3	<u>SEQ ID NO: 324</u>	Len: 556	Check: 501	Weight: 1.00
Name: 00BW3876_9	<u>SEQ ID NO: 325</u>	Len: 556	Check: 773	Weight: 1.00
Name: 00BW3886_8	<u>SEQ ID NO: 326</u>	Len: 556	Check: 2351	Weight: 1.00
Name: 00BW3891_6	<u>SEQ ID NO: 327</u>	Len: 556	Check: 129	Weight: 1.00
Name: 00BW3970_2	<u>SEQ ID NO: 328</u>	Len: 556	Check: 8768	Weight: 1.00
Name: 00BW5031_1	<u>SEQ ID NO: 329</u>	Len: 556	Check: 3966	Weight: 1.00
Name: 96BW01B21	<u>SEQ ID NO: 330</u>	Len: 556	Check: 602	Weight: 1.00
Name: 96BW0407	<u>SEQ ID NO: 331</u>	Len: 556	Check: 9836	Weight: 1.00
Name: 96BW0502	<u>SEQ ID NO: 332</u>	Len: 556	Check: 6402	Weight: 1.00
Name: 96BW06_J4	<u>SEQ ID NO: 333</u>	Len: 556	Check: 254	Weight: 1.00
Name: 96BW11_06	<u>SEQ ID NO: 334</u>	Len: 556	Check: 6801	Weight: 1.00
Name: 96BW1210	<u>SEQ ID NO: 335</u>	Len: 556	Check: 6016	Weight: 1.00
Name: 96BW15B03	<u>SEQ ID NO: 336</u>	Len: 556	Check: 6072	Weight: 1.00
Name: 96BW16_26	<u>SEQ ID NO: 337</u>	Len: 556	Check: 9409	Weight: 1.00
Name: 96BW17A09	<u>SEQ ID NO: 338</u>	Len: 556	Check: 2723	Weight: 1.00
Name: 96BWM01_5	<u>SEQ ID NO: 339</u>	Len: 556	Check: 5051	Weight: 1.00
Name: 96BWM03_2	<u>SEQ ID NO: 340</u>	Len: 556	Check: 496	Weight: 1.00
Name: 98BWMC12_2	<u>SEQ ID NO: 341</u>	Len: 556	Check: 1164	Weight: 1.00
Name: 98BWMC13_4	<u>SEQ ID NO: 342</u>	Len: 556	Check: 4961	Weight: 1.00
Name: 98BWMC14_a	<u>SEQ ID NO: 343</u>	Len: 556	Check: 7351	Weight: 1.00
Name: 98BWM014_1	<u>SEQ ID NO: 344</u>	Len: 556	Check: 288	Weight: 1.00
Name: 98BWM018_d	<u>SEQ ID NO: 345</u>	Len: 556	Check: 6836	Weight: 1.00
Name: 98BWM036_a	<u>SEQ ID NO: 346</u>	Len: 556	Check: 4386	Weight: 1.00
Name: 98BWM037_d	<u>SEQ ID NO: 347</u>	Len: 556	Check: 6900	Weight: 1.00
Name: 99BW3932_1	<u>SEQ ID NO: 348</u>	Len: 556	Check: 292	Weight: 1.00
Name: 99BW4642_4	<u>SEQ ID NO: 349</u>	Len: 556	Check: 1347	Weight: 1.00
Name: 99BW4745_8	<u>SEQ ID NO: 350</u>	Len: 556	Check: 7980	Weight: 1.00
Name: 99BW4754_7	<u>SEQ ID NO: 351</u>	Len: 556	Check: 9892	Weight: 1.00
Name: 99BWMC16_8	<u>SEQ ID NO: 352</u>	Len: 556	Check: 4279	Weight: 1.00
Name: A2_CD_97CD	<u>SEQ ID NO: 353</u>	Len: 556	Check: 9920	Weight: 1.00
Name: A2_CY_94CY	<u>SEQ ID NO: 354</u>	Len: 556	Check: 3070	Weight: 1.00
Name: A2D_97KR	<u>SEQ ID NO: 355</u>	Len: 556	Check: 6350	Weight: 1.00
Name: A2G_CD_97C	<u>SEQ ID NO: 356</u>	Len: 556	Check: 856	Weight: 1.00
Name: A_BY_97BL0	<u>SEQ ID NO: 357</u>	Len: 556	Check: 9315	Weight: 1.00



Name: A_KE_Q23_A	<u>SEQ ID NO: 358</u>	Len: 556	Check: 2442	Weight: 1.00
Name: A_SE_SE659	<u>SEQ ID NO: 359</u>	Len: 556	Check: 8612	Weight: 1.00
Name: A_SE_SE725	<u>SEQ ID NO: 360</u>	Len: 556	Check: 8315	Weight: 1.00
Name: A_SE_SE753	<u>SEQ ID NO: 361</u>	Len: 556	Check: 2915	Weight: 1.00
Name: A_SE_SE853	<u>SEQ ID NO: 362</u>	Len: 556	Check: 9112	Weight: 1.00
Name: A_SE_SE889	<u>SEQ ID NO: 363</u>	Len: 556	Check: 8732	Weight: 1.00
Name: A_SE_UGSE8	<u>SEQ ID NO: 364</u>	Len: 556	Check: 8696	Weight: 1.00
Name: A_UG_92UG0	<u>SEQ ID NO: 365</u>	Len: 556	Check: 6290	Weight: 1.00
Name: A_UG_U455_	<u>SEQ ID NO: 366</u>	Len: 556	Check: 164	Weight: 1.00
Name: AC_IN_2130	<u>SEQ ID NO: 367</u>	Len: 556	Check: 8482	Weight: 1.00
Name: AC_RW_92RW	<u>SEQ ID NO: 368</u>	Len: 556	Check: 977	Weight: 1.00
Name: AC_SE_SE94	<u>SEQ ID NO: 369</u>	Len: 556	Check: 8752	Weight: 1.00
Name: ACD_SE_SE8	<u>SEQ ID NO: 370</u>	Len: 556	Check: 9655	Weight: 1.00
Name: ACG_BE_VI1	<u>SEQ ID NO: 371</u>	Len: 556	Check: 3777	Weight: 1.00
Name: AD_SE_SE69	<u>SEQ ID NO: 372</u>	Len: 556	Check: 732	Weight: 1.00
Name: AD_SE_SE71	<u>SEQ ID NO: 373</u>	Len: 556	Check: 8506	Weight: 1.00
Name: ADHK_NO_97	<u>SEQ ID NO: 374</u>	Len: 556	Check: 5257	Weight: 1.00
Name: ADK_CD_MAL	<u>SEQ ID NO: 375</u>	Len: 556	Check: 5301	Weight: 1.00
Name: AG_BE_VI11	<u>SEQ ID NO: 376</u>	Len: 556	Check: 1610	Weight: 1.00
Name: AG_NG_92NG	<u>SEQ ID NO: 377</u>	Len: 556	Check: 4188	Weight: 1.00
Name: AGHU_GA_VI	<u>SEQ ID NO: 378</u>	Len: 556	Check: 8242	Weight: 1.00
Name: AGU_CD_Z32	<u>SEQ ID NO: 379</u>	Len: 556	Check: 2601	Weight: 1.00
Name: AJ_BW_BW21	<u>SEQ ID NO: 380</u>	Len: 556	Check: 8389	Weight: 1.00
Name: B_AU_VH_AF	<u>SEQ ID NO: 381</u>	Len: 556	Check: 9166	Weight: 1.00
Name: B_CN_RL42_	<u>SEQ ID NO: 382</u>	Len: 556	Check: 3865	Weight: 1.00
Name: B_DE_D31_U	<u>SEQ ID NO: 383</u>	Len: 556	Check: 9464	Weight: 1.00
Name: B_DE_HAN_U	<u>SEQ ID NO: 384</u>	Len: 556	Check: 6999	Weight: 1.00
Name: B_FR_HXB2_	<u>SEQ ID NO: 385</u>	Len: 556	Check: 141	Weight: 1.00
Name: B_GA_OYI_	<u>SEQ ID NO: 386</u>	Len: 556	Check: 7578	Weight: 1.00
Name: B_GB_CAM1_	<u>SEQ ID NO: 387</u>	Len: 556	Check: 8023	Weight: 1.00
Name: B_GB_GB8_A	<u>SEQ ID NO: 388</u>	Len: 556	Check: 2675	Weight: 1.00
Name: B_GB_MANC	<u>SEQ ID NO: 389</u>	Len: 556	Check: 8961	Weight: 1.00
Name: B_KR_WK_AF	<u>SEQ ID NO: 390</u>	Len: 556	Check: 7372	Weight: 1.00
Name: B_NL_3202A	<u>SEQ ID NO: 391</u>	Len: 556	Check: 7117	Weight: 1.00
Name: B_TW_TWCYS	<u>SEQ ID NO: 392</u>	Len: 556	Check: 8767	Weight: 1.00
Name: B_US_BC_LO	<u>SEQ ID NO: 393</u>	Len: 556	Check: 7091	Weight: 1.00
Name: B_US_DH123	<u>SEQ ID NO: 394</u>	Len: 556	Check: 5049	Weight: 1.00
Name: B_US_JRCSE	<u>SEQ ID NO: 395</u>	Len: 556	Check: 975	Weight: 1.00
Name: B_US_MNCG_	<u>SEQ ID NO: 396</u>	Len: 556	Check: 688	Weight: 1.00
Name: B_US_P896_	<u>SEQ ID NO: 397</u>	Len: 556	Check: 8809	Weight: 1.00
Name: B_US_RF_M1	<u>SEQ ID NO: 398</u>	Len: 556	Check: 9306	Weight: 1.00
Name: B_US_SF2_K	<u>SEQ ID NO: 399</u>	Len: 556	Check: 9799	Weight: 1.00
Name: B_US_WEAU1	<u>SEQ ID NO: 400</u>	Len: 556	Check: 9636	Weight: 1.00
Name: B_US_WR27_	<u>SEQ ID NO: 401</u>	Len: 556	Check: 3349	Weight: 1.00
Name: B_US_YU2_M	<u>SEQ ID NO: 402</u>	Len: 556	Check: 8828	Weight: 1.00
Name: BF1_BR_93B	<u>SEQ ID NO: 403</u>	Len: 556	Check: 7935	Weight: 1.00
Name: C_BR_92BR0	<u>SEQ ID NO: 404</u>	Len: 556	Check: 4429	Weight: 1.00
Name: C_BW_96BW0	<u>SEQ ID NO: 405</u>	Len: 556	Check: 1550	Weight: 1.00
Name: C_BW_96BW1	<u>SEQ ID NO: 406</u>	Len: 556	Check: 7158	Weight: 1.00
Name: C_BW_96BW1	<u>SEQ ID NO: 407</u>	Len: 556	Check: 6016	Weight: 1.00
Name: C_BW_96BW1	<u>SEQ ID NO: 408</u>	Len: 556	Check: 6072	Weight: 1.00
Name: C_ET_ETH22	<u>SEQ ID NO: 409</u>	Len: 556	Check: 4314	Weight: 1.00
Name: C_IN_93IN1	<u>SEQ ID NO: 410</u>	Len: 556	Check: 6959	Weight: 1.00
Name: C_IN_93IN9	<u>SEQ ID NO: 411</u>	Len: 556	Check: 9362	Weight: 1.00
Name: C_IN_93IN9	<u>SEQ ID NO: 412</u>	Len: 556	Check: 3298	Weight: 1.00
Name: C_IN_94IN1	<u>SEQ ID NO: 413</u>	Len: 556	Check: 6744	Weight: 1.00
Name: C_IN_95IN2	<u>SEQ ID NO: 414</u>	Len: 556	Check: 8559	Weight: 1.00
Name: CRF01_AE_C	<u>SEQ ID NO: 415</u>	Len: 556	Check: 4763	Weight: 1.00
Name: CRF01_AE_C	<u>SEQ ID NO: 416</u>	Len: 556	Check: 4315	Weight: 1.00
Name: CRF01_AE_C	<u>SEQ ID NO: 417</u>	Len: 556	Check: 3920	Weight: 1.00

Name: CRF01_AE_T	<u>SEQ ID NO: 418</u>	Len: 556	Check: 5074	Weight: 1.00
Name: CRF01_AE_T	<u>SEQ ID NO: 419</u>	Len: 556	Check: 4026	Weight: 1.00
Name: CRF01_AE_T	<u>SEQ ID NO: 420</u>	Len: 556	Check: 2981	Weight: 1.00
Name: CRF01_AE_T	<u>SEQ ID NO: 421</u>	Len: 556	Check: 6648	Weight: 1.00
Name: CRF01_AE_T	<u>SEQ ID NO: 422</u>	Len: 556	Check: 6948	Weight: 1.00
Name: CRF01_AE_T	<u>SEQ ID NO: 423</u>	Len: 556	Check: 6129	Weight: 1.00
Name: CRF02_AG_F	<u>SEQ ID NO: 424</u>	Len: 556	Check: 8134	Weight: 1.00
Name: CRF02_AG_F	<u>SEQ ID NO: 425</u>	Len: 556	Check: 8925	Weight: 1.00
Name: CRF02_AG_G	<u>SEQ ID NO: 426</u>	Len: 556	Check: 9991	Weight: 1.00
Name: CRF02_AG_N	<u>SEQ ID NO: 427</u>	Len: 556	Check: 9388	Weight: 1.00
Name: CRF02_AG_S	<u>SEQ ID NO: 428</u>	Len: 556	Check: 9371	Weight: 1.00
Name: CRF02_AG_S	<u>SEQ ID NO: 429</u>	Len: 556	Check: 3289	Weight: 1.00
Name: CRF03_AB_R	<u>SEQ ID NO: 430</u>	Len: 556	Check: 5554	Weight: 1.00
Name: CRF03_AB_R	<u>SEQ ID NO: 431</u>	Len: 556	Check: 5307	Weight: 1.00
Name: CRF04_cpx	<u>SEQ ID NO: 432</u>	Len: 556	Check: 5488	Weight: 1.00
Name: CRF04_cpx	<u>SEQ ID NO: 433</u>	Len: 556	Check: 6046	Weight: 1.00
Name: CRF04_cpx	<u>SEQ ID NO: 434</u>	Len: 556	Check: 3807	Weight: 1.00
Name: CRF05_DF_B	<u>SEQ ID NO: 435</u>	Len: 556	Check: 6702	Weight: 1.00
Name: CRF05_DF_B	<u>SEQ ID NO: 436</u>	Len: 556	Check: 5563	Weight: 1.00
Name: CRF06_cpx	<u>SEQ ID NO: 437</u>	Len: 556	Check: 8164	Weight: 1.00
Name: CRF06_cpx	<u>SEQ ID NO: 438</u>	Len: 556	Check: 1975	Weight: 1.00
Name: CRF06_cpx	<u>SEQ ID NO: 439</u>	Len: 556	Check: 1486	Weight: 1.00
Name: CRF06_cpx	<u>SEQ ID NO: 440</u>	Len: 556	Check: 4050	Weight: 1.00
Name: CRF11_cpx	<u>SEQ ID NO: 441</u>	Len: 556	Check: 1515	Weight: 1.00
Name: CRF11_cpx	<u>SEQ ID NO: 442</u>	Len: 556	Check: 9474	Weight: 1.00
Name: D_CD_84ZR0	<u>SEQ ID NO: 443</u>	Len: 556	Check: 4739	Weight: 1.00
Name: D_CD_ELI_K	<u>SEQ ID NO: 444</u>	Len: 556	Check: 8533	Weight: 1.00
Name: D_CD_NDK_M	<u>SEQ ID NO: 445</u>	Len: 556	Check: 6100	Weight: 1.00
Name: D_UG_94UG1	<u>SEQ ID NO: 446</u>	Len: 556	Check: 7681	Weight: 1.00
Name: F1_BE_VI85	<u>SEQ ID NO: 447</u>	Len: 556	Check: 8540	Weight: 1.00
Name: F1_BR_93BR	<u>SEQ ID NO: 448</u>	Len: 556	Check: 241	Weight: 1.00
Name: F1_FI_FIN9	<u>SEQ ID NO: 449</u>	Len: 556	Check: 7510	Weight: 1.00
Name: F1_FR_MP41	<u>SEQ ID NO: 450</u>	Len: 556	Check: 9846	Weight: 1.00
Name: F2_CM_MP25	<u>SEQ ID NO: 451</u>	Len: 556	Check: 1247	Weight: 1.00
Name: F2KU_BE_VI	<u>SEQ ID NO: 452</u>	Len: 556	Check: 2186	Weight: 1.00
Name: G_BE_DRCBL	<u>SEQ ID NO: 453</u>	Len: 556	Check: 8049	Weight: 1.00
Name: G_NG_92NG0	<u>SEQ ID NO: 454</u>	Len: 556	Check: 254	Weight: 1.00
Name: G_SE_SE616	<u>SEQ ID NO: 455</u>	Len: 556	Check: 6407	Weight: 1.00
Name: H_BE_VI991	<u>SEQ ID NO: 456</u>	Len: 556	Check: 808	Weight: 1.00
Name: H_BE_VI997	<u>SEQ ID NO: 457</u>	Len: 556	Check: 4749	Weight: 1.00
Name: H_CF_90CF0	<u>SEQ ID NO: 458</u>	Len: 556	Check: 4718	Weight: 1.00
Name: J_SE_SE702	<u>SEQ ID NO: 459</u>	Len: 556	Check: 2564	Weight: 1.00
Name: J_SE_SE788	<u>SEQ ID NO: 460</u>	Len: 556	Check: 2692	Weight: 1.00
Name: K_CD_EQTB1	<u>SEQ ID NO: 461</u>	Len: 556	Check: 6586	Weight: 1.00
Name: K_CM_MP535	<u>SEQ ID NO: 462</u>	Len: 556	Check: 3803	Weight: 1.00
Name: N_CM_YBF30	<u>SEQ ID NO: 463</u>	Len: 556	Check: 8603	Weight: 1.00
Name: O_CM_ANT70	<u>SEQ ID NO: 464</u>	Len: 556	Check: 365	Weight: 1.00
Name: O_CM_MVP51	<u>SEQ ID NO: 465</u>	Len: 556	Check: 9160	Weight: 1.00
Name: O_SN_99SE	<u>SEQ ID NO: 466</u>	Len: 556	Check: 9380	Weight: 1.00
Name: O_SN_99SE	<u>SEQ ID NO: 467</u>	Len: 556	Check: 8796	Weight: 1.00
Name: U_CD_83C	<u>SEQ ID NO: 468</u>	Len: 556	Check: 4633	Weight: 1.00

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<u>SEQ ID NO</u>		1				50
<u>302</u>	00BW0762_1	MGARASILRG	.EKLDKWEKI	RLRPGGRKHY	MIKHIVWASR	ELERFALNPG
<u>303</u>	00BW0768_2	MGARASVLRG	.EKLDKWEKI	RLRPGGKKHY	MLKHLVWASR	ELERFALNPG
<u>304</u>	00BW0874_2	MGARASILRG	.GKLDTWEKI	RLRPGGKKQY	MIKHLVWASR	ELERFALNPG
<u>305</u>	00BW1471_2	MGARASILRG	.GKLDTWEKI	RLRPGGKKHY	MLKHLVWASR	ELERFALNPG

306	00BW1616_2	MGARASILRG	.GKLDEWEKI	RLRPGGKKRY	MMKHLVWASR	ELERFALNPG
307	00BW1686_8	MGARASILRG	.GKLDTWEKI	RLRPGGKKHY	MIKHLVWASR	ELERFALNPG
308	00BW1759_3	MGARASILRG	.GKLDKWERI	RLRPGGKKHY	MLKHLVWASR	ELERFALNPG
309	00BW1773_2	MGASASILRG	.GKLDKWEKI	RLRPGGKKKY	RLKHLVWASR	ELERFALNSG
310	00BW1783_5	MGARASILRG	.GKLDTWEKI	RLRPGGKKHY	MMKHLVWASR	ELERFALNPG
311	00BW1795_6	MGARASILRG	.GKLDKWEKI	RLRPGGKKHY	MMKHLVWASR	ELERFALNPG
312	00BW1811_3	MGARASILRG	.GKLDKWEKI	RLRPGGKKHY	MLKHLVWASR	ELERFALNPG
313	00BW1859_5	MGARASVLKG	.EKLDWEKI	RLRPGGKKGY	MLKHLVWASR	ELERFALNPG
314	00BW1880_2	MGARASILRG	.GKLDKWERI	RLRPGGKKQY	MIKHLVWASR	ELERFALNPG
315	00BW1921_1	MGARASILRG	.GKLDTWEKI	RLRPGGKKRY	MLKHLIWTSR	ELERFALNPD
316	00BW2036_1	MGARASILRG	.EKLDTWERI	KLRPGGKKHY	MLKHLVWASR	ELERFALNPG
317	00BW2063_6	MGARASILRG	.GKLDKWEKI	RLRPGGKKQY	MIKHLVWASR	ELERFALNPG
318	00BW2087_2	MGARASILRG	.GKLDTWEKI	KLRPGGKKSY	KLKHLVWASR	ELERFALNPS
319	00BW2127_2	MGARASILRG	XEKLDEWEKI	RLRPGGRKKY	RLKHLVWASR	ELENFALNPG
320	00BW2128_3	MGARASILRG	.GQLDKWEKI	RLRPGGKKHY	MLKHLVWASG	ELEKFALNPG
321	00BW2276_7	MGARASVLKG	.DKLDAWEKI	KLRPGGKKHY	MLKHLVWASR	ELERFALNPG
322	00BW3819_3	MGARASILRG	.GKLDAWERT	RLRPGGKKHY	RLKHLVWASR	ELERFALNPG
323	00BW3842_8	MGARASVLRG	.EKLDTWERI	KLRPGGKKHY	MLKHIVWASR	ELERFALNPG
324	00BW3871_3	MGARASILRG	.GKLDTWEKI	RLRPGGKKHY	MLKHLVWASR	ELERFALNPG
325	00BW3876_9	MGARASILKG	.GKLDTWEKI	RLRPGGKKHY	MVKHLVWASR	ELERFALNPG
326	00BW3886_8	MGARASILRG	.GKLDKWEKI	RLRPGGKKCY	MIKHIIWASR	ELERFALNPG
327	00BW3891_6	MGARASILRG	.GKLDKWEKI	RLRPGGKKKY	MLKHLVWASR	ELERFALNSG
328	00BW3970_2	MGARASILRG	.GKLDAWERI	KLRPGGKKHY	MLKHLVWASR	ELERFALNPS
329	00BW5031_1	MGARASILRG	.GKLDRWEKI	RLRPGGKKKY	RLKHLVWASR	ELERFALNPS
330	96BW01B21	MGARASILRG	.GKLDQWEKI	RLRPGGKKCY	MLKHLVWASR	ELERFALNPG
331	96BW0407	MGARASILRG	.GKLDAWERI	RLRPGGKKCY	MMKHLVWASR	ELEKFALNPG
332	96BW0502	MGARASILRG	.EKLDKWEKI	RLRPGGKKHY	MLKHLVWASR	ELEGFALNPG
333	96BW06_J4	MGARASILRG	.GNLDTWEKI	RLRPGGKKHY	MLKHLVWASR	ELERFALNPG
334	96BW11_06	MGARASILRG	.GKLDKWEKI	RLRPGGKKRY	MIKHLVWASR	ELERFALNPG
335	96BW1210	MGARASILRG	.EKLDTWEKI	RLRPGGKKRY	MMKHLVWASR	ELENFALNPA
336	96BW15B03	MGARASISRG	.EKLDTWEKI	RSRPGGKKCY	MLKHIVWASR	ELERFALNPG
337	96BW16_26	MGARASILRG	.GKLDKWEKI	RLRPGGKKRY	MLKHLVWASR	ELERFALNPG
338	96BW17A09	MGARASILRG	.GKLDTWEKI	RLRPGGKKHY	MLKHLVWASR	ELERFALNPG
339	96BWM01_5	MGARASILRR	.GKLDKWEKI	RLRPGGKKRY	MIKHLVWASR	ELERYALNPG
340	96BWM03_2	MGARASILRG	.EKLDKWEKI	RLRPGGKKHY	MLKHIVWASR	ELEKFALNPG
341	98BWMC12_2	MGARASILRG	.EKLDTWEKI	RLRPGGKKQY	RIKHLVWASR	ELDRFALNSG
342	98BWMC13_4	MGARASILRG	.GKLDKWEKI	RLRPGGKKHY	MMKHLVWASR	ELGRFALNPG
343	98BWMC14_a	MGARASILRG	.GKLDKWEKI	RLRPGGKKHY	MLKHLVWASR	ELERFALNPG
344	98BWM014_1	MGARASILRG	.GKLDKWERI	RLRPGGKKQY	RLKHLVWASR	ELERFALNPG
345	98BWM018_d	MGARASILRG	.GKLDTWERI	KLRPGGKKHY	MMKHLVWASR	ELERFALNPS
346	98BWM036_a	MGARASILRG	.GKLDTWEKI	RLRPGGKKPY	MLKHLVWASR	ELERFALNPG
347	98BWM037_d	MGARASILRG	.GKLDWEKI	RLRPGGKKHY	MLKHLVWASR	ELERFALNPG
348	99BW3932_1	MGARASILRG	.GKLDEWEKI	RLRPGGKKKY	RLKHLVWASR	ELERFALNPE
349	99BW4642_4	MGARASVLKG	.EKLDTWEKI	RLRPGGRKHY	MLKHLVWASR	ELERFALNPG
350	99BW4745_8	MGARASILRG	.GKLGNERI	KLRPGGRKTY	MLKHLVWASR	ELERFALNPS
351	99BW4754_7	MGARASILRG	.EKLDRWEKI	WLRPGGKNHY	MLKHLVWASR	ELERFALNPA
352	99BWMC16_8	MGARASILRG	.GKLDTWEKI	RLRPGGKKHY	MIKHLVWASR	ELERFALNPG
353	A2_CD_97CD	MGARASVLSG	.GKLEAWEKI	RLRPGGKKKY	RLKHLVWASR	ELEKFSINPS
354	A2_CY_94CY	MGARASILSG	.GKLDWEKI	RLRPGGKKKY	RLKHLVWASR	ELEKFSINPG
355	A2D___97KR	MGARASVLSG	.GKLDWEKI	RLRPGGKKKY	RLKHLVWASR	ELERFAINPG
356	A2G_CD_97C	..ARASILSG	.GKLEAWEKI	RLRPGGKKKY	RLKHLVWASR	ELEKFSINPG

357	A_BY_97BL0	XGARASVLSG	.GKLDA.EKI	RLRPXGKKKY	RIKHLVWASR	ELERFALNPG
358	A_KE_Q23_A	MGARASVLSG	.GKFDAWEKI	RLRPGGKKKY	RMKHLIWASR	ELDRFALNPS
359	A_SE_SE659	...RASVLSG	.GKLDAWEKI	RLRPGGKKKY	RLKHLVWASR	ELERFALNPS
360	A_SE_SE725	...RASVLSG	.GKLDAWEKI	RLRPGGKKKY	RMKHLVWASR	ELERFALNPS
361	A_SE_SE753	MGARASVLSG	.GKLDAWEKI	RLRPGGKKQY	RLKHLVWASR	ELERFALNPS
362	A_SE_SE853	...RASVLSG	.GRLDAWEKI	RLRPGGKKKY	RMKHLVWASR	ELDRFALNPS
363	A_SE_SE889	...RASKLSG	.EKKDAWEKM	RLRPGGKKKY	KLKHMVWARR	ELEKSALNPS
364	A_SE_UGSE8	MGARASVLSG	.GKLDAWEKI	RLRPGGNKKY	RLKHLVWASR	ELEKFALNPG
365	A_UG_92UG0	MGARASVLSG	.GKLDAWEKI	RLRPGGKKKY	RLKHLVWASR	ELERFALNPS
366	A_UG_U455_	MGARASVLSG	.KKLDSWEKI	RLRPGGNKKY	RLKHLVWASR	ELEKFTLNPG
367	AC_IN_2130	MGARASILRG	.GKLDKWEKI	RLRPGGKKHY	MIKHLVWASR	ELERFALNPG
368	AC_RW_92RW	MGARASILRG	.GKLDAWEKI	KLKPGGKKTY	MMKHLVWASR	ELERFALNPD
369	AC_SE_SE94	...RASVLSG	.GKLDAWEKI	RLRPGGKKKY	RMKHLVWASR	ELDRFALNPS
370	ACD_SE_SE8	MGARASILSG	.GKLDAWEKI	RLRPGGKKKY	RLKHLVWASR	ELDRFALNPS
371	ACG_BE_VI1	MGARASVLTG	.GKLDTWERI	RLRPAGKKKY	RMKLLVWASR	ELERFAINPG
372	AD_SE_SE69	MGARASVLSG	.ERLDEWEKI	QLRPGGKKRY	RLKHIVWASR	ELERFALNPG
373	AD_SE_SE71	...RASVLSG	.GKLDAWEKI	RLRPGGRKKY	KLKHIVWASR	ELERFALNPS
374	ADHK_NO_97	MGARASILSG	.GKLDKWEKI	RLRPGGKKQY	RLKHLVWASR	ELDRFALNPS
375	ADK_CD_MAL	MGARASVLSG	.GKLDAWEKI	RLRPGGKKKY	RLKHLVWASR	ELERFALNPG
376	AG_BE_VI11	MGARASVLSG	.GKLDAWEKI	RLRPGGKKKY	RMKHLVWASR	ELERFAINPG
377	AG_NG_92NG	MGARASVLSG	.GKLDAWEKI	RLRPGGKKKY	RMKHLVWASR	ELERFALNPD
378	AGHU_GA_VI	MGARASILSG	.GKLDAWEKI	RLRPGGKKKY	QIKHIVWASR	ELERFALNPG
379	AGU_CD_Z32	MGARASVLSG	.GKLDKWEKI	RLRPGGKKQY	KLKHIVWASR	ELERFALNPG
380	AJ_BW_BW21	MGARASVLSG	.GKLDAWEKI	RLRPGGKKQY	RMKHLVWASR	ELERFALNPG
381	B_AU_VH_AF	MGARASVLSG	.GELDRWEKI	RLRPGGKKTY	KLKHIVWASR	ELERFAVNPG
382	B_CN_RL42_	MGARASVLSG	.GQLDRWEKI	RLRPGGKKKY	RLKHLVWASR	ELERFAVNPG
383	B_DE_D31_U	MGARASVLSG	.GELDRWEKI	RLRPGGKKKY	RLKHIVWASR	ELERFAVNPG
384	B_DE_HAN_U	MGARASVLSG	.GELDKWEKI	RLRPGGKKKY	QLKHIVWASR	ELERFAVNPG
385	B_FR_HXB2_	MGARASVLSG	.GELDRWEKI	RLRPGGKKKY	KLKHIVWASR	ELERFAVNPG
386	B_GA_OYI_	MGARASVLSG	.GELDKWEKI	RLRPGGKKKY	QLKHIVWASR	ELERFAINPG
387	B_GB_CAM1_	MGARASVLSG	.GELDKWEKI	RLRPGGKKKY	KLKHIVWASR	ELERFAVNPG
388	B_GB_GB8_A	MGARASVLSG	.GELDRWEKI	RLRPGGKKKY	RLKHVVWASR	ELERFAVNPG
389	B_GB_MANC_	MGARASVLSG	.GKLDRWEKI	RLRPGGKKKY	KLKHIVWASR	ELERFTVNLG
390	B_KR_WK_AF	MGARASILSG	.GELDQWEKI	RLRPGGKKKY	RLKHLVWASR	ELERFAVNPG
391	B_NL_3202A	MGARASVLSG	.GELDKWEKI	RLRPGGKKRY	KLKHIVWASR	ELERFAVNPG
392	B_TW_TWCYS	MGARASILSA	.GELDKWERV	RLRPGGKKKY	RLKHLVWASR	ELERFAVNPG
393	B_US_BC_L0	MGARASVLSG	.GKLDKWEKI	RLRPGGKKKY	KLKHLVWASR	ELERFAVNPG
394	B_US_DH123	MGARASVLSG	.GKLDSWEKI	RLRPGGKKKY	KLKHIVWASR	ELERFAVNPG
395	B_US_JRCSF	MGARASVLSG	.GELDRWEKI	RLRPGGKKKY	RLKHIVWASR	ELERFAVNPG
396	B_US_MNCG_	MGARASVLSG	.GELDRWENI	RLRPGGKKKY	KLKHVVWASR	ELERFAVNPG
397	B_US_P896_	MGARASVLSG	.GELDRWEKI	RLRPGGKKKY	KLKHIVWASR	ELERFAVNPS
398	B_US_RF_M1	MGARASVLSG	.GKLDKWEKI	RLRPRGKKRY	KLKHIVWASR	ELERFAVNPS
399	B_US_SF2_K	MGARASVLSG	.GELDKWEKI	RLRPGGKKKY	KLKHIVWASR	ELERFAVNPG
400	B_US_WEAU1	MGARASVLSG	.GELDRWEKI	RLRPGGNKKY	KLKHIVWASR	ELERFAVNPG
401	B_US_WR27_	MGARASMLSG	.GELDKWEKI	RLRPGGKKKY	RLKHLVWASR	ELERFAVNPG
402	B_US_YU2_M	MGARASVLSA	.GELDKWEKI	RLRPGGKKQY	RLKHIVWASR	ELERFAVDPG
403	BF1_BR_93B	MGARASVISG	.GELDKWEKI	RLRPGGHKKY	RLKHIVWASR	ELERFAVNPG
404	C_BR_92BR0	MGARASILRG	.GKLDAWERI	KLKPGGKKHY	MMKHLVWASR	ELERFALDPG
405	C_BW_96BW0	MGARASILRG	.GKLDAWEKI	RLRPGGKKQY	RIKHLVWASR	ELERFALNPG
406	C_BW_96BW1	MGARASILRG	.GKLDTWEKI	RLRPGGKKRY	MIKHLVWASR	ELERFALNPG
407	C_BW_96BW1	MGARASILRG	.EKLDTWEKI	RLRPGGKKRY	MMKHLVWASR	ELENFALNPA

408	C_BW_96BW1	MGARASISRG	.EKLDTWEKI	RSRPGGKKCY	MLKHIVWASR	ELERFALNPG
409	C_ET_ETH22	MGARASILRG	.EKLDAWEKI	KLRPGGKKHY	MLKHLVWANR	ELEKFALNPD
410	C_IN_93IN1	MGARASILRG	.GKLDKWERI	RLRPGGKKHY	MLKHLVWASR	ELERFALNPG
411	C_IN_93IN9	MGARASILRG	.EKLDKWEKI	RLRPGGKKHY	MLKHLVWASR	ELDRFALNPG
412	C_IN_93IN9	MGARASILRG	.EKLDKWERI	RLRPGGKKHY	MLKHLVWASR	ELDRFALNPG
413	C_IN_94IN1	MGARASILRG	.GKLDKWEKI	RLRPGGKKHY	MLKHLVWASR	ELEKFALNPG
414	C_IN_95IN2	MGARASILRG	.GKLDKWEKI	RLRPGGKKRY	MLKHLVWASR	ELDRFAVNPG
415	CRF01_AE_C	MGARASVLSG	.GKLDWEKI	RLRPGGKKKY	RMKHLVWASR	ELERFALNPG
416	CRF01_AE_C	MGARASILSG	.GKLDWEKI	RLRPGGKKQY	RMKHLVWASR	ELERFALNPG
417	CRF01_AE_C	MGARASVLSG	.GKLDWEKI	RLRPGGKKKY	RLKHLVWASR	ELERFALNPG
418	CRF01_AE_T	MSARASVLSG	.EKLNAWEKI	RLRPGGRKKY	KLKHLVWASR	ELEKFALNPG
419	CRF01_AE_T	MGARASVLSG	.KLDLEKI	RLRPGGKKKY	KMKHLVWASR	ELERFALNPG
420	CRF01_AE_T	MGARASVLSG	.GKLDWEKI	RLRPGGKKKY	KMKHLVWASR	ELERFALNPG
421	CRF01_AE_T	MGAKASVLSG	.GKLDWEKI	RLRPGGRKKY	HLKHIVWASR	ELERFALNPG
422	CRF01_AE_T	MGARASVLSG	.GKLDWEKI	RLRPGGRKKY	RLKHLVWASR	ELERFALNPS
423	CRF01_AE_T	MGARASILSG	.GKLDWEKI	RLRPGGRKKY	RMKHLVWASR	ELERFALNPG
424	CRF02_AG_F	MGARASVLSG	.GKLDSWEKI	RLRPGGKKKY	RLKHLVWASR	ELERFALNPG
425	CRF02_AG_F	MGARASVLSG	.GKLDSWEKI	RLRPGGKKKY	RLKHLVWASR	ELERFALNPG
426	CRF02_AG_G	MGARVSVLRG	.GQLDTWEKI	RLRPGGKKKY	KMKLLVWASR	ELERFAVNPG
427	CRF02_AG_N	MGARASVLSG	.GKLDWEKI	RLRPGGKKKY	RLKHLVWASR	ELERFALNPG
428	CRF02_AG_S	MGARASVLSG	.GKLDWEKI	RLRPGGKKKY	RLKHLVWASR	ELERFALNPG
429	CRF02_AG_S	.GARASVLSG	.GKLDWEKI	RLRPGGKKKY	RLKHLVWASR	ELERFALNPG
430	CRF03_AB_R	MGARASVLSG	.GKLDWEKI	RLRPGGKKEY	RIKHLVWASR	ELERFALNPS
431	CRF03_AB_R	MGARASVLSG	.GKLDWEKI	RLRPGGKKKY	RIKHLVWASR	ELERFAINPS
432	CRF04_cpx_	MGARASVLSG	.GKLDWEKI	RLRPGGKKKY	RLKHLVWASR	ELERFALNPG
433	CRF04_cpx_	MGARASVLSG	.GKLDWEKI	RLRPGGKKKY	RLKHLVWASR	ELERFALNPG
434	CRF04_cpx_	MGARASVLSG	.GRLDAWEKI	RLRPGGKKRY	RIKHLIWASR	ELERFALNPG
435	CRF05_DF_B	MGARASVLSG	.GKLDWEKI	RLRPGGKKKY	RLKHLVWASR	ELERFALNPG
436	CRF05_DF_B	MGARASVLSG	.GKLDWEKI	RLRPGGKKKY	RLKHIVWASR	ELERFAINPG
437	CRF06_cpx_	MGARASVLSG	.GKLDEWEKI	RLRPGGKKKY	KMKHLVWASR	ELERFAINPG
438	CRF06_cpx_	MGARASVLSG	.GKLDEWEKI	RLRPGGKKKY	RLKHLVWASR	ELERFALNPS
439	CRF06_cpx_	MGARASVLSG	.GKLDEWEKI	RLRPGGKKKY	RMKHLVWASR	ELERFALNPG
440	CRF06_cpx_	MGARASVLSG	.GKLDEWEKI	RLRPGGKKKY	RLKHLVWASR	ELDRFALNPG
441	CRF11_cpx_	MGARASVLSG	.GKLDSWEKI	RLRPGGKKKY	RLKHLVWASR	ELERFALNPS
442	CRF11_cpx_	MGARASVLSG	.GKLDWEKI	RLRPGGKKKY	RLKHLVWASR	ELERFALNPS
443	D_CD_84ZR0	MGARASVLSG	.GKLDWEKI	RLRPGGKKKY	KLKHIVWASR	ELERFALNPG
444	D_CD_ELI_K	MGARASVLSG	.GKLDKWEKI	RLRPGGKKKY	RLKHIVWASR	ELERYALNPG
445	D_CD_NDK_M	MGARASVLSG	.GKLDTWERI	RLRPGGKKKY	ALKHLIWASR	ELERFTLNPG
446	D_UG_94UG1	MGARASVLSG	.GKLDEWEKI	RLRPGGKKKY	RLKHLVWASR	ELERFALNPG
447	F1_BE_VI85	MGARASILSG	.GKLDEWEKI	QLRPGGKKRY	KMKHLIWASR	ELERFALDPG
448	F1_BR_93BR	MGARASVLSG	.GKLDWEKI	RLRPGGKKKY	RLKHLVWASR	ELERFALDPG
449	F1_FI_FIN9	MGARASVLSG	.GKLDWEKI	RLRPGGKKQY	RIKHLVWASR	ELERFAIDPG
450	F1_FR_MP41	MGARASVLSG	.GKLDWEKI	RLRPGGKKKY	RMKHLVWASR	ELERFAVDPG
451	F2_CM_MP25	MGARASVLSG	.GKLDWEKI	RLRPGGKKKY	RLKHIVWASR	ELKRFALNPG
452	F2KU_BE_VI	MGARASVLSG	.GKLDSWEKI	RLRPGGRKKY	RLKHLVWASR	ELERFALNPG
453	G_BE_DRCBL	MGARASVLSG	.GKLDWEKI	RLRPGGKKRY	RMKHLVWASR	ELDRFALNPG
454	G_NG_92NG0	.VGARASVLSG	.GKLDSWEKI	RLRPGGRKKY	KLKHIVWASR	ELGRFALNRD
455	G_SE_SE616	MGARASVLTG	.GKLDWEKI	RLRPGGRKSY	KIKHLVWASR	ELERFALNPD
456	H_BE_VI991	MGARASVLSG	.GKLDWEKI	RLRPGGRKKY	RLKHLVWASR	ELERFALNPD
457	H_BE_VI997	MGARASVLSG	.GRLDTLEKI	RLRPGGKKKY	RLKHIVWASR	ELERFALNPG
458	H_CF_90CF0	MGARASVLSG	.GKLDWEKI	RLRPGGKKKY	RLKHLVWASR	ELERFALNPG

459	J_SE_SE702	MGARASILSG	.GKLDDWEKI	RLRPGGKKQY	RIKHLVWASR	ELDRFALNPG
460	J_SE_SE788	MGARASILSG	.GKLDDWEKI	RLRPGGKKKY	RIKHLVWASR	ELDRFALNPG
461	K_CD_EQTB1	MGARASVLSG	.GKLDKWEKI	QLRPGGKKKY	RLKHLVWASR	ELERFALNPN
462	K_CM_MP535	MGARASVLSG	.GKLDAWEKI	RLRPGGKKKY	KLKHLVWASR	ELERFALNPG
463	N_CM_YBF30	MGARASVLTG	.GKLDQWESI	YLRPGGKKKY	RMKHLVWASR	ELERFACNPG
464	O_CM_ANT70	MGASASVLTG	.SKLDAWEQI	RLKPGSKKKY	RLKHLVWASR	ELERFACNPE
465	O_CM_MVP51	MGARASVLTG	.SKLDAWERI	RLRPGSKKAY	RLKHLVWASR	ELERYACNPG
466	O_SN_99SE_	MGARASVLTG	.SKLDAWEQI	RLKPGCKKKY	RLKHLVWASR	ELDRSACNPE
467	O_SN_99SE_	MGARASVLSG	.SKLDTWEQI	RLKPGCKKKY	RLKHLVWASR	ELERFACNPE
468	U_CD_83C	MGARASVLSG	.GKLDAWEKI	RLRPGGRKKY	RLKHLVWASR	ELEKFAINPG

	51					100
00BW0762_1	LLETSEGCKQ	IIKQLQPALQ	TGTEELRSLY	NTVATLYCVH	KKIDVRDTKE	
00BW0768_2	LLETSEGCKQ	IIKQLQPALQ	TGTEELRSLF	NTVATPYCVH	EKIEVRDTKE	
00BW0874_2	LLETAEGRQ	IIKQLHPALQ	TGTEELRSLY	NTVATLYCVH	RGIEIRDTKE	
00BW1471_2	LLETADGCKQ	IIKQLQPALQ	TGTEELRSLF	NTVATLYCVH	KGIVQDTKE	
00BW1616_2	LLETSDGCKQ	IMKQLQPALQ	TGTEELKSLF	NTVATLYCVH	ANIDVRDTKE	
00BW1686_8	LLETSDGCKQ	IIQQLQPALK	TGTEELRSLF	NTVATLYCAH	KGISIQDTKE	
00BW1759_3	LLETAEGRQ	IIKQLQPALQ	TGTEELKSLH	NTVATLYCVH	KEIDVRDTKE	
00BW1773_2	LLETAEGRQ	IIKQLQPALQ	TGTEELKSLY	NTVATLYCVH	AGIEVRDTKE	
00BW1783_5	LLETSEGCKQ	IIQQLQPALK	TGTEELRSLY	NTVATLYCVH	AKIEVRDTKE	
00BW1795_6	LLETSEGCKQ	IMKQLQPAIQ	TGTEELRSLF	NTVATLYCVH	EGIDVQDTKE	
00BW1811_3	LLETAGCKQ	IIRQLHPALQ	TGTEELRSLY	NTVATLYCVH	AEIEVRDTKE	
00BW1859_5	LLETSEGCRQ	IMRQLQPALQ	TGTEELRSLF	NTVATLYCVH	EKIPVRDTKE	
00BW1880_2	LLETAEGRQ	IIRQLHPALQ	TGTQELRSLY	NTVATLYCVH	KDIEVRDTKE	
00BW1921_1	LLETSEGCKQ	IIQQLQPALQ	TGTEELRSLY	NTVATLYCVH	KGIEVQDTKE	
00BW2036_1	LLETSEGCKQ	IMKQLQPALQ	TGTEELRSLF	NTVATLYCVH	KKIQVQDTKE	
00BW2063_6	LLETADGCKQ	IMKQLQPALQ	TGTEELRSLY	NTVATLYCVH	EGIDVRDTKE	
00BW2087_2	LLETSEGCKQ	IIKQLQPALQ	TGTEELRSLF	NTVATLYCVH	KGIEVRDTKE	
00BW2127_2	LLETSEGCRQ	IIKQLQPALQ	TGTEELRSLY	NTIATLYCAH	QRIKVQDTKE	
00BW2128_3	LLETSEGCKQ	IIKQLHPALQ	TGTEELKSLY	NTVATLYCVH	AGIAVRDTKE	
00BW2276_7	LLETSEGCKQ	IMQQLQPALK	TGTEELISLY	NTVATLYCVH	EKIQVQDTKE	
00BW3819_3	LLETSEGCKQ	IIKQLQPALQ	TGTEELRSLY	NTVATLYCVH	QKIEIRDTKE	
00BW3842_8	LMETSEGCKQ	IIQQLQPALQ	TGTEELRSLF	NTIATLYCVH	KGIVQDTKE	
00BW3871_3	LLETSDGCKQ	IIKQLQPALQ	TGTEELRSLF	NTVATLYCVH	KGIVQDTKE	
00BW3876_9	LLETSEGCEQ	IMKQLQPALQ	TGTEELRSLY	NTVATLYCVH	ARIEVKDTKE	
00BW3886_8	LLETAEGRQ	IMKQLQPALQ	TGTEELRSLF	NTVATLYCVH	AGIDVRDTKE	
00BW3891_6	LLETSDGCKQ	IIQQLQPALK	TGTEELRSLY	NTVATLYCVH	NNIEIRDTKE	
00BW3970_2	LLETSEGCKQ	IIKQLQPALQ	TGTEELKSLF	NTVATLYCVH	EKIEIRDTKE	
00BW5031_1	LLETADGCKQ	IIKQLQPALK	TGTEELRSLY	NTVATLYCVH	RNIEVQDTKE	
96BW01B21	LLETSEGCKQ	IMEQLQPALQ	TGTEELKSLY	NTVATLYCVH	ENIEVRDTKE	
96BW0407	LLETSEGCKQ	IIRQLHPALQ	TGSEELKSLF	NTVATLYCVH	EKIEVRDTKE	
96BW0502	LLETAEGRQ	IMKQLQPALQ	TGTEELRSLY	NTVATLYCVH	AGIEVRDTKE	
96BW06_J4	LLETSEGCKQ	IMQQLQPALQ	TGTEELRSLF	NTVATLYCVH	KGIVQDTKE	
96BW11_06	LLETSEGCKQ	IMKQLQPALQ	TGTEEIRSLY	NTVATLYCVH	EGIEVQDTKE	
96BW1210	LLETAEGRQ	IMKQLQPALK	TGTEELKSLY	NTVATLYCVH	EKIEVRDTKE	
96BW15B03	LLETSEGCKQ	IMKQLQPALQ	TGTEELRSLF	NTVATLYCVH	EKIKVKDTKE	
96BW16_26	LLETSEGCRQ	IMIQLQPALK	TGTEELKSLY	NTVATLYCVH	AGIEVQDTKE	
96BW17A09	LLETAEGRQ	IIKQLQPALQ	TGTEELKSLY	NTVATLYCVH	QGIEVRDTKE	
96BWM01_5	LLETSEGCKQ	IIKQLQPTIQ	TGTEELKSLY	NTVATLYCVH	KGIDVRDTKE	
96BWM03_2	LLETSEGCKQ	IIKQLQPALQ	TGTEELRSLY	NTVATLYCVH	EKIEVRDTKE	
98BWMC12_2	LLETAEGRQ	IMRQLQPALQ	TGTEELRSLY	NTVATLYCVL	KGIVKVRDTKE	
98BWMC13_4	LLETSEGCKQ	IMRQLQPAIQ	TGTEELRSLF	NTVATLYCVH	EGIDVKDTKE	
98BWMC14_a	LLETSEGCRQ	IMKQLQPALQ	TGTEELRSLF	NTVATLYCVH	MGIEVRDTKE	
98BWM014_1	LLETAEGRQ	IIQQLQPALK	TGTEELRSLF	NTVATLYWVH	KNVEVRDTKE	
98BWM018_d	LLETSEGCRK	IMKQLQPSIQ	TGTEELRSLY	NTIATLYCVH	EKIEVRDTKE	
98BWM036_a	LLETAEGRQ	ILQQLQPALK	TGTEELKSLY	NTVATLYCVH	QGIEVRDTKE	

98BWM037_d	LLENSEGCKQ	IMKQLQPALQ	TGTEELKSFL	NTVATLYCVH	EKIEVRDTKE
99BW3932_1	LLETADGCKQ	IIKQLQPAFQ	TGTEEIRSLY	NSIAVLYCVH	RRLTIQDTKE
99BW4642_4	LLETSEGCKQ	IMKQLQPALQ	TGTEELRSLY	NTVATLYCVH	ERIQVRDTKE
99BW4745_8	LLETTEGCRQ	IIRQLQPALQ	TGTEELKSFL	NTVATLYCVH	NNIEIRDTE
99BW4754_7	LLETAEGCKQ	IIKQLHPALQ	TGTEELRSLY	NTVATLYCVH	NKIEVQDTKE
99BWMC16_8	LLETSEGCKQ	IMKQLQPALQ	TGTEELRSLY	NTIATLYCVH	ESIEVRDTKE
A2_CD_97CD	LLETETGCRQ	IFGQLQPALE	TGTEELRSLY	NTIAVLYFVH	QKIEVKDTKE
A2_CY_94CY	LLETPEGCRQ	IIRQLQPALQ	TGTEELKSFL	NTVVVLYWVH	QRVDVKDTKE
A2D___97KR	LLETSEGCKQ	IIQGLEPSIK	TGSEEIKSLF	NAVVTLYCVH	QRIEVRDTKE
A2G_CD_97C	LLETAAGCRQ	ILGQLQPALQ	TGTEELRSLY	NTVAVLYCVH	QKIEVKDTKE
A_BY_97BL0	LLETSEGCKQ	ILEQLQPTLK	TGSEELKSFL	NTVATLYCVH	QRIEIKDTKE
A_KE_Q23_A	LLETADGCQ	IMEKLQPALK	TGTEEIKSLF	NTVATLYCVH	QRIDVKDTKE
A_SE_SE659	LLETTEGCQ	IIEQQLPALN	TGTEEIKSLF	NTVATLYCVH	QRIDVKDTKE
A_SE_SE725	LLETTEGCQ	IMEQLQSALK	TGTEELRSLF	NTVAVLYCVH	QRIEIKDTKE
A_SE_SE753	LLETAEGCQ	IMKQLQPALK	TGTEELRSLY	NTVATLYCVH	QRINVTDTKE
A_SE_SE853	LLETTEGCQ	IIQQLQPAFK	TGTEELKSFL	NTVATLWCVH	QRIDVKDTKE
A_SE_SE889	LLETTEGCQ	IMDKLQPALK	TGTEELRSLY	NTVATLYCVH	QKIAVKDTKE
A_SE_UGSE8	LLETAEGCQ	IIEQQLSAPK	TGTEELRSLY	NTVATLYCVH	QRIDVKDTKE
A_UG_92UG0	LLETTEGCQ	IMEQLQSALK	TGTEELRSLY	NTVATLYCVH	QRIEIKDTKE
A_UG_U455_	LLETAEGCQ	ILGQLQPALQ	TGTEELRSLY	NTVAVLYCVH	QRIDVKDTKE
AC_IN_2130	LLETSEGCKQ	IIKQLQPALQ	TGTEELRSLH	NTVATLYCVH	AGIEIRDTE
AC_RW_92RW	LLETPEGCKQ	IMRQLQPALQ	TGTEELRSLY	NTVATLYCVH	QKIDVKDTKE
AC_SE_SE94	LLETSEGCKQ	ILEQLQPALK	TGTEEIKSLF	NTVATLYCVH	QRIEIKDTKE
ACD_SE_SE8	LLETTEGCQ	IMDQLQPALK	TGTEELRSLY	NTVATLWCVH	KRIDVKDTKE
ACG_BE_VI1	LLETAEGCQ	IIEQQLSTLK	TGSEELKSFL	NTVATLWCVH	LRIEIKDTKE
AD_SE_SE69	LLETPEGCKQ	IMGQLQPAIQ	TGSEELKSFL	NTVATLYCVH	AKIKVTDTE
AD_SE_SE71	LLETTKGCQ	IMEQLQPAFK	TGTEELKSFL	NTVATLYCVH	QQIEVKDTKE
ADHK_NO_97	LLETSEGCKQ	VMEQLQPALK	TGSEELKSFL	NLVAVLWCVH	QRIDVRDTKE
ADK_CD_MAL	LLETGEGCQ	IMEQLQSTLK	TGSEEIKSLY	NTVATLYCVH	QRIDVKDTKE
AG_BE_VI11	LLETAEGCQ	IIEQQLSTLR	TGSEELKSFL	NTLATLWCVH	KKIEVRDTKE
AG_NG_92NG	LLETTEGCQ	IMRQLQPSLQ	TGTEEIKSLF	NTVATLYCVH	QRIEIKDTKE
AGHU_GA_VI	LLETAEGCQ	IMEQLQSALK	TGSEELKSFL	NTVATLYCVH	QKIDVKDTKE
AGU_CD_Z32	LLETTEGCQ	ILSQFQPALK	TGTEEIIISLY	NTVATLYCVH	QNIEVRDTKE
AJ_BW_BW21	LLETAEGCQ	IMEQLQSALK	TGSEELRSLY	NTVATLYCVH	QRIEIKDTKE
B_AU_VH_AF	LLETSEGCRQ	ILVQLQPSLP	TGSEELKSFL	NTVATLYCVH	QKIEIRDTE
B_CN_RL42_	LLETSEGCRQ	ILEQLQPALQ	TGSEELRSLF	NTVATLYCVH	LRIEIKDTKE
B_DE_D31_U	LLETSEGCRQ	ILGQLQPSLQ	TGSEELRSLF	NTVATLYCVH	QRIEIKDTKE
B_DE_HAN_U	LLETSEGCRQ	IMGQLQPSLQ	TGSEELRSLY	NTVATLYCVH	QKIEVKDTKE
B_FR_HXB2_	LLETSEGCRQ	ILGQLQPSLQ	TGSEELRSLY	NTVATLYCVH	QRIEIKDTKE
B_GA_OYI_	LLETSEGCRQ	ILGQLQPSLK	TGSEEIRSLY	NTVATLYCVH	QKIEVKDTKE
B_GB_CAM1_	LLETSEGCRQ	ILGQLQPSLQ	TGSEELRSLY	NTVATLYCVH	QKIDVKDTKE
B_GB_GB8_A	LLETSEGCRQ	ILEQLQPSLQ	TGSEERRSLF	NTVATLYCVH	QRIDVKDTKE
B_GB_MANC_	LLETSEGCRQ	ILVQLQPSLQ	TGSEELKSFL	NTVAVLYCVH	QGIEVKDTKE
B_KR_WK_AF	LLETSEGCRQ	ILGQLQPSLQ	TGSEELKSFL	NAVAVLYCVH	QRIEIKDTKE
B_NL_3202A	LLETAEGCRQ	ILGQLQPALQ	TGSEELRSLF	NTVAVLYCVH	QRIEIKDTKE
B_TW_TWCYS	LLETSEGCRQ	ILGQLQSSSQ	TGSEELRSLY	NTVATLYCIH	QKIEIKDTKD
B_US_BC_L0	LLETAEGCRQ	ILGQLQPSLQ	TGSEELKSFL	NTIAVLYCVH	QMIDVKDTKE
B_US_DH123	LLETSEGCRQ	ILGQLQPSLQ	TGSEELRSLY	NTVATLYCVH	ERIEVKDTKE
B_US_JRCSF	LLESSEGCRQ	ILGQLQPSLK	TGSEELTSLY	NTVATLYCVH	QRIEIKDTKE
B_US_MNCG_	LLETSEGCRQ	ILGQLQPSLQ	TGSEELKSFL	NTVATLYCVH	QKIEIKDTKE
B_US_P896_	LLETSEGCRQ	ILGQLQSSSQ	TGSEELKSFL	NTVATLYCVH	QRIEIKDTKE
B_US_RF_M1	LLETAEGCRQ	ILGQLQPALQ	TGSEELKSFL	NAVATLYCVH	QNIEVRDTKE
B_US_SF2_K	LLETSEGCRQ	ILGQLQPSLQ	TGSEELRSLY	NTVATLYCVH	QRIDVKDTKE
B_US_WEAU1	LLETSEGCRQ	ILGQLQPSLQ	TGSEELRSLY	NTVAVLYCVH	QKIEVKDTKE
B_US_WR27_	LLETAEGCRQ	ILRQLQPSLQ	TGSEELRSLF	NTVATLYCVH	QRIGVKDTKE
B_US_YU2_M	LLETSEGCRQ	ILGQLQPSLQ	TGSEELRSLY	NTVATLYCVH	QKIEVKDTKE
BF1_BR_93B	LLETSEGCRQ	ILEQLQPALK	TGSEELRSLY	NTVATLYCVH	QKIDVKDTKE
C_BR_92BR0	LLETSEGCKQ	IMKQLQPALQ	TGTEELISLH	NTVATLYCVH	EKIDVRDTKE
C_BW_96BW0	LLETSEGCKQ	IIQQLQPALQ	TGTEELRSLF	NTVATLYCVH	KKIEVRDTKE
C_BW_96BW1	LLGTSEGCKQ	IMKQLQPALQ	TGTEEIRSLY	NTVATLYCVH	EGIEVQDTKE

C_BW_96BW1	LLETAEGCKQ	IMKQLQPALK	TGTEELKSLY	NTVATLYCVH	EKIEVRDTKE
C_BW_96BW1	LLETSEGCKQ	IMKQLQPALQ	TGTEELRSLF	NTVATLYCVH	EKIKVKDTKE
C_ET_ETH22	LLDTSAGCKQ	IIKQLQPALQ	TGTEELKSLF	NTVATLYCVH	QKIEIKDTKE
C_IN_93IN1	LLETAEGCKQ	IIKQLQPALQ	TGTEELKSLH	NTVATLYCVH	AGIEVRDTKE
C_IN_93IN9	LLETSEGCKQ	IIKQLQPALQ	TGTEELRSLH	NTVVTLYCVH	AGIEVRDTKE
C_IN_93IN9	LLEAAEGCKQ	IIKQLQPALQ	TGTEELRSLH	NTVATLYCVH	EGIEVRDTKE
C_IN_94IN1	LLETSEGCKQ	IMKQLQPALQ	TGTEELRSLF	NTVATLYCVH	AEIEVRDTKE
C_IN_95IN2	LLETAEGCKQ	IIKQLQPALQ	TGTEELRSLF	NTVATLYCVH	AGIEVRDTKE
CRF01_AE_C	LLETAEGCQQ	LIEQLQSNLK	TGSEEIKSLF	NTIATLWCVH	QRIDVKDTKE
CRF01_AE_C	LLETAEGCQQ	LIEQLQSTIK	TGSEELKSLF	NTIATLWCVH	QRIDVKDTKE
CRF01_AE_C	LLETAEGCQQ	LLEQLQSTLK	TGSEELKSLF	NTIATLWCVH	QRINVTDTKE
CRF01_AE_T	LLETAEGCQQ	LIEQLQSTLK	TGSEELKSLF	NTIATLWCVH	QKIEVKDTKK
CRF01_AE_T	LLETAEGCQQ	IIIEQLQSALK	TGSEELKSLY	NTVVTLWCVH	QRIDVKDTKE
CRF01_AE_T	LLETAEGCQQ	LIEQLQSTLK	TGSEELKSLY	NTIATLWCVH	QRIEIKDTKE
CRF01_AE_T	LLETAEGCQQ	LIEQLQSTLK	TGSEELRSLF	NTIVTLWCVH	QRIEIKDTKE
CRF01_AE_T	FLETAEGCQQ	IIIEQLQSTLK	TGLEELKSLF	NTVATLWCVH	QRIEIKDTKE
CRF01_AE_T	LLETAEGCQQ	LIGQLQSNLK	TGSEELRSLF	NTVATLWCVH	QRIEIKDTKE
CRF02_AG_F	LLETAEGCQQ	LIEQLQTAG	TGSEELKSLY	NTIATLWCVH	KRIDIKDTKE
CRF02_AG_F	LLETAEGCQQ	LMKQLQSALG	TGSEELKSLY	NTIATLWCVH	QRIDIKDTKE
CRF02_AG_G	LLETTEGCQQ	ILEQLQPALK	AGSEELKSLY	NTVATLYCVH	QKIDVRDTKE
CRF02_AG_N	LLETAEGCQQ	LMEQLQSALR	TGSEELKSLF	NTIATLWCVH	QRIDIKDTKE
CRF02_AG_S	LLETAEGCQQ	LMEQLQSTLR	TGSEELKSLF	NTIATLWCVH	QRIDIKDTKE
CRF02_AG_S	LLETAEGCQQ	IIIEQLQSTLK	TGSEELKSLF	NTVATLYCVH	QRIEIKDTKE
CRF03_AB_R	LLETSEGCKQ	ILEQLQPTLK	TGSEELKSLY	NTVATLYCVH	QRIEIKDTKE
CRF03_AB_R	LLETSEGCKQ	ILEQLQPTLK	TGSEELKSLY	NTVATLYCVH	RRIEIKDTKE
CRF04_cpx_	LLETAEGCQQ	LMEQLQSTLK	TGSEELRSLY	NTITTLWCVH	QRIDVQDTKE
CRF04_cpx_	LLETAEGCQQ	LMEQLQPTLR	TGSEEVKSLF	NTLATLWCVH	QRIDVKDTKE
CRF04_cpx_	LLETAEGCQQ	LMEQLQSTLK	TGSEELKSLF	NLIATLWCVH	QRIEIKDTKE
CRF05_DF_B	LLETSEGCKQ	IISQLQPAIQ	TGTEELKSLY	NTVATLYCVH	ERIEVKDTKE
CRF05_DF_B	LLETSEGCKQ	IIAQQLQPAIQ	TGSEELRSLY	NTVATLYCVH	EKIEVKDTKE
CRF06_cpx_	LLETAEGCQQ	IIIEQLQSTLK	TGSEELKSLF	NTVATLYCVH	QRIKVTDTKE
CRF06_cpx_	LLETAEGCQQ	IMEQLQSALR	TGSEELKSLY	NTVATLYCVH	QRIKVTDTKE
CRF06_cpx_	LLETPEGCKQ	IMEQLQSTLR	TGSEELKSLY	NTVATLYCVH	QRIKVTDTKE
CRF06_cpx_	LLETAEGCQQ	IIIEQLQSALK	TGSEELRSLF	NTVATLYCVH	QRIKVTDTKE
CRF11_cpx_	LLETGEGCQQ	LMGQLQPALG	TGTEELRSLY	NTLATLYCVH	HRIEIKDTKE
CRF11_cpx_	LLETGEGCKQ	IMGQLQPALG	TGTEELRSLY	NTVAALYCVH	LRIEIKDTKE
D_CD_84ZR0	LLETSEGCKQ	IMEQLQPALK	TGSEELRSIY	NTVATLYCVH	KRIEIKDTKE
D_CD_ELI_K	LLETSEGCKQ	IIGQLQPAIQ	TGTEELRSLY	NTVATLYCVH	KGIDVKDTKE
D_CD_NDK_M	LLETSEGCKQ	IIGQLQPSIQ	TGSEEIRSLY	NTVATLYCVH	ERIEVKDTKE
D_UG_94UG1	LLETSEGCRQ	IIRQLQPSIQ	TGSEEIKSLY	NTVVTLYCVH	ERIKVASTKE
F1_BE_VI85	LLETSEGCRQ	IIRQLQPSIQ	TGSEELKSLF	NTVAVLYYVH	QRAGVTDTKE
F1_BR_93BR	LLETSEGCRQ	IIGQLQPSIQ	TGSEELKSLY	NTI AVLYYVH	QKVEVKDTKE
F1_FI_FIN9	LLETSEGCRQ	IIAQIQPSIQ	TGSEELRSLY	NTI AVLYYVH	QKIEVKDTKE
F1_FR_MP41	LLETPEGCKQ	IIRQLQPSIQ	TGSEELRSLF	NTVAVLYCVH	QKIEIKDTKE
F2_CM_MP25	LLETTEGCKK	IIGQLQPSIQ	TGSEELKSLF	NTIVVLYYVH	QKIEVRDTKE
F2KU_BE_VI	LLESANGCRQ	IIIEQIQPALQ	TGSEELRSLF	NTVVTLYWVH	QRIEIKDTKE
G_BE_DRCBL	LLETAEGCQK	IMAQLQPALQ	TGTEEIKSLF	NTVATLYCVH	QKIEVRDTKE
G_NG_92NG0	LLETAEGCVQ	IMKQLQP .AL	TGTEELRSLF	NTVATLYCVH	QKIEVKDTKE
G_SE_SE616	LLETAEGCQQ	IMRQLQPSIQ	TGTEEIKSLY	NAVATLYCVH	QRIEIKDTKE
H_BE_VI991	LLETADGCQQ	ILGQLQPALK	TGTEDLQSLY	NTI AVLYYVH	QRIDVKDTKE
H_BE_VI997	LLESAGCLQ	IIIEQLRPSIK	TGTEELXSLF	NTVATLYCVL	QRIEIKDTKE
H_CF_90CF0	LLETPEGCLQ	IIIEQIQPAIK	TGTEELKSLF	NLVAVLYCVH	RKIDVKDTKE
J_SE_SE702	LLESAGCQK	ILVQLQPALQ	TGTEEIKSLY	NTVATLYCVH	QRIEIKDTKE
J_SE_SE788	LLESAGCQK	ILVQLQPALQ	TGTQEIKSLY	NTVATLYCVH	QRIEIKDTKE
K_CD_EQTB1	LLETVEGCRQ	IIRQLQPSIQ	TGSEELRSLF	NTVATLYWVH	QSIQVRDTKE
K_CM_MP535	LLETTEGCRQ	IITQIQPSIQ	TGSEEIKSLY	NTI AVLYYVH	QKIEVKDTKE
N_CM_YBF30	LMDTADGCAK	LLNQLEPALK	TGSEELRSLY	NALAVLYCVH	SRIQIHNTQE
O_CM_ANT70	LLETAEGNEK	LLQQLEPALK	TGSDSLQSLW	NAIVVLWCVH	NRYKIGDTQQ
O_CM_MVP51	LLETAEGTEQ	LLQQLEPALK	TGSEDLSLW	NAI AVLWCVH	NRFDIRDTQQ
O_SN_99SE_	LLETAEGNEK	LLQQLEPALK	TGSESLQSLW	NTI AVLWCVH	NRIKVEDTQQ



O_SN_99SE_	LLETAEGNEE	LLQQLPALK	TGSESLQSLW	NTIAVLWCVH	KRFKVEDTQQ
U_CD___83C	LLETAEGCQQ	IIGQLPALQ	TGSEELKSIY	NLVATLYCVH	QRIEVKDTKE

	101		150
00BW0762_1	ALDQIEKEQN	QSQQK.....	.TQQAETADK K..... VSQNYPIVQN
00BW0768_2	ALDKMEEEQN	KSQQK.....	TQQAEEAA.AG K..... VSQNYPIVQN
00BW0874_2	ALDKIEKEQN	.....ESQQ	KTQQAQAADG K..... VSQNYPIVQN
00BW1471_2	ALDKIEEEQN	K.....	CQQQAKAAEG K..... VSQNYPIVQN
00BW1616_2	ALDKLEEEQN	KSQQE.....	TQQQTKAADG KIS..... ..HNYPIVQN
00BW1686_8	ALDKIEEEQN	KSQQ.....	KTQQVAAAAG Q..... VSQNYPIVQN
00BW1759_3	ALDKIEEEQK	KSQQK.....	.LQQEEAADR KV.....S ..QNYPIVQN
00BW1773_2	ALDKIEEEQN	KCQQK.....	.TQQAKEADG K..... VSQNYPIVQN
00BW1783_5	ALDKIEEEQN	KCQQK.....	.TQQAECTQQ AGAA...GGK VSQNYPIVQN
00BW1795_6	ALDKVEEEQN	KSQQ.....	KMQQAEEADK KVS..... ..QNYPIVQN
00BW1811_3	ALDKIEEEQN	KSQQK.....	.TQQAQEATA TG.....K VSQNYPIVQN
00BW1859_5	ALDKIEEEQN	KCQQ.....	KTQQTEAAAG K..... VSQNYPIVQN
00BW1880_2	ALDKIEEEQN	KSQQK.....	.AQQAEEADK Q..... VSQNYPIVQN
00BW1921_1	ALDKIEEEQN	KSQQ.....	KTQQAEEAAAG K..... VSQNYPIVQN
00BW2036_1	ALDKIEEEQN	TCQQ.....	KTQQAEEAAAG K..... ISQNYPIVQN
00BW2063_6	ALDKIEEEQQ	KSQQ.....	KTQQAEEADK KVS..... ..QNYPIVQN
00BW2087_2	ALDKIEEEQN	KCQQK.....	.TQQAKAADK G.....E VSQNYPIVQN
00BW2127_2	ALDEIEEEQN	KCQQK.....	.AQQEKATDG .....K VSQNYPIVQN
00BW2128_3	ALDKIEEEQN	KIQK.....	.TQQAKEADK .....K VSQNYPIVQN
00BW2276_7	ALDKIEEEQN	KSQQKSQQ..	KTQQAQAADG K..... VSQNYPIVQN
00BW3819_3	ALDKIEEEQN	KCQQK.....	.TQQGKAADK .....K ISQNYPIVQN
00BW3842_8	ALDKIEEEQN	KSQQKTQQQQ	KTQQTEAAAG K..... VSQNYPIVQN
00BW3871_3	ALDKIEEEQN	KSQQ.....	KTQQAEEAAAE K..... VSQNYPIVRN
00BW3876_9	ALDKIEEEQN	KRQK.....	.AQQEKAADG .....K VSQNYPIVQN
00BW3886_8	ALDKIEEEQN	KSQQK.....	.TQQAQAADK .....K VSQNYPIVQN
00BW3891_6	ALDRIEEEQK	KCQQK.TQQQ	KTQQVEAADG K..... VSQNYPIVQN
00BW3970_2	ALDKIEEEQK	KSQQK.....	.TQQAKAADG KI.....S ..QNYPIVQN
00BW5031_1	ALDKVEEEQN	NCQQK.....	.TQQAEEAAG .....K ISQNYPIVQN
96BW01B21	ALDKIEEEQN	KSQQK.....	.TQQAKTDD. .G.....K ISPNYPIVQN
96BW0407	ALDKIEEEQN	KCQQK.....	.IQQAEEADK G.....K VSQNYPIVQN
96BW0502	ALDKIEEEQN	KSQQK.....	.TQQAKEADG K..... VSQNYPIVQN
96BW06_J4	ALDKIEEEQN	KSQQ.....	KTQQAEEAAAG K..... VSQNYPIVQN
96BW11_06	AVDKIEEEQN	KSQQ.....	KTQQAEEADK KVS..... ..QNYPIVQN
96BW1210	ALDKIEEEQN	KCQQK.....	.EQQAEEAAK G.....K VSQNYPIVQN
96BW15B03	ALDKIEEEQN	KSQE.....	KTQQAEEAAAG K..... ISQNYPIVQN
96BW16_26	ALDKIEEEQN	KSQQK.....	.TQQAKEATG K..... VSQNYPIVQN
96BW17A09	ALDKIEEEQN	K.....	FQQQAKAADG K..... VSQNYPIVQN
96BWM01_5	ALDKIEEEQN	KIQK.....	KMQQAEEADK KISQ...DKK ISQNYPIVQN
96BWM03_2	ALDRIEEEQN	KCQQK.....	AQQQEEA.AA K..... VSQNYPIVQN
98BWMC12_2	ALDKIKEEQN	.....KSKQ	KTQQAQAADK K..... VSQNYPIVQN
98BWMC13_4	ALDKVEEEQN	KIQK.....	KMQQAESADK KVS..... ..QNYPIVQN
98BWMC14_a	ALDKIEEEQN	KVQQ.....	KTQQAEEAAAG K..... VSQNYPIVQN
98BWM014_1	ALDKIEEEQN	KSQQK.....	TQQAEEAADKG K..... VSQNYPIVQN
98BWM018_d	ALDKVEEEQK	QCQQR.....	.TQQAEEADK G.....K VSQNYPIVQN
98BWM036_a	ALDKIEEEQN	KIQK.....	.TQKATAADK G.....K VSQNYPIVQN
98BWM037_d	ALDKIEEEQN	KSQQ.....	..K.TQQADG KV.....S ..QNYPIVQN
99BW3932_1	ALDKIEEEQN	KCQQK.....	.TQQEKMAEG .....K VSQNYPIVQN
99BW4642_4	ALDKIEEEQN	KCQS.....	KTQQAEEAAAE K..... VSQNYPIVQN
99BW4745_8	ALDRIEEEQN	.....KSQQ	KAQQAQAAG K..... VSQNYPIVQN
99BW4754_7	ALDKIEEEQN	KSQQK.....	.TTQAEEADK K..... VSQNYPIVQN
99BWMC16_8	ALDKIEEEQN	KCQQK.....	.TQQAEEADK .G.....K VSQNYPIVQN
A2_CD_97CD	ALDKIEEEQN	KCKK.....	.TQQAADTG SSSSQNYRGS SSQNYPIVQN
A2_CY_94CY	ALDKIEEEQN	..KQK.....	.TQHAAADTG NS.....S S.QNYPIVQN
A2D___97KR	ALDKLEEEQN	KHKQK.....	.TQPAAADTG SS..... GSQNYPIVQN
A2G_CD_97C	ALDKIEEEQN	TCKQR.....	.TQHAAADTG SSRSQDYRGS SSQNYPIVQN
A_BY_97BL0	ALDKIEEQN	XSKQ.....	KTQQAATGTG S.....SS.K VSQNYPIXQN

A_KE_Q23_A	ALDKIEEIKN	KSKQ.....	KTQQAAADTG	N.....SS.N	VSQNYPIVQN
A_SE_SE659	ALDKIEEMQK	KSKQ.....	KTSQATADTG	S.....SS.K	VSQNYPIVQN
A_SE_SE725	ALDKIEEIQK	KSKQ.....	KAQQAAADTG	N.....SS.K	VSQNYPIVQN
A_SE_SE753	ALDKIEEIQN	KSEQ.....	KTQQAAADTG	N.....S..K	VSQNYPIVQN
A_SE_SE853	ALDKLEEEIQK	KSKQ.....	KTQQAVADTG	S.....SS.K	VSHNYPVVQN
A_SE_SE889	ALDKIEEIQN	KNKQ.....	KTQQAAADTG	N.....SS.N	VSRNYPIVQN
A_SE_UGSE8	ALDKIEEIQN	KSKQ.....	KKEQAAADTG	N.....SS.K	VSQNYPIVQN
A_UG_92UG0	ALDKIEEIQK	KSKQ.....	KTQQAAADTG	S.....SS.K	VSQNYPIVQN
A_UG_U455_	ALNKIEEMQN	KNKQR.....	.TQQAAANTG	SS.....	..QNYPIVQN
AC_IN_2130	ALDKIEEEQE	KSQK.....	.TQQAKEADG	K.....	VSQNYPIVQN
AC_RW_92RW	ALDKIEEEQN	KSQK.....	.TQQAEEADK	G.....K	VSQNYPIVQN
AC_SE_SE94	ALDKIEEIKN	KSKQ.....	KAQQAAADTG	N.....SG.K	VSQNYPIVQN
ACD_SE_SE8	ALDKIEEIQK	KSKQ.....	KAQQAAADTG	N.....SS.N	VSQNYPIVQN
ACG_BE_VI1	ALDKLEEVQN	KSKQR.....	.TQQAAAATG	.....S	GSQNFPIVQN
AD_SE_SE69	ALDKIEEEQT	KSK.....K	KAQQATADTK	N.....SS.Q	VSQNYPIVQN
AD_SE_SE71	ALDKIEEMQN	RSKQ.....	KTQQAAADTG	N.....NS.K	VSQNYPIVQN
ADHK_NO_97	ALDKIEEIQN	KSKQ.....	KTQQAAAATG	N.....GS.N	ISQNYPIVQN
ADK_CD_MAL	ALDKIEEIQN	KSRQKTQQA	AAQQAAAATK	N.....SS.S	VSQNYPIVQN
AG_BE_VI11	AVDKIEEMQN	KSKQ.....	KTQQAAAADT	G.....S	SSQNYPIVQN
AG_NG_92NG	ALEEVEKIQK	NSQQE.....	.TQKAAMGKG	N.....SS.Q	VSQNYPIVQN
AGHU_GA_VI	ALDKIEEIQN	KSKQ.....	KTQQAAAATG	N.....SS.K	VSQNYPIVQN
AGU_CD_Z32	ALDEVEKAQK	SSQK.....	.TQKATMAEE	N.....SSNQ	VSKNFPPIVQN
AJ_BW_BW21	ALDKIEEIQN	KSKQ.....	KAQQAAAATG	N.....SS.S	VSQNYPIVQN
B_AU_VH_AF	ALEKIEEEN	KSKKKAQQ.A	AADAAAADAG	N.....SS.K	VSQNYPIVQN
B_CN_RL42_	ALEKIEEEN	KSKK.....	KAQQTAAAGT	NNS.....Q	ASQNYPIVQN
B_DE_D31_U	ALDKIEEEN	KSKK.....	KAQPAARDAG	N.....NS.Q	VSQNYPIVQN
B_DE_HAN_U	ALDKVEEEN	NSKK.....	KAQQAADAG	N.....RN.Q	VSQNYPIVQN
B_FR_HXB2_	ALDKIEEEN	KSKK.....	KAQQAAADTG	H.....SN.Q	VSQNYPIVQN
B_GA_OYI_	ALDKIEEEN	KSKK.....	KAQQTAAADT	NSS.....Q	VSQNYPIVQN
B_GB_CAM1_	ALEKIEEEN	KSKK.....	KAQQAAAAGT	N.....SS.Q	VSQNYPIVQN
B_GB_GB8_A	ALDKIEEES	KSKK.....	KAQQAAADKG	NSNS...N.Q	VSQNYPIVQN
B_GB_MANC	ALDKIEEEN	KSKK.....	KAQPAADTG	N.....SS.Q	VSHNYPPIVQN
B_KR_WK_AF	ALEKIEEES	KSKK.....	KAQQATADTG	S.....SS.Q	VSQNYPIVQN
B_NL_3202A	ALDKIEEEN	KSKK.....	KAQQAAADTG	N.....SS.Q	VSQNYPIVQN
B_TW_TWCYS	ALEKIEEEN	KSKK.....	KAQQAATGTG	NNS.....P	VSQNYPIVQN
B_US_BC_L0	ALEKIEEEN	NSKK.....	KAQQAAADTG	N.....SS.Q	VSRNYPPIVQN
B_US_DH123	ALDKVEEEN	KSKK.....	KAQQAAADTG	N.....SS.Q	VSQNYPIVQN
B_US_JRCSF	ALEKIEEET	KSMK.....	KAQQAAADTG	N.....SS.Q	VSQNYPIVQN
B_US_MNCG_	ALEKIEEEN	KSKK.....	KAQQAAADTG	NRG.N.SS.Q	VSQNYPIVQN
B_US_P896_	ALDKIEEEN	KSKK.....	KAQQAAADTG	N.....SS.Q	VSQNYPIVQN
B_US_RF_M1	ALDKIEEEN	KSKK.....	KAQQAAADTG	N.....GS.Q	VSQNYPIVQN
B_US_SF2_K	ALEKIEEEN	KSKK.....	KAQQAAAAAG	TG..N.SS.Q	VSQNYPIVQN
B_US_WEAU1	ALDKIEEEN	KSKK.....	KAQQAAADTE	N.....RN.Q	VSQNYPIVQN
B_US_WR27_	ALEKIEEEN	KSKK.....	KAQQAADTG	N.....NS.K	VSQNYPIVQN
B_US_YU2_M	ALEKIEEEN	KSKK.....	KAQQAAADTG	N.....SS.Q	VSQNYPIVQN
BF1_BR_93B	ALEKIEEEN	.SKK.....	KAQQAAANTG	NNS.....Q	VSQNYPIVQN
C_BR_92BR0	ALDKIEEEN	KSQK.....	.TQQAEEADK	G.....K	VSQNYPIVQN
C_BW_96BW0	ALDKIEEEN	KCQK.....	.IQQAEEADK	G.....K	VSQNYPIVQN
C_BW_96BW1	AVDKIEEEN	KSQK.....	KTQQAEEADK	RVS.....	..QNYPIVQN
C_BW_96BW1	ALDKIEEEN	KCQK.....	.EQQAEEAAK	G.....K	VSQNYPIVQN
C_BW_96BW1	ALDKIEEEN	KSQE.....	KTQQAEEAAK	K.....	ISQNYPIVQN
C_ET_ETH22	ALDKIEEEN	ESQK.....	.TQAGAADR	G.....K	DSQNYPIVQN
C_IN_93IN1	ALDKIEEEN	KIQK.....	.TQQAKEADG	K.....	VSQNYPIVQN
C_IN_93IN9	ALDKIEEEN	KNQK.....	.TQQAKEADE	K.....	VSQNYPIVQN
C_IN_93IN9	ALDKIEEEN	KSQK.....	.TQQAKEADG	K.....	VSQNYPIVQN
C_IN_94IN1	ALDKIEEEN	KSQK.....	.TQQAKEADS	.....	..QNYPIVQN
C_IN_95IN2	ALDKIEEEN	KIKQK.....	.TQQAKEDDG	K.....	VSQNYPIVQN
CRF01_AE_C	ALDKIEEVQN	KNKQ.....	KTQQAAAAGT	S.....NS.K	VSQNYPIVQN
CRF01_AE_C	ALDKIEEVQN	KSKQ.....	KAQQAAAAGT	S.....SS.K	VSQNYPIVQN
CRF01_AE_C	ALDKIEEIQN	KNKQ.....	KTQQAAADTG	S.....SS.K	VSQNYPIVQN

CRF01_AE_T	ALDKIEEVQK	KSQQ.....	KTQQAAAAGTG	S.....SS.K	VSQNYPIVQN
CRF01_AE_T	ALDKIEEVQN	KSQQ.....	KTQQAAAAGTG	S.....SS.K	VSQNYPIVQN
CRF01_AE_T	ALDKIEEVQK	KSQQ.....	KKQQAAAADTG	S.....SS.K	VSQNYPIVQN
CRF01_AE_T	ALDKIEEVQN	KSQQ.....	KTQQAAAAGTG	S.....SS.T	VSHNYPIVQN
CRF01_AE_T	ALDKIEEVQN	KSQR.....	KTQQAAAAGTG	S.....SS.K	VSQNYPIVQN
CRF01_AE_T	ALDKIEEAQK	KSQQ.....	KTQQAAAAGTG	S.....SS.K	VSQNYPIVQN
CRF02_AG_F	ALEKIEEVQN	KSKQ.....	KTQQAAAATG	.....S	SSQNYPIVQN
CRF02_AG_F	ALDKIEEVQN	KSKQ.....	KTQQAEEATG	.....S	SSQNYPIVQN
CRF02_AG_G	ALDKLEEIQN	KSKQK.....	.TQQAAANS.	.....Q	VSQNYPIVQN
CRF02_AG_N	ALDKMEEIQN	KSKQ.....	KVQQTAAATG	.....S	SSQNYPIVQN
CRF02_AG_S	ALDKVEEVQK	KSKQ.....	KTQQAAAAAAG	.....S	SSQNYPIVQN
CRF02_AG_S	ALDKLEEIQE	KSKQ.....	KTQQAAAATG	.....S	SSQNFPIVQN
CRF03_AB_R	ALDKIEEIQN	KSKQ.....	KTQQAATGTG	S.....SS.K	VSQNYPIVQN
CRF03_AB_R	ALDKIEEIQN	KSKQ.....	KTQQAATGTG	S.....SS.K	VSQNYPIVQN
CRF04_cpx_	ALDKIEEIQS	KSKQ.....	KTQQAAAAAAG	G.....SS.N	VSQNYPIVQN
CRF04_cpx_	ALDKVEEVQK	KSKQ.....	KTQQAAAADTG	G.....SS.K	VSQNYPIVQN
CRF04_cpx_	ALDKVEEMQN	KSKQ.....	KTQQAAAAGN.	.....SS.N	VSQNYPIAQN
CRF05_DF_B	ALEKIEEEQN	KSKR.....K	KAQQAEEAGAG	N.....SS.Q	ASQNYPIVQN
CRF05_DF_B	ALEKIEEEQN	KSKS.....K	RAQQAEEAGTK	N.....SG.P	VSQNFPIVQN
CRF06_cpx_	AIDKIEEIQK	KSKQK.....	.AHQAAAATG.	N.....SS.N	LSQNYPIVQN
CRF06_cpx_	ALDKIEEIQN	KSKQK.....	.AQQAAAATG	N.....SS.N	LSQNYPIVQN
CRF06_cpx_	ALHKIEEIQN	KSKQK.....	.VQQAAAATG	N.....SS.Q	LSQNYPIVQN
CRF06_cpx_	AVDKVEEIQN	KSKQK.....	.TQQTAAATG	N.....SS.N	LSQNYPIVQN
CRF11_cpx_	ALDKIEEIQN	KSKQ.....	KKQQAAAADTG	N.....SS.N	VSQNYPIVQN
CRF11_cpx_	ALDKVEEIQN	KSK.....	.KQQAAAADSG	N.....SN.K	VSQNYPIVQN
D_CD_84ZR0	ALDKIEEEQN	NSKK.....	RAQQAAAAGTG	N.....SS.Q	VSQNYPIVQN
D_CD_ELI_K	ALEKMEEQN	KSK.....K	KAQQAAAADTG	N.....NS.Q	VSQNYPIVQN
D_CD_NDK_M	AVEKMEEQN	KSK.....K	KTQQAAAADS.	.....S.Q	VSQNYPIVQN
D_UG_94UG1	ALDKIEEEQA	KSK.....K	KAQQATADTR	N.....SS.Q	VSQNYPIVQN
F1_BE_VI85	ALDKLEEEQN	KSQQ.....	.KTQQAAAADK	.....G	VSQNYPIVQN
F1_BR_93BR	ALEKLEEEQN	KGRQ.....	.KTQQATAEK	.....G	VSQNYPIVQN
F1_FI_FIN9	ALDKLEEEQN	KSQOKT....	.QAAAAAADK	.....G	VSQNYPIVQN
F1_FR_MP41	ALEKLEEEQN	KGQQ.....	.KTQQAAAADK	.....G	VSQNYPIVQN
F2_CM_MP25	ALDKLQEEQD	KHQQ.....	.KTQQATADK	GVSK.....G	VSQNYPIVQN
F2KU_BE_VI	ALDKLEEEQK	TQKQQ.....	.KTQQEAAGK	.....G	VSQNYPIVQN
G_BE_DRCBL	ALEEVEKIQK	KSQQ.....	.....KEN	S.....SS.Q	VSQNYPIVQN
G_NG_92NG0	APEEVEKIQK	NSQQE.....	.IQQAANKNEG	N.....SN.P	VSQNYPIVQN
G_SE_SE616	ALEEVEKIQK	KSQEK.....	.IQQAAMDKG	N.....SN.Q	VSQNYPIVQN
H_BE_VI991	ALGKIEEIQN	KNKQR.....	.TQQAPAAAD	K.EK...DSK	ISQNYPIVQN
H_BE_VI997	ALGKIEEIQN	KRQOK.....	.TQQATANK.	..ER...DNK	VSQNYPIVQN
H_CF_90CF0	ALDKIEEIQN	KSQOK.....	.TQQAAAADK.	..EK...DNK	VSQNYPIVQN
J_SE_SE702	ALDKIEEIQN	KNKQQ.....	.TQKAETDKK	DNS.....Q	VSQNYPIVQN
J_SE_SE788	ALEKIEEIQN	KNKQQ.....	.AQKAETDKK	DNS.....Q	VSQNYPIVQN
K_CD_EQTB1	ALDKLEEEQ	NRTQQ.....	.KTQQKGADK	.....G	VSQNYPIVQN
K_CM_MP535	ALDKLEEEQ.	NKSQR.....	.KTQQEAADK	.....G	VSQNYPIVQN
N_CM_YBF30	ALDKIKEKQE	QHKPE....P	KNPEAGAAAA	TDS.....N	ISRNYPLVQT
O_CM_ANT70	AIQKLKEVMG	SRKS.....	.ADAAKEDTS	A....R..Q	AGQNYPIVSN
O_CM_MVP51	AIQKLKEVMA	SRKS.....	.AEAAKEETS	P....R..Q	TSQNYPIVTN
O_SN_99SE_	AIQKLKEVMG	SRKS.....	.AGTAKEDTS	A....R..Q	TGQNYPIVTN
O_SN_99SE_	AIQKLKEVMG	SRKS.....	.AGAAKEDTS	A....R..Q	TGQNYPVVAN
U_CD___83C	ALDKIEEVQN	KGKQK.....	.AQQAAAADK.	..GS...NSQ	VSQNYPIVQN

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200

00BW0762_1	IQQQMVHQSL	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
00BW0768_2	LQQQMVHQAL	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
00BW0874_2	LQQQMVHNPI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
00BW1471_2	AQQQMVHQSI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPSDLNTM
00BW1616_2	LQQQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
00BW1686_8	LQQQMVHQAI	SPRTLNAWVK	VIEEKGFNPE	VIPMFTALSE	GATPQDLHTM
00BW1759_3	LQQQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPSDLNTM

00BW1773_2	LQGQMVHQPI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
00BW1783_5	LQGQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPGDLNTM
00BW1795_6	LQGQMVHQAI	SPRTLNAWVK	VEDKAFSPE	VIPMFTALSE	GATPQDLNTM
00BW1811_3	AQGQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALPE	GATPQDLNTM
00BW1859_5	LQGQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
00BW1880_2	LQGQMVHQPL	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
00BW1921_1	LQGQMVHQSI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
00BW2036_1	LQGQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	IIPMFTALSE	GATPQDLNTM
00BW2063_6	LQGQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
00BW2087_2	AQGQMVHQTI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
00BW2127_2	LQGQMVHQAL	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
00BW2128_3	LQGQMVHQPL	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDSNTM
00BW2276_7	IQGQMVHQPL	SPRTLNAWVK	VVEEKAFSPE	VIPMFTALSE	GATPQDLNTM
00BW3819_3	LQGQMVHQNI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
00BW3842_8	LQGQMVHQAI	SPRTLNAWVK	VVEEKGFNPE	VIPMFTALSE	GATPQDLNTM
00BW3871_3	LQGQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GAAPQDLNTM
00BW3876_9	LQGQMVHQSL	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
00BW3886_8	LQGQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
00BW3891_6	LQGQMVHQSL	SPRTLNAWVK	VIEEKAFSPE	IIPMFTALSE	GATPQDLNTM
00BW3970_2	LQGQMVHQPI	APRTLNAWVK	VIEEKNFSP	VIPMFTALSE	GATPQDLNSM
00BW5031_1	LQGQMVHQAI	SPRTLNAWVK	VIEKAFNPE	IIPIFTALSE	GATPRDLNTM
96BW01B21	LQGQMVHQPL	SPRTLNAWVK	VIKAFSPE	VIPMFTALSE	GATPQDLNTM
96BW0407	LQGQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
96BW0502	LQGQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
96BW06_J4	LQGQMVHQPI	SPRTLNAWVK	VIEEKGFSP	VIPMFTALSE	GATPQDLNTM
96BW11_06	LQGQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
96BW1210	LQGQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	IIPMFTALSE	GATPQDLNTM
96BW15B03	LQGQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
96BW16_26	LQGQMVHQAI	SPRTSNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
96BW17A09	AQGQMVHQAI	SPRTLNAWVK	VVEEKAFSPE	VIPMFTALSE	GATPQDLNTM
96BWM01_5	LQGQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQILNTM
96BWM03_2	LQGQMVHQAI	SPRTLNAWVK	VVQEKGFNPE	VIPMFTALSE	GATPQDLNTM
98BWMC12_2	VQGQMVHQPI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLTTM
98BWMC13_4	LQGQMVHQAL	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
98BWMC14_a	LQGQMVHQAI	SPRTLNAWVK	VIEEKGFNPE	VIPMFTALSE	GATPQDLNTM
98BWM014_1	IQGQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
98BWM018_d	LQGQVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
98BWM036_a	LQGQMVHQAP	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
98BWM037_d	LQGQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
99BW3932_1	LQGQMVHQSL	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
99BW4642_4	LQGQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
99BW4745_8	LQGQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
99BW4754_7	LQGQMVHQAI	SPRTLNAWVK	VVEEKAFSPE	VIPMFSALSE	GATPQDLNTM
99BWMC16_8	LQGQMVHQAI	SPRTLNAWVK	VVEEKAFSPE	VIPMFTALSE	GATPQDLNTM
A2_CD_97CD	AQGQMVHQAV	SPRTLNAWVK	VVEEKAFSPE	VIPMFTALSE	GATPQDLNTM
A2_CY_94CY	AQGQMVHQAI	SPRTLNAWVK	VVEEKAFSPE	VIPMFTALSE	GATPQDLNTM
A2D_97KR	AQGQMTYQNL	SPRTLNAWVK	VVEEKAFSPE	VIPMFSALSE	GATPQDLNTM
A2G_CD_97C	AQGQMVHQAI	SPRTLNAWVK	VVEEKAFSPE	VIPMFSALSE	GATPQDLNTM
A_BY_97BL0	AQGQMT HQSM	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GATPQDLNMM
A_KE_Q23_A	AQGQMIHQSL	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GATPQDLNMM
A_SE_SE659	AQGQMIHQSL	SPRTLNAWVK	VIEEKGFNPE	VIPMFSALSE	GATPQDLNMM
A_SE_SE725	AQGQMVHQSL	SPRTLNAWVK	VIEEKAFSPE	VIPVFSALSE	GATPQDLNMM
A_SE_SE753	AQGQMVHQSL	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GATPQDLNMM
A_SE_SE853	AQGQMIHQNL	SPRTLNAWVK	VIEEKGFNPE	VIPMFSALSE	GATPQDLNTM
A_SE_SE889	AQGQMVHQSL	SPRTLNAWVK	VIEEKGFSP	VIPMFSALSE	GATPGDLNMM
A_SE_UGSE8	AQGQMVHQVM	SPRTLNAWVK	VIEERAFSPE	VIPMFSALSE	GATPHDLNMM
A_UG_92UG0	AQGQMIHQSL	SPRTLNAWVK	VIEEKALSPE	VIPMFSALSE	GATPQDLNMM
A_UG_U455_	AQGQPVHQAL	SPRTLNAWVK	VVEDKAFSPE	VIPMFSALSE	GATPQDLNMM
AC_IN_2130	LQGQMVHQAL	SPRTLNAWVK	VIEEKAFSPE	IIPMFTALSE	GATPQDLNTM
AC_RW_92RW	AQGQMVHQAI	SPRTLNAWVK	VIEEKAFSQE	VIPMFTALSE	GATPQDLNTM

AC_SE_SE94	PQGQMVHQPI	SPRTLNAWVK	VEDKAFSPE	VIPMFTALSE	GATPQDLNTM
ACD_SE_SE8	AQGQMVHQSL	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GATPQDLNMM
ACG_BE_VI1	AQEQMVHQSM	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GATPQDLNMM
AD_SE_SE69	LQGQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GAAPQDLNTM
AD_SE_SE71	AQGQMIHQAL	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GATPQDLNMM
ADHK_NO_97	AQGQMVHQAI	SPRTLNAWVK	AIEEKAFSPE	VIPMFSALSD	GATPQDLNMM
ADK_CD_MAL	AQGQMIHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GATPQDLNMM
AG_BE_VI11	AQGQMVHQSM	SPRTLNAWVK	VIEEKGFSPE	VIPMFSALSE	GATPQDLNMM
AG_NG_92NG	AQGQVVHQPI	SPRTLNAWVK	VIEEKNFSPE	VIPMFTALSE	GATPQDLNTM
AGHU_GA_VI	AQGQMVHQAM	SPRTLNAWVK	VIEEKGFSPE	VIPMFSALSE	GATPQDLNMM
AGU_CD_Z32	AQGQMVHQAL	TPRTLNAWVK	VVEEKNFSPE	VIPMFSALSE	GATPQDLNTM
AJ_BW_BW21	AQGQMVHQAV	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GATPQDLNMM
B_AU_VH_AF	LQGQMVHQPI	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GATPQDLNTM
B_CN_RL42_	LQGQMVHQPI	SPRTLNAWVK	VVEEKAFSPE	VIPMFSALSE	GATPQDLNTM
B_DE_D31_U	LQGQMVHQPI	SPRTLNAWVK	VVEEKAFSPE	VIPMFSALSE	GATPQDLNTM
B_DE_HAN_U	LQGQMVHQAI	SPRTLNAWVK	VVEEKAFSPE	VIPMFSALSE	GATPQDLNTM
B_FR_HXB2_	IQGQMVHQAI	SPRTLNAWVK	VVEEKAFSPE	VIPMFSALSE	GATPQDLNTM
B_GA_OYI_	LQGQMVHQPI	SPRTLNAWVK	VVEEKAFSPE	VIPMFSALAE	GATPQDLNTM
B_GB_CAM1_	LQGQMVHQAI	SPRTLNAWVK	VVEEKAFSPE	VIPMFSALSE	GATPQDLNTM
B_GB_GB8_A	LQGQMVHQAI	SPRTLNAWVK	VVEEKAFSPE	VIPMFSALAE	GATPQDLNTM
B_GB_MANC_	LQGQMVHQSI	SPRTLNAWVK	VVEEKAFSPE	VIPMFSALSE	GAIPQDLNTM
B_KR_WK_AF	LQGQMVHQPI	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GATPQDLNTM
B_NL_3202A	LQGQMVHQAL	SPRTLNAWVK	VVEEKAFSPE	VIPMFSALSE	GATPQDLNTM
B_TW_TWCYS	LQGQMVHQAI	SPRTLNAWVK	VVEEKAFSPE	VIPMFSALSE	GATPQDLNTM
B_US_BC_L0	IQGQMVHQAI	SPRTLNAWVK	VVEEKAFSPE	VIPMFSALSE	GATPQDLNTM
B_US_DH123	IQGQMVHQAL	SPRTLNAWVK	VVEEKAFSPE	VIPMFSALSE	GATPQDLNTM
B_US_JRCSF	LQGQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GATPQDLNTM
B_US_MNCG_	IEGQMVHQAI	SPRTLNAWVK	VVEEKAFSPE	VIPMFSALSE	GATPQDLNTM
B_US_P896_	IQGQMVHQAI	SPRTLNAWVK	VVEEKAFSPE	VIPMFSALSE	GATPQDLNTM
B_US_RF_M1	LQGQMVHQAI	SPRTLNAWVK	VVEEKAFSPE	VIPMFSALSE	GATPQDLNTM
B_US_SF2_K	LQGQMVHQAI	SPRTLNAWVK	VVEEKAFSPE	VIPMFSALSE	GATPQDLNTM
B_US_WEAU1	LQGQMVHQAL	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GATPQDLNTM
B_US_WR27_	LQGQMVHQAL	SPRTLFAWVK	VVEEKAFSPE	VIPMFSALSE	GATPQDLNTM
B_US_YU2_M	LQGQMVHQAI	SPRTLNAWVK	VVEEKAFSPE	VIPMFSALSE	GATPQDLNTM
BF1_BR_93B	LQGQMVHQAI	SPRTLNAWVK	VVEEKAFSPE	VIPMFSALSE	GATPQDLNTM
C_BR_92BR0	LQGQMVHQPI	SARTLNAWVK	VVEEKAFSPE	VIPMFTALSE	GATPQDLNTM
C_BW_96BW0	LQGQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
C_BW_96BW1	LQGQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
C_BW_96BW1	LQGQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	IIPMFTALSE	GATPQDLNTM
C_BW_96BW1	LQGQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
C_ET_ETH22	MQGQMVHQPI	SARTLNAWVK	VVEEKAFSPE	VIPMFTALSE	GATPQDLNTM
C_IN_93IN1	LQGQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
C_IN_93IN9	LQGQMVHQAL	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
C_IN_93IN9	LQGQMVHQPI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
C_IN_94IN1	LQGQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
C_IN_95IN2	LQGQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
CRF01_AE_C	AQGQMVHQPL	SPRTLNAWVK	VVEEKGFNPE	VIPMFSALSE	GATPQDLNMM
CRF01_AE_C	AQGQMVHQAL	SPRTLNAWVK	VVEEKGFNPE	VIPMFSALSE	GATPQDLNMM
CRF01_AE_C	AQGQMIHQAL	SPRTLNAWVK	VVEEKGFNPE	VIPMFSALSE	GATPQDLNMM
CRF01_AE_T	AQGQMVHQPV	SPRTLNAWVK	VVEEKGFNPE	VIPMFSALSE	GATPQDLNMM
CRF01_AE_T	AQGQMVHQPL	SPRTLNAWVK	VVEEKGFNPE	VIPMFSALSE	GATPQDLNMM
CRF01_AE_T	AQGQMVHQPL	SPRTLNAWVK	VIEEKGFNPE	VIPMFSALSE	GATPQDLNMM
CRF01_AE_T	AQGQMVHQPI	SPRTLNAWVK	VIEEKGFSPE	VIPMFSALSE	GATPQDLNMM
CRF01_AE_T	AQGQMAHQPL	SPRTLNAWVK	VVEEKGFNPE	VIPMFSALSE	GATPQDLNMM
CRF01_AE_T	AQGQMVHQPV	SPRTLNAWVK	VVEEKGFNPE	VIPMFSALSE	GATPQDLNMM
CRF02_AG_F	AQGQMT HQPM	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNMM
CRF02_AG_F	AQGQMT HQPM	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNMM
CRF02_AG_G	AQGQMVHQAI	SPRTLNAWVK	VVEEKAFSPE	VIPMFTALSE	GATPQDLNMM
CRF02_AG_N	AKGQMT HQSM	SPRTLNAWVK	VIEEKGFSPE	VIPMFSALSE	GATPQDLNMM
CRF02_AG_S	AQGQMT HQSI	SPRTLNAWVK	VVEEKAFSPE	VIPMFSALSE	GATPQDLNMM

CRF02_AG_S	AQGQMVHQSI	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GATPQDLNMM
CRF03_AB_R	AQGQMTHQSM	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GATPQDLNMM
CRF03_AB_R	AQGQMTHQSM	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GATPQDLNMM
CRF04_cpx_	AQGQMVHQSI	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GATPQDLNMM
CRF04_cpx_	AQGQMVHQAM	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GATPQDLNMM
CRF04_cpx_	AQGQMVHQSI	SPRTLNAWVK	VVEEKGFSPE	VIPMFSALSE	GATPQDLNMM
CRF05_DF_B	IQGQMVHQAL	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GATPQDLNMT
CRF05_DF_B	LQGQMVHQAL	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNMT
CRF06_cpx_	AQGQMVHQAM	SPRTLNAWVK	VIDEKAFSPE	VIPMFTALSE	GATPQDLNMM
CRF06_cpx_	AQGQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GATPQDLNMM
CRF06_cpx_	AQGQMIHQAI	SPRTLNAWVK	AIEEKAFSPE	VIPMFSALSE	GATPQDLNMM
CRF06_cpx_	AQGQMVHQAI	SPRTLNAWVK	AIEEKAFSPE	VIPMFSALSE	GATPQDLNMM
CRF11_cpx_	AQGQMVHQPV	SPRTLNAWVK	VVEEKAFSPE	VIPMFSALSE	GATPQDLNMM
CRF11_cpx_	AQGQMVHQAM	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GATPQDLNMM
D_CD_84ZR0	LQGQMVHQAL	SPRTLNAWVK	VIEEKAFNPE	VIPMFSALSE	GATPQDLNMT
D_CD_ELI_K	LQGQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GATPQDLNMT
D_CD_NDK_M	LQGQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GATPQDLNMT
D_UG_94UG1	LQGQMVHHPL	SPRTLNAWVK	VIEEKAFNPE	VIPMFSALSE	GATPQDLNMT
F1_BE_VI85	LQGQMVHQSL	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GATPTDLNMT
F1_BR_93BR	LQGQMVHQSL	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GATPQDLNMT
F1_FI_FIN9	LQGQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GATPQDLNMT
F1_FR_MP41	LQGQMVHQPI	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GATPQDLNMT
F2_CM_MP25	LQGQMVHQSL	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GATPQDLNMT
F2KU_BE_VI	LQGQMVHQAL	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNMT
G_BE_DRCBL	AQGQMVHQAI	SPRTLNAWVK	VVEEKAFSPE	VIPMFTALSE	GATPQDLNMT
G_NG_92NG0	AQGQMIHQAI	SPRTLNAWVK	VVEEKAFSPE	VIPMFSALSE	GATPQDLNMT
G_SE_SE616	AQGQMVHQAI	TPRTLNAWVK	VVEEKAFSPE	VIPMFSALSE	GATPQDLNLM
H_BE_VI991	AQGQMVHQAI	SPRTLNAWVK	VVEEKAFSPE	VIPMFSALSE	GATPQDLNAM
H_BE_VI997	AQGQMVHQPI	SXRTLNAWVK	VVEEKAFSPE	VIPMFSALSE	GATPQDLNAM
H_CF_90CF0	AQGQMVHQAI	SPRTLNAWVK	VVEEKAFSPE	VIPMFSALSE	GATPQDLNAM
J_SE_SE702	LQGQPVHQAL	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GATPQDLNMT
J_SE_SE788	LQGQPVHQAL	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GATPQDLNMT
K_CD_EQTB1	LQGQMVHQAL	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GATPQDLNMT
K_CM_MP535	LQGQMVHQAL	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNMT
N_CM_YBF30	AQGQMVHQPL	TPRTLNAWVK	VIEEKAFSPE	VIPMFMALSE	GATPSDLNMT
O_CM_ANT70	AQGQMVHQAI	SPRTLNAWVK	AVEEKAFNPE	IIPMFMALSE	GAISYDINTM
O_CM_MVP51	AQGQMVHQAI	SPRTLNAWVK	AVEEKAFNPE	IIPMFMALSE	GAVPYDINTM
O_SN_99SE_	AQGQMVHQSL	SPRTLNAWVK	AVEEKAFNPE	IIPMFMALSE	GAIPYDTNTM
O_SN_99SE_	AQGQMVHQSL	SPRTLNAWVK	AVEEKAFNPE	IIPMFMALSE	GAIPYDTNTM
U_CD___83C	MQGQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GATPQDLNMT

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00BW0762_1	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPIAPG	QMREPRGSDI
00BW0768_2	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR VH	PAHAGPVAPG	QMREPRGSDI
00BW0874_2	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR VH	PVHAGPVAPG	QMREPRGSDI
00BW1471_2	LNTVGGHQ.A	AMQMLKDTIN	EEVAEWDR LH	PVQAGPIAPG	QMRDPRGSDI
00BW1616_2	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR MH	PVQAGPVAPG	QMRDPRGSDI
00BW1686_8	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPIAPG	QMREPRGSDI
00BW1759_3	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPIAPG	QMREPRGSDI
00BW1773_2	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPVAPG	QMREPRGSDI
00BW1783_5	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVQAGPVAPG	QIREPRGSDI
00BW1795_6	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPVAPG	QMREPRGSDI
00BW1811_3	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPIAPG	QMREPRGSDI
00BW1859_5	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR VH	PVHAGPIAPG	QMREPRGSDI
00BW1880_2	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPVAPG	QMRDPRGSDI
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00BW2036_1	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPNPAG	QMREPRGSDI
00BW2063_6	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPAAPG	QMREPRGSDI
00BW2087_2	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPVAPG	QMREPRGSDI
00BW2127_2	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPIAPG	QMREPRGSDI

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00BW2128_3	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDVRH	PVHAGPIAPG	QMREPRGSDI
00BW2276_7	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDRLH	PVHAGPVAPG	QMREPRGSDI
00BW3819_3	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDRLH	PVHAGPVAPG	QMREPRGSDI
00BW3842_8	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDVRH	PVQAGPVAPG	QIREPRGSDI
00BW3871_3	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDRLH	PVHAGPIAPG	QMREPRGSDI
00BW3876_9	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDRIH	PVHAGPVAPG	QMRDPRGSDI
00BW3886_8	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDRLH	PVHAGPIAPG	QMREPRGSDI
00BW3891_6	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDRLH	PVHAGPVAPG	QMREPRGSDI
00BW3970_2	LNAVGGHQ.A	AMQMLKDTIN	EEAAEWDRLH	PVHAGPIAPG	QLREPRGSDI
00BW5031_1	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDRLH	PVHAGPVAPG	QMREPRGSDI
96BW01B21	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDRTH	PVHAGPVAPG	QLREPRGSDI
96BW0407	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDVRH	PVHAGPIAPG	QMREPRGSDI
96BW0502	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDRLH	PVQAGPVAPG	QMRDPRGSDI
96BW06_J4	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDRLH	PVQAGPVAPG	QMRDPRGSDI
96BW11_06	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDRLH	PVHAGPVAPG	QMREPRGSDI
96BW1210	LNTVGGHQ.A	AMQMLKDTIN	EEAAGWDLRH	PVHAGPVAPG	QMREPRGSDI
96BW15B03	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDRLH	PVHAGPIAPG	QMREPRGSDI
96BW16_26	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDVRH	PVHAGPIAPG	QMREPRGSDI
96BW17A09	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDRLH	PVHAGPIAPG	QMREPRGSDI
96BWM01_5	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDRLH	PVHAGPVAPG	QMREPRGSDI
96BWM03_2	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDRLH	PVHAGPVAPG	QMREPRGSDI
98BWMC12_2	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDRLH	PVHAGPVAPG	QMREPRGSDI
98BWMC13_4	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDRLH	PVQAGPVAPG	QIREPRGSDI
98BWMC14_a	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDRLH	PVHAGPVAPG	QMRDPRGSDI
98BWM014_1	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDRTH	PVHAGPVAPG	QMREPRGSDI
98BWM018_d	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDRLH	PVHAGPVAPG	QMREPRGSDI
98BWM036_a	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDRLH	PVHAGPVAPG	QMREPRGSDI
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99BW4642_4	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDRLH	PVHAGPVAPG	QMREPRGSDI
99BW4745_8	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDRIH	PVHAGPVAPG	QMREPRGSDI
99BW4754_7	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDVRH	PVHAGPIAPG	QIREPRGSDI
99BWMC16_8	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDRTH	PVHAGPIAPG	QMREPRGSDI
A2_CD_97CD	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDRLH	PVQAGPIPPG	QMREPRGSDI
A2_CY_94CY	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDVRH	PVHAGPIPPG	QMREPRGSDI
A2D_97KR	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDRLH	PVHAGPIPPG	QMREPRGSDI
A2G_CD_97C	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDVRH	PVHAGPIPPG	QMREPRGS..
A_BY_97BL0	LNIVGGHQ.A	AMQMLKDTIN	EEAAXXDRLH	PAQAGPFPFG	QMREPRGSDI
A_KE_Q23_A	LNIVGGHQ.A	AMQMLKDTIN	EEAAEWDRLH	PVHAGPIPPG	QMREPRGSDI
A_SE_SE659	LNIVGGHQ.A	AMQMLKDTIN	EEAAEWDRLH	PVHAGPIPPG	QMREPRGS..
A_SE_SE725	LNIVGGHQ.A	AMQMLKDTIN	EEAAEWDRLH	PAHAGPVAPG	QMREPRGS..
A_SE_SE753	LNIVGGHQ.A	AMQMLKDTIN	EEAAEWDRLH	PVHAGPIPPG	QMREPRGSDI
A_SE_SE853	LNIVGGHQ.A	AMQMLKDTIN	EEAAEWDRLH	PVHAGPIPPG	QMREPRGS..
A_SE_SE889	LNIVGGHQ.A	AMQMLKDTIN	EEAAEWDRLH	PVHAGPIPPG	QMREPRGS..
A_SE_UGSE8	LNIVGGHQ.A	AMEMLKDTIN	EEAAEWDRTH	PIHAGPVAPG	QMREPRGSDI
A_UG_92UG0	LNIVGGHQ.A	AMQMLKDTIN	EEAAEWDRLH	PVHAGPVAPG	QMREPRGSDI
A_UG_U455_	LNIVGGHQ.A	AMQMLKDTIN	EEAAEWDRLH	PVHAGPIPPG	QMREPRGSDI
AC_IN_2130	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDRLH	PAQAGPIAPG	QMREPRGSDI
AC_RW_92RW	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDVRH	PVQAGPVAPG	QIREPRGSDI
AC_SE_SE94	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDRLH	PAQAGPVAPG	QMREPRGS..
ACD_SE_SE8	LNIVGGHQ.A	AMQMLKDTIN	EEAAEWDRIH	PVHAGLIAPG	QMREPRGSDI
ACG_BE_VI1	LNIVGGHQ.A	AMQMLKDTIN	EEAADWDRTH	PVHAGPNPPG	QMREPRGSDI
AD_SE_SE69	LSTVGGHQ.A	AMQILKETIN	EEAADWDRTH	PVHAGPNAPG	QMREPRGSDI
AD_SE_SE71	LNIVGGHQ.A	AMQMLKDTIN	EEAAEWDRLH	PVHAGPIPPG	QMREPRGS..
ADHK_NO_97	LNIVGGHQ.A	AMQMLKDTIN	EEAADWDRTH	PVHAGPIPPG	QMREPRGSDI
ADK_CD_MAL	LNIVGGHQ.A	AMQMLKDTIN	EEAADWDRTH	PVHAGPIPPG	QMREPRGSDI
AG_BE_VI11	LNIVGGHQ.A	AMQMLKDTIN	EEAAEWDVRH	PVHAGPIPPG	QMREPRGSDI
AG_NG_92NG	LNTVGGHQ.A	AMQMLKDSIN	EEAAEWDRLH	PQAGPIPPG	QIREPRGSDI
AGHU_GA_VI	LNIVGGHQ.A	AMQMLKDTIN	EEAAEWDRIH	PVQAGPIPPG	QIREPRGSDI
AGU_CD_Z32	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDVRH	PPQAGPIPPG	QIREPRGSDI

AJ_BW_BW21	LNIVGGHQ .A	AMQMLKDTIN	EAAA EWDR LH	PVHAGPIPPG	QMREPRGSDI
B_AU_VH_AF	LNTVGGHQAA	AMQMLKETIN	EEAADWDR LH	PVHAGPIAPG	QMREPRGSDI
B_CN_RL42	LNTVGGHQ .A	AMQMLKETIN	EAAA EWDR LH	PVHAGPVAPG	QMREPRGSDI
B_DE_D31_U	LNTVGGHQ .A	AMQMLKETIN	EAAA EWDR LH	PVHAGPIAPG	QMREPRGSDI
B_DE_HAN_U	LNTVGGHQ .A	AMQMLKETIN	EAAA EWDR LH	PVHAGPIAPG	QMREPRGSDI
B_FR_HXB2_	LNTVGGHQ .A	AMQMLKETIN	EAAA EWDR VH	PVHAGPIAPG	QMREPRGSDI
B_GA_OYI_	LNTVGGHQ .A	AMQMLKETIN	EAAA EWDR LH	PVHAGPIAPG	QMREPRGSDI
B_GB_CAM1_	LNTVGGHQ .A	AMQMLKETIN	EAAA EWDR LH	PVHAGPIAPG	QMREPRGSDI
B_GB_GB8_A	LNTVGGHQ .A	AMQMLKETIN	EAAA EWDR VH	PVHAGPVAPG	QMREPRGSDI
B_GB_MANC_	LNTVGGHQ .A	AMQMLKETIN	EAAA EWDR LH	PVHAGPVAPG	QMREPRGSDI
B_KR_WK_AF	LNTVGGHQ .A	AMQMLKETIN	EEAADWDR LH	PVHAGPIAPG	QMREPRGS D
B_NL_3202A	LNTVGGHQ .A	AMQMLKETIN	EAAA EWDR LH	PVHAGPIAPG	QMREPRGSDI
B_TW_TWCYS	LNTVGGHQ .A	AMQMLKETIN	EAAA EWDR LH	PVHAGPIAPG	QMREPRGSDI
B_US_BC_L0	LNTVGGHQ .A	AMQMLKETIN	EAAA EWDR LH	PVQAGPVAPG	QMREPRGSDI
B_US_DH123	LNTVGGHQ .A	AMQMLKETIN	EAAA EWDR LH	PVHAGPIAPG	QMREPRGSDI
B_US_JRCFS	LNTVGGHQ .A	AMQMLKETIN	EAAA EWDR LH	PVHAGPIAPG	QMREPRGSDI
B_US_MNCG_	LNTVGGHQ .A	AMQMLKETIN	EAAA EWDR LH	PVHAGPITPG	QMREPRGSDI
B_US_P896_	LNTVGGHQ .A	AMQMLKETIN	EAAA EWDR LH	PVQAGPVAPG	QMREPRGSDI
B_US_RF_M1	LNTVGGHQ .A	AMQMLKETIN	EAAA EWDR LH	PVHAGPIAPG	QMREPRGSDI
B_US_SF2_K	LNTVGGHQ .A	AMQMLKETIN	EAAA EWDR VH	PVHAGPIAPG	QMREPRGSDI
B_US_WEAU1	LNTVGGHQ .A	AMQMLKETIN	EAAA EWDR LH	PVHAGPIAPG	QMREPRGSDI
B_US_WR27_	LNTVGGHQ .A	AMQMLKETIN	DEAAEWDR LH	PVQAGPVAPG	QMREPRGSDI
B_US_YU2_M	LNTVGGHQ .A	AMQMLKETIN	EAAA EWDR LH	PVHAGPIAPG	QMREPRGSDI
BF1_BR_93B	LNTVGGHQ .A	AMQMLKETIN	EAAA EWDR VH	PVHAGPIPPG	QMREPRGSDI
C_BR_92BR0	LNTVGGHQ .A	AMQMLKDTIN	EAAA EWDR LH	PVHAGPVAPG	QMREPRGSDI
C_BW_96BW0	LNTVGGHQ .A	AMQMLKDTIN	EAAA EWDR LH	PVHAGPIAPG	QMREPRGSDI
C_BW_96BW1	LTTVGGHQ .A	AMQMLKDTIN	EAAA EWDR LH	PVHAGPVAPG	QMREPRGSDI
C_BW_96BW1	LNTVGGHQ .A	AMQMLKDTIN	EAAAGWDR LH	PVHAGPVAPG	QMREPRGSDI
C_BW_96BW1	LNTVGGHQ .A	AMQMLKDTIN	EAAA EWDR LH	PVHAGPIAPG	QMREPRGSDI
C_ET_ETH22	LNTVGGHQ .A	AMQMLKDTIN	EAAA EWDR LH	PVHAGPVAPG	QMRDPRGSDI
C_IN_93IN1	LNTVGGHQ .A	AMQMLKDTIN	EAAA EWDR LH	PIHAGPIAPG	QMREPRGSDI
C_IN_93IN9	LNTVGGHQ .A	AMQMLKDTIN	EAAA EWDR LH	PIHAGPIAPG	QMREPRGSDI
C_IN_93IN9	LNTVGGHQ .A	AMQMLKDTIN	EAAA EWDR LH	PVHAGPIAPG	QIREPRGSDI
C_IN_94IN1	LNTVGGHQ .A	AMQMLKDTIN	EAAA EWDR IH	PVHAGPIAPG	QMREPRGSDI
C_IN_95IN2	LNTVGGHQ .A	AMQMLKDTIN	EAAA EWDR LH	PVPAGPIAPG	QLREPRGSDI
CRF01_AE_C	LNIVGGHQ .A	AMQMLKDTIN	EAAA EWDR LH	PVHAGPIPPG	QMREPRGSDI
CRF01_AE_C	LNIVGGHQ .A	AMQILKDTIN	EAAA EWDR VH	PVHAGPIPPG	QMREPRGADI
CRF01_AE_C	LNIVGGHQ .A	AMQMLKDTIN	EAAA EWDR VH	PVHAGPIPPG	QMREPRGSDI
CRF01_AE_T	LNIVGEHQ .A	AMQMLKETIN	EAAA EWDR VH	PVHAGPIPPG	QMREPRGSDI
CRF01_AE_T	LNIVGGHQ .A	AMQMLKETTN	EAAA EWDR VH	PVHAGPIPPG	QMREPRGSDI
CRF01_AE_T	LNIVGGHQ .A	AMQMLKETIN	EAAA EWDR VH	PVHAGPIPPG	QMREPRGSDI
CRF01_AE_T	LNIVGGHQ .A	AMQMLKETIN	EEPAEWDR VH	PVHAGPIPPG	QIREPRGSDI
CRF01_AE_T	LNIVGGHQ .A	AMQMLKETIN	EEPAEWDR VH	PVHAGPIPPG	QMREPRGSDI
CRF01_AE_T	LNIVGGHQ .A	AMQMLKETIN	EAAA EWDR VH	PVHAGPIPPG	QMREPRGSDI
CRF02_AG_F	LNIVGGHQ .A	AMQMLKDTIN	EAAA EWDR VH	PVHAGPIPPG	QMREPRGSDI
CRF02_AG_F	LNIVGGHQ .A	AMQMLKDTIN	EAAA EWDR VH	PVHAGPIPPG	QMREPRGSDI
CRF02_AG_G	LNIVGGHQ .A	AMQMLKDTIN	EAAA EWDR TH	PIHAGPNPPG	QMREPRGSDI
CRF02_AG_N	LNIVGGHQ .A	AMQMLKDTIN	EAAA EWDR VH	PVHAGPIPPG	QMREPRGSDI
CRF02_AG_S	LNIVGGHQ .A	AMQMLKDTIN	EAAA EWDR VH	PVHAGPIPPG	QMREPRGSDI
CRF02_AG_S	LNIVGGHQ .A	AMQMLKDTIN	EEAADWRTH	PVHAGPIPPG	QMREPRGSDI
CRF03_AB_R	LNIVGGHQ .A	AMQMLKDTIN	EAAA EWDR LH	PAQAGPFPPG	QMREPRGSDI
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CRF04_cpx_	LNIVGGHQ .A	AMQMLKDTIN	EEAADWRTH	PVHAGPIPPG	QMREPRGSDI
CRF04_cpx_	LNIVGGHQ .A	AMQMLKDTIN	EEASEWDRAH	PVHAGPIPPG	QMREPRGSDI
CRF04_cpx_	LNIVGGHQ .A	AMQMLKDTIN	EAAA EWDR VH	PAHAGPNPAG	QMREPRGSDI
CRF05_DF_B	LNTVGGHQ .A	AMQMLKETIN	EAAA EWDR LH	PVQAGPVAPG	QMRDPRGSDI
CRF05_DF_B	LNTVGGHQ .A	AMQMLKETIN	EAAA EWDR VH	PAQAGPIAPG	QIREPRGSDI
CRF06_cpx_	LNIVGGHQ .A	AMQMLKDTIN	EAAA EWDR VH	PVHAGPIPPG	QIREPRGSDI
CRF06_cpx_	LNIVGGHQ .A	AMQMLKDTIN	EAAA EWDR VH	PVHAGPIPPG	QMREPRGSDI
CRF06_cpx_	LNIVGGHQ .A	AMQMLKDTIN	EAAA EWDR MH	PVQAGPMPPG	QMREPRGSDI



CRF06_cpx_	LNIVGGHQ.A	AMQMLKDTIN	EEAAEWDRVH	PAQAGPIPPG	QIRDPRGSDI
CRF11_cpx_	LNIVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVQAGPIAPG	QMRDPRGSDI
CRF11_cpx_	LNIVGGHQ.A	AMQMLKDTIN	EEAAEWDRVH	PVHAGPAPPG	QMREPRGSDI
D_CD_84ZR0	LNTVGGHQ.A	AMQMLKETIN	EEAAEWDR LH	PVQAGPVAPG	QMREPRGSDI
D_CD_ELI_K	LNTVGGHQ.A	AMQMLKETIN	EEAAEWDR LH	PVHAGPIAPG	QMREPRGSDI
D_CD_NDK_M	LNTVGGHQ.A	AMQMLKETIN	DEAAEWDR LH	PVHAGPVAPG	QMREPRGSDI
D_UG_94UG1	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPVAPG	QLREPRGSDI
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F1_BR_93BR	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PTQAGPIPPG	QIREPRGSDI
F1_FI_FIN9	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPIPPG	QMREPRGSDI
F1_FR_MP41	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PAHAGPILPG	QMREPRGSDI
F2_CM_MP25	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPIPPG	QMREPRGSDI
F2KU_BE_VI	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPIAPG	QMREPRGSDI
G_BE_DRCBL	LNTVGGHQ.A	AMQMLKETIN	DEAAEWDR LH	PQQAGPIAPG	QIRDPTGSDI
G_NG_92NG0	LNTVGGHQ.A	AMQMLKDTIN	DEAAEWDR IH	PQQAGPIPPG	QIREPSGSDI
G_SE_SE616	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR MH	PQQAGPFPPG	QIREPRGSDI
H_BE_VI991	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPIPPG	QMREPRGSDI
H_BE_VI997	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPIPPG	QMREPRGSDI
H_CF_90CF0	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR VH	PVHAGPIPPG	QMREPRGSDI
J_SE_SE702	LNTIGGHQ.A	AMQMLKDTIN	EEAAEWDR VH	PVHAGPVAPG	QVREPRGSDI
J_SE_SE788	LNTIGGHQ.A	AMQMLKDTIN	EEAAEWDR VH	PVHAGPIAPG	QVREPRGSDI
K_CD_EQTB1	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR MH	PVQAGPIPPG	QIREPRGSDI
K_CM_MP535	LNTVGGHQ.A	AMQMLKDTIN	DEAAEWDR LH	PVHAGPIPPG	QMREPRGSDI
N_CM_YBF30	LNTVGGHQ.A	AMQMLKEVIN	EEAADWDR TH	PVPVGPLPPG	QLRDPRGSDI
O_CM_ANT70	LNAIGGHQ.G	ALQVLKEVIN	EEAVEWDR TH	PPPVGPLPPG	QIREPTGSDI
O_CM_MVP51	LNAIGGHQ.G	ALQVLKEVIN	EEAAEWDR TH	PPAMGPLPPG	QIREPTGSDI
O_SN_99SE_	LNAIGGHQ.G	ALQVLKEVIN	EEAAEWDR TH	PPAAGPLPVG	QIREPTGSDI
O_SN_99SE_	LNAIGGHQ.G	ALQVLKEVIN	EEAAEWDR TH	PQAAGPLPPG	QIREPTGSDI
U_CD___83C	LNTVGGHQ.A	AMQMLKDTIN	EEAADWDR LH	PVHAGPIPPG	QMREPRGSDI

	251				300
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00BW0768_2	AGTTSNLQEQ	IAWMTA.NPP	VPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
00BW0874_2	AGTTSTLQEQ	IAWMTS.NPP	IPVGDYKRW	IILGLNKIVR	MYSPPVSILDI
00BW1471_2	AGTTSTLQEQ	VAWMTS.NPP	VPVGDYKRW	IILGLNKIVR	MYSPPVSILDI
00BW1616_2	AGTTSTLQEQ	IAWMTS.NPP	VPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
00BW1686_8	AGTTSNLQEQ	VAWMTS.NPP	IPVGDYKRW	IILGLNKIVR	MYSPPVSILDI
00BW1759_3	AGTTSTLQEQ	IAWMTS.NPP	VPVGDYKRW	IILGLNKIVR	MYSPPVSILDI
00BW1773_2	AGTTSTLQEQ	ITWMTS.NPP	VPVGDYKRW	IILGLNKIVR	MYSPPVSILDI
00BW1783_5	AGTTSTLQEQ	ITWMTS.NPP	IPVGDYKRW	IVLGLNKIVR	MYSPPVSILDI
00BW1795_6	AGTTSTLQEQ	IAWMTS.NPP	IPVGDYKRW	IILGLNKIVR	MYSPPVSILDI
00BW1811_3	AGTTSTLQEQ	IAWMTN.NPP	IPVGDYKRW	IILGLNKIVR	MYSPPVSILDI
00BW1859_5	AGTTSTLQEQ	IAWMTG.NPP	VPVGDYKRW	IILGLNKIVR	MYSPPVSILDI
00BW1880_2	AGTTSTLQEQ	ITWMTS.NPP	IPVGDYKRW	IVLGLNKIVR	MYSPPVSILDI
00BW1921_1	AGTTSTLQEQ	IAWMTN.NPP	VPVGDYKRW	IILGLNKIVR	MYSPPVSILDI
00BW2036_1	AGTTSTLQEQ	IAWMTS.NPP	IPVGDYKRW	IILGLNKIVR	MYSPPVSILDI
00BW2063_6	AGTTSTLAEQ	IAWMTS.NPP	IPVGDYKRW	IILGLNKIVR	MYSPPVSILDI
00BW2087_2	AGTTSTLQEQ	IAWMTN.NPP	IPVGDYKRW	IILGLNKIVR	MYSPPVSILDI
00BW2127_2	AGTTTTLQEQ	INWMTS.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
00BW2128_3	AGTTSTLQEQ	IAWMTS.NPP	IPVGDYKRW	IILGLNKIVR	MYSPPVSILDI
00BW2276_7	AGTTSTLQEQ	IAWMTS.NPA	IPVGDYKRW	IILGLDKIVR	MYSPPVSILDI
00BW3819_3	AGTTSTLQEQ	VAWMTS.NPP	VPVGDYKRW	IILGLNKIVR	MYSPPVSILDI
00BW3842_8	AGTTSNLQEQ	ITWMTS.NPP	IPVGEIYKRW	IVLGLNKIVR	MYSPPVSILDI
00BW3871_3	AGTTSTLQEQ	IDWMTN.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
00BW3876_9	AGTTSTLQEQ	IAWMTS.NPP	VPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
00BW3886_8	AGTTSTLQEQ	IAWMTN.NPP	VPVGDYKRW	IILGLNKIVR	MYSPPVSILDI
00BW3891_6	AGTTSNLQEQ	INWMTA.NPP	IPVGDYKRW	IILGLNKIVR	MYSPPVSILDI
00BW3970_2	AGTTSTLQEQ	IAWMTN.NPP	VPVGDYKRW	IVLGLNKIVR	MYSPPVSILDI
00BW5031_1	AGTTSTLQEQ	IAWMTS.NPP	VPVGDYKRW	IILGLNKIVR	MYSPPVSILDI
96BW01B21	AGTTSNLQEQ	IAWMTA.NPP	VPVGDYKRW	IILGLNKIVR	MYSPPVSILDI
96BW0407	AGTTSTLQEQ	IAWMTS.NPP	IPVGDYKRW	IILGLNKIVR	MYSPPVSILDI
96BW0502	AGATSTLQEQ	IAWMTS.NPP	VPVGDYKRW	IILGLNKIVR	MYSPPVSILDI
96BW06_J4	AGTTSTLQEQ	IGWMTN.NPP	IPVGDYKRW	IILGLNKIVR	MYSPPVSILDI
96BW11_06	AGTTSTLQEQ	IAWMTS.NPP	IPVGDYKRW	IILGLNKIVR	MYSPPVSILDI
96BW1210	AGTTSNLQEQ	INWMTS.NPP	IPVGDYKRW	IILGLNKIVR	MYSPPVSILDI
96BW15B03	AGTTSTLQEQ	IAWMTS.NPP	IPVGDYKRW	IILGLNKIVR	MYSPPVSILDI
96BW16_26	AGTTSTLQEQ	IAWMTS.NPP	VPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
96BW17A09	AGTTSTLQEQ	IAWMTN.NPP	IPVGDYKRW	ITMGLNKIVR	MYSPPVSILDI
96BWM01_5	AGTTSTLQEQ	IAWMTS.NPP	IPVGDYKRW	IILGLNKIVR	MYSPPVSILDI
96BWM03_2	AGSTSTLQEQ	IAWMTS.NPP	VPVGDYKRW	IILGLNKIVR	MYSPPVSILDI
98BWMC12_2	AGSTSNLQEQ	IAWMTS.NPP	IPVGDYKRW	IILGLNKIVR	MYSPPVSILDI
98BWMC13_4	AGTTSTLQEQ	IAWMTR.NPP	VPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
98BWMC14_a	AGTTSTLQEQ	VGWMTS.NPP	IPVGDYKRW	IILGLNKIVR	MYSPPVSILDI
98BWM014_1	AGTTSTLQEQ	IAWMTS.NPP	VPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
98BWM018_d	AGTTSTLQEQ	IAWMTS.NPP	IPVGDYKRW	IILGLNKIVR	MYSPPVSILDI
98BWM036_a	AGTTSTLQEQ	IAWMTS.NPP	IPVGDYKRW	IIMGLNKIVR	MYSPPVSILDI
98BWM037_d	AGTNSTLQEQ	IAWMTN.NPP	VPVGDYKRW	IILGLNKIVR	MYSPPVSILDI
99BW3932_1	AGTTSTLQEQ	IQWMTS.NPP	IPVGDYKRW	IILGLNKIVR	MYSPPVSILDI
99BW4642_4	AGTTSTLQEQ	VTWMTS.NPP	VPVGDYKRW	IILGLNKIVR	MYSPPVSILDI
99BW4745_8	AGTTSTLQEQ	INWMTG.NPP	IPVGDYKRW	IIMGLNKIVR	MYSPPVSILDI
99BW4754_7	AGTTSTLQEQ	ITWMTN.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
99BWMC16_8	AGTTSTLQEQ	IAWMTS.NPP	VPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
A2_CD_97CD	AGATSNLQEQ	IGWMTS.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
A2_CY_94CY	AGTTSTLQEQ	IGWMTS.DPP	IPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
A2D_97KR	AGTTSTLQEQ	IGWMTS.NPP	VPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
A2G_CD_97C	.....	.....	.....	.....	.....
A_BY_97BL0	AGTTSTLQEQ	IGXMTS.NPP	IPXGDYKRW	IILGLNKIVR	MYSPPVSILDI
A_KE_Q23_A	AGTTSTPQEQ	IGWMTG.NPP	IPVGDYKRW	IILGLNKIVR	MYSPPVSILDI
A_SE_SE659	.....	.....	.....	.....	.....
A_SE_SE725	.....	.....	.....	.....	.....

A_SE_SE753	AGTTSTPQEQ	IGWMTG.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
A_SE_SE853	.....	.....	.....	.....	.....
A_SE_SE889	.....	.....	.....	.....	.....
A_SE_UGSE8	AGTTSTLQEQ	IAWMTS.NPP	VPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
A_UG_92UG0	AGTTSTPQEQ	IAWMTG.NPP	IPVGDIYKRW	MILGLNKIVR	MYSPPVSILDI
A_UG_U455_	AGTTSTVQEQ	IGWMTG.NPP	IPVGDIYRRW	IILGLNKIVR	MYSPPVSILDI
AC_IN_2130	AGTTSTLQEQ	IAWMTG.NPP	VPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
AC_RW_92RW	AGTTSTLQEQ	IAWMTN.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
AC_SE_SE94	.....	.....	.....	.....	.....
ACD_SE_SE8	AGTTSTLQEQ	IAWMTS.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
ACG_BE_VI1	AGTTSTLQEQ	IGWMTS.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
AD_SE_SE69	AGTTSTLQEQ	IGWMTS.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
AD_SE_SE71	.....	.....	.....	.....	.....
ADHK_NO_97	AGTTSTLQEQ	IGWMTS.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
ADK_CD_MAL	AGTTSTLQEQ	IGWMTS.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
AG_BE_VI11	AGTTSTLQEQ	VGWMTS.NPP	VPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
AG_NG_92NG	AGTTSTLQEQ	ITWMTS.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
AGHU_GA_VI	AGTTSTTQEQ	IGWMTG.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
AGU_CD_Z32	AGTTSTLQEQ	IRWMTS.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
AJ_BW_BW21	AGTTSTLQEQ	IGWMTS.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
B_AU_VH_AF	AGTTSTLQEQ	IGWMTN.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPTSILDI
B_CN_RL42_	AGTTSTLQEQ	IGWMTN.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPTCILDI
B_DE_D31_U	AGTTSTLQEQ	IGWMTN.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPTSILDI
B_DE_HAN_U	AGTTSTLQEQ	IGWMTN.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPTSILDI
B_FR_HXB2_	AGTTSTLQEQ	IGWMTN.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPTSILDI
B_GA_OYI_	AGTTSTLQEQ	IGWMTN.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPTSILDI
B_GB_CAM1_	AGTTSTLQEQ	IGWMTN.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPTSILDI
B_GB_GB8_A	AGTTSTLQEQ	IGWMTN.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
B_GB_MANC_	AGTTSTLQEQ	IGWMTN.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPTSILDI
B_KR_WK_AF	AGTTSTLQEQ	IGWMTN.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPPASILDI
B_NL_3202A	AGTTSTLQEQ	IGWMTN.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPTSILDI
B_TW_TWCYS	AGTTSTLQEQ	IGWMTN.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPTSILDI
B_US_BC_L0	AGTTSTLQEQ	IGWMTN.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPPSSILDI
B_US_DH123	AGTTSTLQEQ	IGWMTN.NPP	IPVGEIYKRW	IIMGLNKIVR	MYSPTSILDI
B_US_JRCSF	AGTTSTLQEQ	IGWMTN.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
B_US_MNCG_	AGTTSTLQEQ	IGWMTN.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPPSSILDI
B_US_P896_	AGTTSTLQEQ	IGWMTN.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPPSSILDI
B_US_RF_M1	AGTTSTLQEQ	IGWMTN.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPPISILDI
B_US_SF2_K	AGTTSTLQEQ	IGWMTN.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPTSILDI
B_US_WEAU1	AGTTSTLQEQ	IAWMTN.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
B_US_WR27_	AGXTSTLXXX	IGWMTN.XPP	IPVGEIYKRW	IILGLNKIVR	MYSPTSILDI
B_US_YU2_M	AGTTSTLQEQ	IGWMTN.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPTSILDI
BF1_BR_93B	AGTTSTLQEQ	IQWMTS.NPP	VPVGEIYKRW	IILGLNKIVR	MYSPTSILGI
C_BR_92BR0	AGTTSTLQEQ	ITWMTN.NPP	VPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
C_BW_96BW0	AGTTSTLQEQ	IAWMTS.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
C_BW_96BW1	AGTTSTLQEQ	IAWMTS.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
C_BW_96BW1	AGTTSTLQEQ	INWMTS.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
C_BW_96BW1	AGTTSTLQEQ	IAWMTS.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
C_ET_ETH22	AGTTSTLQEQ	IAWMTG.NPP	VPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
C_IN_93IN1	AGTTSSLQEQ	IAWMTG.NPP	VPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
C_IN_93IN9	AGTTSSLQEQ	IAWMTG.NPP	VPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
C_IN_93IN9	AGTTSTLQEQ	IAWMTG.NPP	VPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
C_IN_94IN1	AGTTSTLQEQ	IAWMTS.NPP	VPVGEIYKRW	IILGLNKIVR	MYSPPVSILDT
C_IN_95IN2	AGTTSTLQEQ	IAWMTN.NPP	VPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
CRF01_AE_C	XGTTSTNLQEQ	IGWMTS.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
CRF01_AE_C	AGTTSTLHEQ	IGWMTS.NPP	IPVGEIYKKW	IILGLNKIVR	MYSPPVSILDI
CRF01_AE_C	AGTTSTLQEQ	IGWMTS.NPP	VPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
CRF01_AE_T	AGTTSTLQEQ	IGWMTN.NPP	IPVGDIYKRW	IILGLNKIVR	MYRPPVSILDI
CRF01_AE_T	AGTTSTLQEQ	IGWMTN.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
CRF01_AE_T	AGTTSTLQEQ	IGWMTN.NPP	IPVGDIYKRW	IILGLNKIVR	MYQPPVSILDI

CRF01_AE_T	AGTTTTLQEQ	IGWMTN.NPP	IPVGSIIYKRW	IILGLNKIVR	MYSPPVSILDI
CRF01_AE_T	AGTTSTLQEQ	IGWMTN.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
CRF01_AE_T	AGTTSTLQEQ	IGWMTS.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
CRF02_AG_F	AGTTSTPQEQ	IGWMTS.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
CRF02_AG_F	AGTTSTLQEQ	IGWMTS.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
CRF02_AG_G	AGTTSNLQEQ	IAWMTG.NPP	IPVGEIYKRW	IVLGLNKIVR	MYSPPVGILDI
CRF02_AG_N	AGTTSTLQEQ	IGWMTS.NPP	IPVGEIYKRW	IVLGLNKIVR	MYSPPVSILDI
CRF02_AG_S	AGTTSTLQEQ	IGWMTS.NPP	IPVGEIYKRW	IVLGLNKIVR	MYSPPVSILDI
CRF02_AG_S	AGTTSTLQEQ	IGWMTS.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
CRF03_AB_R	AGSSSTLQEQ	IGWMTS.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
CRF03_AB_R	AGTTSTLQEQ	IGWMTS.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
CRF04_cpx_	AGTTSTLQEQ	IGWMTS.NPP	VPVGEIYKRW	IILGLNKIVR	TYSPISILDI
CRF04_cpx_	AGTTSTLQEQ	IGWMTS.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
CRF04_cpx_	AGTTSTLQEQ	VGWMTS.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
CRF05_DF_B	AGTTSTLQEQ	IAWMTN.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
CRF05_DF_B	AGTTSTLQEQ	ITWMTN.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
CRF06_cpx_	AGTTSTLQEQ	IGWMTS.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPPVGILDI
CRF06_cpx_	AGTTSTLQEQ	IGWMTG.NPP	VPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
CRF06_cpx_	AGTTSTLLEQ	IGWMTS.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
CRF06_cpx_	AGTTSTLQEQ	IRWMTS.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
CRF11_cpx_	AGTTSTLQEQ	IGWMTG.NPP	IPVGDIYRRW	IILGLNKIVR	MYSPPVSILDI
CRF11_cpx_	AGTTGNLQEQ	IGWMTG.NPP	IPVGEIYRRW	IILGLNKIVR	MYSPPVSILDI
D_CD_84ZR0	AGTTSTLQEQ	IGWMTS.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
D_CD_ELI_K	AGTTSTLQEQ	IAWMTS.NPP	IPVGEIYKRW	IIVGLNKIVR	MYSPPVSILDI
D_CD_NDK_M	AGTTSTLQEQ	IAWMTS.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
D_UG_94UG1	AGTTSNLQEQ	IGWMTS.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
F1_BE_VI85	AGTTSTLQEQ	IQWMTG.NPP	VPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
F1_BR_93BR	AGTTSTLQEQ	IQWMTG.NPP	VPVGEMYKRW	IILGLNKIVR	MYSPPVGILDI
F1_FI_FIN9	AGTTSTLQEQ	IQWMTS.NPP	VPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
F1_FR_MP41	AGTTSTLQEQ	IQWMTS.NPP	VPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
F2_CM_MP25	AGTTSTLQEQ	IAWMTS.NPP	VPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
F2KU_BE_VI	AGATSNLQEQ	IAWMTS.NPP	VPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
G_BE_DRCBL	AGATSTLQEQ	IRWMTS.NPP	VPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
G_NG_92NG0	AGTTSTLQEQ	IRWMTS.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
G_SE_SE616	AGTTSSLQEQ	ITWMTG.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
H_BE_VI991	AGTTSTLQEQ	VAWMTG.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
H_BE_VI997	AGTTSTLQEQ	IAWMTG.NPS	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
H_CF_90CF0	AGTTSTLQEQ	IAWMTG.NPA	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
J_SE_SE702	AGTTSNLQEQ	IGWMTG.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
J_SE_SE788	AGTTSTLQEQ	IGWMTG.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
K_CD_EQTB1	AGTTSTLQEQ	ITWMTS.NPP	IPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
K_CM_MP535	AGTTSTLQEQ	IAWMTS.NPP	VPVGEIYKRW	IILGLNKIVR	MYSPPVSILDI
N_CM_YBF30	AGTTSTLAEQ	VAWMTA.NPP	VPVGDIYRRW	IVLGLNRIVR	MYSPPVSILEI
O_CM_ANT70	AGTTSTQQEQ	IHWTTTRPNQP	IPVGDIYRKW	IVLGLNKMVK	MYSPPVSILDI
O_CM_MVP51	AGTTSTQQEQ	IIWTTTRGANS	IPVGDIYRKW	IVLGLNKMVK	MYSPPVSILDI
O_SN_99SE_	AGTTSTQQEQ	VHWITRPNQP	IPVGDIYRKW	IVLGLNKVVK	MYSPPVSILDI
O_SN_99SE_	AGTTSTQQEQ	VHWITRPNQP	IPVGDIYRKW	IVLGLNKVVK	MYSPPVSILDI
U_CD___83C	AGTTSTLQEQ	IGWMTS.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI

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00BW0762_1	KQGPKEPFRD	YVDRFFKTLR	AEQATQEVKN	WMTDTLLVQN	ANPDCKTILR
00BW0768_2	KQGPKEPFRD	YVDRFFKTLR	AEQATQDVKN	WMTDTLLVQN	ANPDCKTILR
00BW0874_2	KQGPKEPFRD	YVDRFFKTLR	AEQATQEVKN	WMTDTLLVQN	ANPDCKTILR
00BW1471_2	KQGPKEPFRD	YVDRFFKTLR	AEQATQDVKN	WMTDTLLVQN	ANPDCKTILR
00BW1616_2	KQGPKEPFRD	YVDRFFKTLR	AEQATQDVKN	WMTDTLLVQN	ANPDCKTILR
00BW1686_8	KQGPKEPFRD	YVDRFFKTLR	AEQATQDVKN	WMTDTLLVQN	ANPDCKAILR
00BW1759_3	RQGPKEPFRD	YVDRFFKTLR	AEQATQEVKN	WMTDTLLIQN	ANPDCKTILK
00BW1773_2	KQGPKEPFRD	YVDRFFKTLR	AEQATQDVKN	WMTDTLLVQN	ANPDCKTILR
00BW1783_5	KQGPKEPFRD	YVDRFFKTLR	AEQSTQEVKN	WMTDTLLIQN	ANPDCKTILR
00BW1795_6	KQGPKEPFRD	YVDRFFKTLR	AEQSTQEVKN	WMTDTLLVQN	ANPDCKTILK

00BW1811_3	KQGPKEPFRD	YVDRFFKTLR	AEQATQDVKN	WMTETLLVQN	ANPDCKTILR
00BW1859_5	RQGPKEPFRD	YVDRFFKTLR	AEQATQDVKN	WMTDTLLVQN	ANPDCKTILR
00BW1880_2	KQGPKEPFRD	YVDRFFKTLR	AEQATQEVKN	WMTDTLLVQN	ANPDCKTILR
00BW1921_1	KQGPKEPFRD	YVDRFFKTLR	AEQSSQEVKN	WMTDTLLVQN	ANPDCKTILR
00BW2036_1	RQGPKEPFRD	YVDRFFKTLR	AEQATQDVKN	WMTDTLLVQN	ANPDCKTILR
00BW2063_6	KQGPKEPFRD	YVDRFFKTLR	AEQSTQEVKN	WMTDTLLVQN	ANPDCKTILR
00BW2087_2	KQGPKEPFRD	YVDRFFKTLR	AEQATQDVKN	WMTDTLLVQN	ANPDCKTILK
00BW2127_2	KQGPKEPFRD	YVDRIFFKTLR	AEQATQDVKN	WMTETLLVQN	ANPDCKTILR
00BW2128_3	RQGPKEPFRD	YVDRFFKTLR	AEQATQDVKN	WMTKTLLVQN	ANPDCKTILR
00BW2276_7	KQGPKEPFRD	YVDRFFKTLR	AEQATQDVKN	WMTDTLLVQN	ANPDCKTILR
00BW3819_3	RQGPKEPFRD	YVDRFFKTLR	AEQATQDVKN	WMTDTLLVQN	ANPDCKTILR
00BW3842_8	RQGPKEPFRD	YVDRFFKTLR	AEQATQDVKN	WMTETLLVQN	ANPDCKTILR
00BW3871_3	KQGPKEPFRD	YVDRFFKTLR	AEQATQDVKN	WMTGTLLVQN	ANPDCKTILR
00BW3876_9	KQGPKEPFRD	YVDRFFKTLR	AEQATQDVKN	WMTDTLLVQN	ANPDCKTILK
00BW3886_8	KQGPKEPFRD	YVDRFFKTLR	AEQATQDVKN	WMTDTLLVQN	ANPDCKTILR
00BW3891_6	KQGPKEPFRD	YVDRFFKTLR	AEQATQDVKN	WMTDTLLVQN	ANPDCKTILR
00BW3970_2	RQGPKEPFRD	YVDRFFKTLR	AEQATQDVKN	WMTDTLLVQN	ANPDCKTILR
00BW5031_1	KQGPKEPFRD	YVDRFFKTLR	AEQATQDVKN	WMTDTLLVQN	GNPDCKNILR
96BW01B21	KQGPKEPFRD	YVDRFFKTLR	AEQATQDVKN	WMTDTLLVQN	ANPDCKTILR
96BW0407	KQGPKEPFRD	YVDRFFKTLR	AEQSTQEVKN	WMTDTLLVQN	ANPDCKTILR
96BW0502	RQGPKEPFRD	YVDRFFKTLR	AEQATQDVKN	WMTETLLVQN	ANPDCKTILR
96BW06_J4	KQGPKEPFRD	YVDRFFKTLR	AEQCTQDVKN	WMTDTLLVQN	ANPDCKTILR
96BW11_06	KQGPKEPFRD	YVDRFFKTLR	AEQSSQEVKN	WMTDTLLVQN	ANPDCKTILK
96BW1210	KQGPKEPFRD	YVDRFFKTLR	AEQATQDVKN	WMTDTLLVQN	ANPDCKTILR
96BW15B03	RQGPKEPFRD	YVDRFFKTLR	AEQATQDVKN	WMTDTLLVQN	ANPDCKPILR
96BW16_26	RQGPKEPFRD	YVDRFFKTLR	AEQATQDVKN	WMTDTLLVQN	ANPDCKTILR
96BW17A09	KQGPKEPFRD	YVDRFFKTLR	AEQATQDVKN	WMTDTLLVQN	ANPDCKTILR
96BWM01_5	KQGPKEPFRD	YVDRFFKTLR	AEQSSQEVKN	WMTDTLLVQN	ANPDCKTILR
96BWM03_2	KQGPKEPFRD	YVDRFFKTLR	AEQATQDVKN	WMTDTLLVQN	ANPDCKTILR
98BWMC12_2	KQGPKEPFRD	YVDRFFKTLR	AEQATQEVKG	WMTDTLLIQN	ANPDCKTILR
98BWMC13_4	KQGPKEPFRD	YVDRFFKTLR	AEQATREVKN	WMTDTLLVQN	ANPDCKTILR
98BWMC14_a	KQGPKEPFRD	YVDRFFKTLR	AEQATQEVKD	WMTETLLVQN	ANPDCKTILR
98BWM014_1	RQGPKEPFRD	YVDRFFKTLR	AEQATQDVKN	WMTDTLLVQN	ANPDCKTILR
98BWM018_d	KQGPKEPFRD	YVDRFFKTLR	AEQSTQEVKN	WMTDTLLVQN	ANPDCKTILR
98BWM036_a	RQGPKEPFRD	YVDRFFKTLR	AEQATQEVKN	WMTDTLLVQN	ANPDCKTILR
98BWM037_d	RQGPKEPFRD	YVDRFFKTLR	AEQATQEVKN	WMTDTLLVQN	ANPDCKTILR
99BW3932_1	RQGPKEPFRD	YVDRFFKTLR	AEQATQDVKN	WMTETLLVQN	ANPDCKTILR
99BW4642_4	RQGPKEPFRD	YVDRFFKTLR	AEQATQEVKN	WMTDTLLVQN	ANPDCKTILR
99BW4745_8	KQGPKEPFRD	YVDRFFKTLR	AEQATQEVKN	WMADTLLVQN	ANPDCKTILR
99BW4754_7	KQGPKEPFRD	YVDRFFKTLR	AEQSTQDVKN	WMTDTLLVQN	ANPDCKTILR
99BWMC16_8	KQGPKEPFRD	YVDRFFKTLR	AEQASQDVKN	WMTDTLLVQN	ANPDCKTILR
A2_CD_97CD	KQGPKEPFRD	YVDRFFKTLR	AEQATQEVKN	WMTDTLLVQN	ANPDCKSILR
A2_CY_94CY	RQGPKEPFRD	YVDRFFKTLR	AEQATQEVKN	WMTDTLLVQN	ANPDCKSILR
A2D_97KR	RQGPKEPFRD	YVDRFFKTLR	AEQATQEVKN	WMTETLLVQN	ANPDCKSILR
A2G_CD_97C	.....	.....	.....	.....	.....
A_BY_97BL0	RQGPKEPFRD	YVDRFFKTLX	AEQATQDVKN	WMTETLLVQN	ANPDCKTILR
A_KE_Q23_A	KQGPKEPFRD	YVDRFFKTLR	AEQATQDVKN	WMTDTLLVQN	ANPDCKAILR
A_SE_SE659	.....	.....	.....	.....	.....
A_SE_SE725	.....	.....	.....	.....	.....
A_SE_SE753	KQGPKEPFRD	YVDRFFKTLR	AEQASQDVKN	WMTETLLIQN	ANPDCKSILR
A_SE_SE853	.....	.....	.....	.....	.....
A_SE_SE889	.....	.....	.....	.....	.....
A_SE_UGSE8	KQGPKEPFRD	YVDRFFKALR	AEQATQEVKG	WMTDTLLVQN	ANPDCKSILR
A_UG_92UG0	KQGPKEPFRD	YVDRFFKTLR	AEQATQEVKG	WMTETLLIQN	ANPDCKSILR
A_UG_U455_	RQGPKEPFRD	YVDRFFKTLR	AEQATQDVKN	WMTETLLVQN	ANPDCKSILR
AC_IN_2130	KQGPKEPFRD	YVDRFFKTLR	AEQATQDVKN	WMTDTLLVQN	ANPDCKTILR
AC_RW_92RW	KQGPKEPFRD	YVDRFFKTLR	AEQASQDVKN	WMTDTLLVQN	ANPDCKTILR
AC_SE_SE94	.....	.....	.....	.....	.....
ACD_SE_SE8	RQGPKEPFRD	YVDRFFKTLR	AEQATQEVKN	WMTETLLVQN	ANPDCKTILK
ACG_BE_VI1	RQGPKEPFRD	YVDRFFKTLR	AEQATQDVKN	WMTDTLLVQN	ANPDCKTILR



CRF04_cpx_	RQGPKEPFRD	YVDRFFKCLR	AEQATQEVKN	WMTETLLVQN	ANPDCKSILK
CRF04_cpx_	RQGPKEPFRD	YVDRFFKCLR	AEQATQEVKN	WMTETLLVQN	ANPDCKSILK
CRF04_cpx_	RQGTKEPFRD	YVDRFFKCLR	AEQATQDVKN	WMTETLLVQN	ANPDCKSILK
CRF05_DF_B	RQGPKEPFRD	YVDRFYKTLR	AEQATQEVKN	WMTETLLVQN	ANPDCKTILK
CRF05_DF_B	RQGPKEPFRD	YVDRFYKTLR	AEQASQDVKN	WMTETLLVQN	ANPDCKTILK
CRF06_cpx_	KQGPKEPFRD	YVDRFFKTLR	AEQATQEVKN	WMTDTLLVQN	ANPDCKTILR
CRF06_cpx_	RQGPKEPFRD	YVDRFFKTLR	AEQATQEVKN	WMTDTLLVQN	ANPDCKTILK
CRF06_cpx_	RQGPKEPFRD	YVDRFFKTLR	AEQATQEVKN	WMTDTLLVQN	ANPDCKTILK
CRF06_cpx_	RQGPKEPFRD	YVDRFFKTLR	AEQATQEVKN	WMTDTLLVQN	ANPDCKTILK
CRF11_cpx_	KQGPKEPFRD	YVDRFFKALR	AEQATQEVKG	WMTDTLLIQN	ANPDCKSILR
CRF11_cpx_	RQGPKEPFRD	YVDRFFKTLR	AEQASQEVKN	WMTETLLVQN	ANPDCKSILR
D_CD_84ZR0	RQGPKEPFRD	YVDRFYKTLR	AEQASQEVKN	WMTETLLVQN	ANPDCKTILK
D_CD_ELI_K	RQGPKEPFRD	YVDRFYKTLR	AEQASQDVKN	WMTETLLVQN	ANPDCKTILK
D_CD_NDK_M	RQGPKEPFRD	YVDRFYKTLR	AEQASQDVKN	WMTETLLVQN	ANPDCKTILK
D_UG_94UG1	RQGPKEPFRD	YVDRFYKTLR	AEQASQDVKN	WMTETLLVQN	ANPDCKTILK
F1_BE_VI85	KQGPKEPFRD	YVDRFFKVLR	AEQASQDVKG	WMTDTLLVQN	ANPDCKTILK
F1_BR_93BR	RQGPKEPFRD	YVDRFFKTLR	AEQATQEVKG	WMTDTLLVQN	ANPDCKTILK
F1_FI_FIN9	RQGPKEPFRD	YVDRFFKALR	AEQATQEVKG	WMTDTLLVQN	ANPDCKIILK
F1_FR_MP41	RQGPKEPFRD	YVDRFFKTLR	AEQASQEVKN	WMTESLLVQN	SNPDCKTILK
F2_CM_MP25	KQGPKEPFRD	YVDRFFKTLR	AEQATQEVKG	WMTETLLVQN	ANPDCKTILK
F2KU_BE_VI	KQGPKEPFRD	YVDRFFKTLR	AEQATQEVKN	WMTDTLLIQN	ANPDCKTILK
G_BE_DRCBL	RQGPKEPFRD	YVDRFFKTLR	AEQATQEVKS	WMTDTLLIQN	ANPDCKIILK
G_NG_92NG0	RQGPKEPFRD	YVDRFFKTLR	AEQATQEVKG	WMTDTLLVQN	ANPDCKTILR
G_SE_SE616	RQGPKEPFRD	YVDRFFKCLR	AEQASQDVKG	WMTDTLLVQN	ANPDCKTILR
H_BE_VI991	KQGPKEPFRD	YVDRFFRVLR	AEQATQDVKN	WMTDTLLVQN	ANPDCTRILK
H_BE_VI997	KQGPKEPFRD	YVDRFFKTLR	AEQATQEVKN	WMTDTLLVQN	ANPDCKTILR
H_CF_90CF0	KQGPKEPFRD	YVDRFFKTLR	AEQATQDVKN	WMTETLLVQN	ANPDCKTILR
J_SE_SE702	RQGPKEPFRD	YVDRFFKALR	AEQATQDVKN	WMTDTLLVQN	ANPDCKTILK
J_SE_SE788	RQGPKEPFRD	YVDRFFKALR	AEQATQDVKN	WMTDTLLVQN	ANPDCKTILK
K_CD_EQTB1	RQGPKEPFRD	YVDRFFRVLR	AEQATQEVKN	WMTETLLVQN	ANPDCTRILK
K_CM_MP535	RQGPKEPFRD	YVDRFFKTLR	AEQATQEVKN	WMTDTLLVQN	ANPDCKTILK
N_CM_YBF30	KQGPKEPFRD	YVDRFYKTLR	AEQATQEVKN	WMTETLLVQN	ANPDCKQLLK
O_CM_ANT70	RQGPKEPFRD	YVDRFYKTLR	AEQATQEVKN	WMTETLLVQN	ANPDCKQILK
O_CM_MVP51	RQGPKEPFRD	YVDRFYKTLR	AEQATQEVKN	WMTETLLVQN	SNPDCKQILK
O_SN_99SE_	RQGPKEPFRD	YVDRFYKTLR	AEQATQEVKN	WMTETLLVQN	ANPDCKQILK
O_SN_99SE_	RQGPKEPFRD	YVDRFYKTLR	AEQATQEVKN	WMTETLLVQN	ANPDCKQILK
U_CD_83C	KQGPKEPFRD	YVDRFFKVLR	AEQSSQEVKN	WMTDTLLIQN	ANPDCKTILK

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400

00BW0762_1	ALGPGASLEE	MMTACQGVGG	PSHKARVLAE	AMSQANN...	...TNIMLQK
00BW0768_2	ALGPGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQHN...	...TSIMMQK
00BW0874_2	GLGPGASLEE	MMTACQGVGG	PSHKARVLAE	AMSQSN...	...S.IMMQR
00BW1471_2	ALGPGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQANN...	...TNVMMQK
00BW1616_2	ALGPGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQAGN...	...ATIMMQK
00BW1686_8	ALGPGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQANS...	...PNILMQR
00BW1759_3	ALGPGASLEE	MMTACQGVGG	PGHKARVLAE	AMSKANN...	...ANILMQR
00BW1773_2	ALGPAASLEE	MMTACQGVGG	PSHKARVLAE	AMSQANT...	...TNIMMQK
00BW1783_5	ALGQGASLEE	MMTACQGVGG	PGHKARVLAE	AMSQVGN...	...PQVMMQR
00BW1795_6	ALGSGASLEE	MMTACQGVGG	PSHKARVLAE	AMSQANN...	...VQIMMQK
00BW1811_3	ALGPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQTTS...	...MQIMMQR
00BW1859_5	ALGPGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQANN...	...ANIMMQR
00BW1880_2	ALGPGASLEE	MMTACQGVGG	PSHKARVLAE	AMSQATN...	...TSIMMQK
00BW1921_1	ALGPGATLEE	MMTACQGVGG	PSHKARALAE	AMSQANN...	...TNIMMQK
00BW2036_1	ALGPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVNG...	...SNVLMQR
00BW2063_6	ALGPGASLEE	MMTACQGVGG	PGHKARVLAE	AMSQANN...	...INVMMQK
00BW2087_2	ALGSGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQANS...	...TNIMIQR
00BW2127_2	ALGSGVTLLEE	MMSACRGVGG	PSHKARVLAE	AMSQANN...	...TNIMMQR
00BW2128_3	ALGPAATLVE	MMTACQGVGG	PSHKARVLAE	AMSQTAS...	...TNILMQR
00BW2276_7	ALGPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQAN...	...SNIMMQR
00BW3819_3	ALGPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQANN...	...INVMMQR

00BW3842_8	ALGPGASLEE	MMTACQGVGG	PGHKARVLAE	AMSQANS...	...TNIMMQR
00BW3871_3	ALGPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQANN...	...SNIMMQR
00BW3876_9	ALGPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQAGS...	...VNILMQR
00BW3886_8	ALGPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQANN...	...INVMMQR
00BW3891_6	ALGPGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQTN....	...SNIMMQN
00BW3970_2	AIGPGASLEE	MMTACQGVGG	PSHKARVLAE	AMSQTH....	...SNIMMQR
00BW5031_1	ALGPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQANN...	...INIMMQR
96BW01B21	ALGPGASIEE	MMTACQGVGG	PSHKARVLAE	AMSQANS...	...MNIMMQR
96BW0407	ALGPGASLEE	MMTACQGVGG	PSHKARVLGE	AMSQA.N...	...TNVMMQR
96BW0502	ALGPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQANS...	...VNIMMQR
96BW06_J4	ALGPGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQANS...	...TSILMQR
96BW11_06	TLGPGASLEE	MMTACQGVGG	PSHKARILAE	AMSQANN...	...PNIMMQR
96BW1210	ALGPGASLEE	MMTACQGVGG	PSHKARVLAE	AMSHAGN...	...AGIMMQR
96BW15B03	ALGPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQATS...	...ANILMQR
96BW16_26	ASGPGASLEE	MMTACQGVGG	PGHKARVLAE	AMSQANN...	...TNIMIQR
96BW17A09	ALGPGATLEE	MMTACQGVGG	PSHKARVLAE	AMSHANN...	...TSIMMQR
96BWM01_5	ALGPGASLEE	MMTACQGVGG	PSHKARVLAE	AMSQANN...	...IQVMMQR
96BWM03_2	ALGPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQAN....	...TNIMMQR
98BWMC12_2	ALGPGATLEE	MMTACQGVGG	PSHKARVLAE	AMSHTN....	...S.IMMQR
98BWMC13_4	ALGPGASLEE	MMTACQGVGG	PGHKARVLAE	AMSQANN...	...INIMMQR
98BWMC14_a	SLGTGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQAN....	...TSIMMQR
98BWM014_1	ALGPGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQANS...	...TNILIQR
98BWM018_d	ALGPGASLEE	MMTACQGVGG	PSHKARVLAE	AMSQAGN...	...ANIMMQR
98BWM036_a	ALGPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQANN...	...ANIMMQR
98BWM037_d	ALGPGASLEE	MMTACQGVGG	PGHKARVLAE	AMSQAN....	...SNIMMQR
99BW3932_1	ALGPGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQANN...	...ASVMMQR
99BW4642_4	ALGPGATLEE	MMTACQGVGG	PGHKARVLAE	AMGQVNS...	...TNIMMQR
99BW4745_8	GLGPGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQTN....	...SNIMMQR
99BW4754_7	ALGPGASLEE	MMTACQGVGG	PSHKARVLAE	AMSQANN...	...PNIMMQR
99BWMC16_8	ALGPGASIEE	MMTACQGVGG	PSHKARVSAE	AMSQANQ...	...ANIMMQR
A2_CD_97CD	ALGPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVQNT..	...NIMIQR
A2_CY_94CY	ALGPGASLEE	MMTACQGVGG	PSHKARVLAE	AMSHVQSTN.	..T.NIMMQR
A2D_97KR	ALGPGASLEE	MMTACQGVGG	PSHKARVLAE	AMSQVQNTN.	..SNIMMMQR
A2G_CD_97C	.....	.....	.....	.....	.....
A_BY_97BL0	ALGSEATLEE	MMTACQGVGG	PGHKAXVXAE	AMSQVQN...	...ANIMMQR
A_KE_Q23_A	ALGPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVQH...	...TNIMMQR
A_SE_SE659	.....	.....	.....	.....	.....
A_SE_SE725	.....	.....	.....	.....	.....
A_SE_SE753	ALGAGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVQH...	...PNIMMQR
A_SE_SE853	.....	.....	.....	.....	.....
A_SE_SE889	.....	.....	.....	.....	.....
A_SE_UGSE8	GLGAGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQAQQ...	...TNIMMQR
A_UG_92UG0	ALGAGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVQH...	...TNIMMQR
A_UG_U455_	ALGPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVQQT..	...SIMMQR
AC_IN_2130	ALGPGASLEE	MMTACQGVGG	PSHKARVLAE	AMSQTN....	...NSILMQR
AC_RW_92RW	ALGPGASLEE	MMTACQGVGG	PGHKARVLAE	AMSQVQQ...	...PNIMMQR
AC_SE_SE94	.....	.....	.....	.....	.....
ACD_SE_SE8	ALGPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQAN....	..ANTAIMMQR
ACG_BE_VI1	ALGPGASLEE	MMTACQGVGG	PSHKARVLAE	AMSQANN...	...TVMMQR
AD_SE_SE69	ALGPAATLEE	MMTACQGVGG	PGHKARVLAE	AMSQATNN..	..INAAIMMQR
AD_SE_SE71	.....	.....	.....	.....	.....
ADHK_NO_97	ALGPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVQN...	...VSVMMQR
ADK_CD_MAL	ALGPGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQATN...	..STAAIMMQR
AG_BE_VI11	ALGTGATLEE	MVTACQGVGG	PGHKARVLAE	AMSQVH....	..QTNIMMQR
AG_NG_92NG	ALGAGATLEE	MLTACQGVGG	PSHKARVLAE	AMSRAT.G..	..TSAAIMMQR
AGHU_GA_VI	GLGAGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVHN...	...TSIMMQR
AGU_CD_Z32	ALGPGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQAS.S..	..TAAAIMMQR
AJ_BW_BW21	ALGAGATLEE	MMTACQGVG.	PGHKAKILAE	AMSQVQN...	...TNIMMQR
B_AU_VH_AF	ALGPAATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVT....	..NSATIMMQR
B_CN_RL42_	ALGPAATLEE	MMTACQGVGG	PSHKARILAE	AMSQVTNSAI	TNSATIMMQR



B_DE_D31_U	ALGPAATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVT....	.NSATVMMQR
B_DE_HAN_U	ALGPAATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVT....	.GSAAIMMQR
B_FR_HXB2_	ALGPAATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVT....	.NSATIMMQR
B_GA_OYI_	ALGPAATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVN....	..SVTVMMQK
B_GB_CAM1_	ALGPAATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVT....	.NSATIMMQR
B_GB_GB8_A	ALGPAATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVN....	..SATIMMQR
B_GB_MANC_	ALGPAATLEE	MMTACQGVGG	PSHKARILAE	AMSQVT....	.NSATIMMQR
B_KR_WK_AF	ALGPGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQAT....	.NSATIMMQR
B_NL_3202A	ALGPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVT....	.NSATIMMQR
B_TW_TWCYS	ALGPAATLEE	MMTACQGVGG	PSHKARVLAE	AMSRVP....	.NSTNIMMQR
B_US_BC_L0	ALGPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVT....	.NSATIMMQR
B_US_DH123	ALGPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQITN...	.TSATIMMQG
B_US_JRCSF	ALGPAATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVT....	.NPATIMMQR
B_US_MNCG_	ALGPAATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVT....	.NSATIMMQR
B_US_P896_	ALGPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVT....	.NSATIMMQR
B_US_RF_M1	ALGPAATLEE	MMTACQGVGG	PSHKARILAE	AMSQVT....	.NSATIMLQK
B_US_SF2_K	ALGPAATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVT....	.NPANIMMQR
B_US_WEAU1	ALGPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVT....	.NTATMMMQR
B_US_WR27_	ALGPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVT....	.GSNAIMMQR
B_US_YU2_M	ALGPAATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVT....	.NSATIMMQR
BF1_BR_93B	ALGPAATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVT....	.NSGTIMMQR
C_BR_92BR0	ALGPGASLEE	MMTACQGVGG	PGHKARVLAE	AMSKVNN...	...TNIMMQR
C_BW_96BW0	ALGPGASLEE	MMTACQGVGG	PSHKARVLAE	AMSQT.N...	...TNVMMQR
C_BW_96BW1	ALGPGASLEE	MMTACQGVGG	PSHKARILAE	AMSQANN...	...SNIMMQR
C_BW_96BW1	ALGPGASLEE	MMTACQGVGG	PSHKARVLAE	AMSHAGN...	...AGIMMQR
C_BW_96BW1	ALGPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQATS...	...ANILMQR
C_ET_ETH22	ALGPGASLEE	MMTACQGVGG	PAHKARVLAE	AMSQVNN...	...TTIMMQR
C_IN_93IN1	ALGPGASLEE	MMTACQGVGG	PGHKARVLAE	AMSQAN....	...STILMQR
C_IN_93IN9	ALGPGASLEE	MMTACQGVGG	PSHKARVLAE	AMSQTN....	...SAILMQR
C_IN_93IN9	ALGPGASLEE	MMTACQGVGG	PGHKARVLAE	AMSQAN....	...SNILMQR
C_IN_94IN1	ALGPGASLEE	MMTACQGVGG	PSHKARVLAE	AMSQTN....	...SAILMQR
C_IN_95IN2	ALGPGASLEE	MMTACQGVGG	PSHKARVLAE	AMSQTN....	...SAILMQR
CRF01_AE_C	ALGTGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVQ....	...HANIMMQR
CRF01_AE_C	ALGTGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVH....	...HTNIMMQR
CRF01_AE_C	ALGTGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVQ....	...HANIMMQR
CRF01_AE_T	SLGTGATLEE	MMTACQGVGG	PSHKARVLAE	AMSHAQ....	...HANIMMQR
CRF01_AE_T	ALGTGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQAQ....	...HANIMMQR
CRF01_AE_T	ALGTGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQAQ....	...HANIMMQR
CRF01_AE_T	ALGTGATLEE	MMTACQGVGG	PSHKARVLAE	AMSHAQ....	...QANIMMQR
CRF01_AE_T	ALGTGATLEE	MMTACQGVGG	PSHKARVLAE	AMSHAQ....	...HATIMMQR
CRF01_AE_T	ALGTGATLEE	MMTACQGVGG	PSHKARVLAE	AMSHVQ....	...QANIMMQR
CRF02_AG_F	ALGPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVQ....	...QSNIMMQR
CRF02_AG_F	ALGPGASLEE	MMTACQGVGG	PGHKARVLAE	AMSQVQ....	...QSNIMMQR
CRF02_AG_G	ALGPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVQSP..	...NILMQR
CRF02_AG_N	ALGTGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVQ....	...QANVMMQR
CRF02_AG_S	ALGPGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQVQ....	...QPNIMMQR
CRF02_AG_S	ALGPGATLEE	MMSACQGVGG	PGHKARVLAE	AMSQAQ....	...QSNIMMQR
CRF03_AB_R	ALGSGATLEE	MMTVCQGVGG	PGHKARVLAE	AMSQVQN...	...ANIMMQR
CRF03_AB_R	ALGSGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVQN...	...ANIMMQR
CRF04_cpx_	ALGTGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQASN...	...AAAAIMMQR
CRF04_cpx_	ALGTGATLEE	MMTACQGVGG	PAHKARVLAE	AMSQASN...	...AAAAIMMQR
CRF04_cpx_	ALGTGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQASS...	...AAAAIMMQR
CRF05_DF_B	ALGQQATLEE	MMTACQGVGG	PSHKARVLAE	AMSQATN...	...SAATAMMQR
CRF05_DF_B	ALGPQATLEE	MMTACQGVGG	PSHKARVLAE	AMSQATG...	...SPAVMMQ.R
CRF06_cpx_	ALGPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQAS...	...VGAIMMQ.K
CRF06_cpx_	ALGPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQASGT..	...LTAIMMQ.K
CRF06_cpx_	ALGPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQASGT..	...VAAAIMMQR
CRF06_cpx_	ALGPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVSGA..	...TAAIMMQ.K
CRF11_cpx_	ALGTGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQVQQ...	...TNVMMQR
CRF11_cpx_	ALGVGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQAQH...	...TNIMMQR

D_CD_84ZR0	ALGPGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQATS...	.ASAAIMMQK
D_CD_ELI_K	ALGPQATLEE	MMTACQGVGG	PSHKARVLAE	AMSQATN...	.SVTTAMMQR
D_CD_NDK_M	ALGPQATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVTG...	.SATAVMMQR
D_UG_94UG1	ALGPAATLEE	MMTACQGVGG	PSHKARVLAE	AMSQATN...	.ANTAIMMQR
F1_BE_VI85	ALGTGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQAN....	...SAIMMQK
F1_BR_93BR	ALGPGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQATN...	...TAIMMQK
F1_FI_FIN9	GLGIGATLEE	MMTACRGVGG	PGHKARILAE	AMSQAN....	...TTIMMQK
F1_FR_MP41	ALGPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQATN...	...AAIMMQK
F2_CM_MP25	ALGPGATLEE	MMTACQGVGG	PSHKARILAE	AMSKATG...	...AAIMMQK
F2KU_BE_VI	ALGPGASLEE	MMTACQGVGG	PAHKARVLAE	AMSQATN...	...TAIMMQK
G_BE_DRCBL	GLGQGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQAS.G..	.AAAAIMMQK
G_NG_92NG0	ALGPGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQASGA..	.AAAAIMMQK
G_SE_SE616	ALGQGASLEE	MMTACQGVGG	PSHKARVLAE	AMSQAS.G..	.AAAAIMMQR
H_BE_VI991	ALGRGASIEE	MMTACQGVGG	PSHKARVLAE	AMSQVTNAS..	...AAIMMQK
H_BE_VI997	ALGQGASIEE	MMTACQGVGG	PSHKARVLAE	AMSQVTNAN..	...AAIMMQK
H_CF_90CF0	ALGQGASIEE	MMTACQGVGG	PSHKARVLAE	AMSQVTNTN..	...TAIMMQK
J_SE_SE702	ALGSGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVTN...	...TNIMMQR
J_SE_SE788	ALGSGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVTN...	...TNIMMQR
K_CD_EQTB1	ALGSGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVTN...	...SAVMMQR
K_CM_MP535	ALGPGASLEE	MMTACQGVGG	PSHKARILAE	AMSQVTN...	...PVVMMQK
N_CM_YBF30	ALGPGATLEE	MMTACQGVGG	PAHKARVLAE	AMSQVQPP..	..TTSVFAQR
O_CM_ANT70	SLGPGATLEE	MMVACQGVGG	PTHKARVLAE	AMATAQQDLK	GGYTAVFMQR
O_CM_MVP51	ALGPEATLEE	MMVACQGVGG	PTHKAKILAE	AMASAQQDLK	GGYTAVFMQR
O_SN_99SE_	SLGPGATLEE	MMIACQGVGG	PTHKARVLAE	AMA.AAQDLK	GGYTAVFMQR
O_SN_99SE_	SLGPGATLEE	MMIACQGVGG	PTHKARVLAE	AMS.AAQDLK	GGYSAVFMQR
U_CD___83C	ALGTGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQTN....	...TAIMMQR

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450

00BW0762_1	NNFKGPRRIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
00BW0768_2	SNFKGPKRIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
00BW0874_2	SNFKGCHKRIV	KCFNCGKEGH	IAKNCRAPRK	KGCWKCCKEG	HQMKDCT..E
00BW1471_2	GNFKGPRRVI	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKECT..E
00BW1616_2	SNFKGPRRIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
00BW1686_8	SNFKGSK.RV	KCFNCGKEGH	IARNCRAPRK	RGCWKCCKEG	HQMKDCT..E
00BW1759_3	SNFKGPKRIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
00BW1773_2	SNFKGPRRTV	KCFNCGKEGH	IAKNCRAPRK	KGCWKCCKEG	HQMKDCT..E
00BW1783_5	NNLKGTTRTV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
00BW1795_6	NNFKGPRRII	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
00BW1811_3	SNFKGSKRSV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKDG	HQMKDCT..E
00BW1859_5	SNFKGPRKII	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
00BW1880_2	SNFKGPRRIV	KCFNCGKEGH	IAKNCRAPRK	KGCWKCCKEG	HQMKDCT..E
00BW1921_1	SNFKGPRRIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
00BW2036_1	GNFKGPKRII	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
00BW2063_6	NNFKGPRRLV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
00BW2087_2	SNFKGSKRIV	KCFNCGKEGH	IAKNCRAPRK	KGCWKCCKEG	HQMKDCT..E
00BW2127_2	GNFRGAKRSV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
00BW2128_3	SNFKGSKRSV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
00BW2276_7	SNFKGPRKIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCTN.D
00BW3819_3	SNFKGSKRIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDYT..E
00BW3842_8	GNFKGPKRTI	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
00BW3871_3	SNFKGPRRII	KCFNCGKEGH	LARNCRAPRK	RGCWKCCKEG	HQMKDCTT.E
00BW3876_9	SNFKGSKRIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
00BW3886_8	GNFKGAKRIV	KCFNCGKEGH	IAKNCRAPRK	KGCWKCCKEG	HQMKDCT..E
00BW3891_6	SNFKGSRRIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
00BW3970_2	SNFKGPKRIV	KCFNCGKEGH	IAKNCRAPRK	KGCWKCCKEG	HQMKDCT..E
00BW5031_1	NNFKGPKRIV	KCFNCGKEGH	IAKNCRAPRK	KGCWKCCKEG	HQMKDCT..E
96BW01B21	SNFKNPKRIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
96BW0407	SNFKGPRRIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
96BW0502	SNFKGPRRNV	KCFNCGKEGH	IAKNCRAPRK	KGCWKCCKEG	HQMKDCT..E
96BW06_J4	GNFKGPKRII	KCFNCGKEGH	IAKNCRAPRK	KGCWKCCKEG	HQMKDCT..E

96BW11_06	NNFKGPRRIV	KCFNCGKEGH	IARNCKAPRK	KGCWKCCKEG	HQMKDCT..E
96BW1210	GNFKGPRKIP	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCS..E
96BW15B03	SNFKGPKRII	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
96BW16_26	SNFKGPRRSV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
96BW17A09	GNFKGPRRTI	KCFNCGKEGH	LAKNCRAPRK	XGCWKCCKEG	HQMKECT..E
96BWM01_5	NNFKGPRRTI	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
96BWM03_2	GNFKGPKRII	KCFNCGKEGH	IAKNCRAPRK	KGCWKCCKEG	HQMKDCNN.E
98BWMC12_2	SNFKGPKRIV	KCFNCGKEGH	IAKNCRAPRK	KGCWKCCKEG	HQMKDCN..E
98BWMC13_4	SNFKGPKRII	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
98BWMC14_a	GNFKGPRRII	KCFNCGKEGH	IAKNCRAPRK	KGCWKCCKEG	HQMKDCT..E
98BWM014_1	SHFKGSKRTV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
98BWM018_d	GNFKGPRRII	KCSNCGKEGH	IAKNCRAPRK	KGCWKCCKEG	HQMKDCT..E
98BWM036_a	SNFKGPKRTV	KCFNCGKEGH	VARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
98BWM037_d	GNFKGSKRIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
99BW3932_1	SNFKGPKRII	KCFNCGKEGH	IAKNCRAPRK	KGCWKCCKEG	HQMKDCT..E
99BW4642_4	SNFKGPKRII	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
99BW4745_8	SNFKGPRRTV	KCFNCGKEGH	IAKNCRAPRK	KGCWKCCKEG	HQMKDCT..E
99BW4754_7	XNFKGPRRIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
99BWMC16_8	SNFKGPKRIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
A2_CD_97CD	GNFKGQKR.I	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
A2_CY_94CY	GNFRGQKR.I	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
A2D_97KR	GNFRGQK..I	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
A2G_CD_97C	.....	.....	.....	.....	.....
A_BY_97BL0	SNFRGPKR.I	KCXNCGKEGH	LARNCRAPRK	XGCWKCCKEG	HQMKDCTE..
A_KE_Q23_A	GNFKGQKR.I	KCFNCGKEGH	LARNCRALRK	KGCWKCCKEG	HQMKDCTE..
A_SE_SE659	.....	.....	.....	.....	.....
A_SE_SE725	.....	.....	.....	.....	.....
A_SE_SE753	GNFRGQKR.I	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCTE..
A_SE_SE853	.....	.....	.....	.....	.....
A_SE_SE889	.....	.....	.....	.....	.....
A_SE_UGSE8	GNFRGQKK.I	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCTE..
A_UG_92UG0	GNFKGQKR.I	KCFNCGKEGH	LAKNCRAPRK	KGCWKCCKEG	HQMKDCTE..
A_UG_U455_	GNFRGPRR.I	KCFNCGKEGH	LAKNCRAPRK	KGCWKCCKEG	HQMKDCT..E
AC_IN_2130	SNFKGFKRTV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
AC_RW_92RW	GNFKGQRRII	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
AC_SE_SE94	.....	.....	.....	.....	.....
ACD_SE_SE8	GNFKGPKKII	KCFNCGKEGH	IAKNCRAPRK	KGCWKCCKEG	HQMKDCTE..
ACG_BE_VI1	GNFKGPKRII	KCFNCGKEGH	VARNCRAPRK	KGCWKCCKEG	HQMKDCTT.E
AD_SE_SE69	GNFKGQRKII	KCFNCGKLGH	IARNCKAPRK	KGCWKCCKEG	HQMKDCTE..
AD_SE_SE71	.....	.....	.....	.....	.....
ADHK_NO_97	GNFKGQKR.I	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCTE..
ADK_CD_MAL	GNFKGQKR.I	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCTE..
AG_BE_VI11	GNFRGQKT.I	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCTE..
AG_NG_92NG	NNFKGPRRGI	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCTE..
AGHU_GA_VI	GNFKGQKR.I	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCTE..
AGU_CD_Z32	SNFKGPRKTI	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDC.E..
AJ_BW_BW21	SNFKGQKR.I	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCTE..
B_AU_VH_AF	GNFRNQRKTV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCTE..
B_CN_RL42_	GNFRNQRKIV	KCFNCGKEGH	IAKNCRAPRK	KGCWKCCKEG	HLMKDCTE..
B_DE_D31_U	GNFRNQRKTV	KCFNCGKEGH	IAKNCRAPRK	KGCWKCCKEG	HQMKDCTE..
B_DE_HAN_U	GNFRNQRKTV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCTE..
B_FR_HXB2_	GNFRNQRKIV	KCFNCGKEGH	TARNCRAPRK	KGCWKCCKEG	HQMKDCTE..
B_GA_OYI_	GNFKNQRKTV	KCFNCGKEGH	IAKNCRAPRK	KGCWKCCKEG	HQMKDCTE..
B_GB_CAM1_	GNFRNQRKTV	KCFNCGKVGH	IAKNCRAPRK	KGCWKCCKEG	HQMKDCNE..
B_GB_GB8_A	GNFRSQRKTV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKECTE..
B_GB_MANC_	GNFRNQRKTV	KCFNCGKEGH	IAKNCRAPRK	KGCWKCCKEG	HQMKDCTE..
B_KR_WK_AF	GNFRNQRRTV	KCFNCGKEGH	IAKNCRAPRK	KGCWKCCKEG	HQMKDCTE..
B_NL_3202A	GNFRNQRKIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCTE..
B_TW_TWCYS	GNFRNQRKTV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCTE..
B_US_BC_LO	GNFRNQRKTV	KCFNCGKEGH	IARNCKAPRK	KGCWKCCKEG	HQMKDCTE..

B_US_DH123	GNFRNQRK.I	KCFNCGKEGH	ISKNCRAPRK	KGCWKCCKEG	HQMKDCTE..
B_US_JRCSF	GNFRNQRKIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKECTE..
B_US_MNCG	GNFRNQRKII	KCFNCGKEGH	IAKNCRAPRK	RGCWKCCKEG	HQMKDCTE..
B_US_P896	GNFRNQRKTV	KCFNCGKEGH	IAKNCRAPRK	KGCWKCCKEG	HQMKDCTE..
B_US_RF_M1	GNFRDQRKIV	KCFNCGKVGH	IAKNCRAPRK	KGCWKCCKEG	HQMKDCTNEG
B_US_SF2_K	GNFRNQRKTV	KCFNCGKEGH	IAKNCRAPRK	KGCWRCGREG	HQMKDCTE..
B_US_WEAU1	GNFRSPRKTI	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCTE..
B_US_WR27	GNFRNQRKTV	KCXXCGKEGH	XARXCKAPRK	RGCWKCCKEG	HQMXDXXE..
B_US_YU2_M	GNFRNQRKTV	KCFNCGKEGH	IAKNCRAPRK	KGCWKCCKEG	HQMKDCTE..
BF1_BR_93B	GNFRNQRKTI	KCFNCGKEGH	IAKNCRAPRK	KGCWKCCKEG	HQMKDCTE..
C_BR_92BR0	SNCKGPKRTI	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQVKDCT..E
C_BW_96BW0	SNFKGPRRIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
C_BW_96BW1	NNFKGPRTRIV	KCFNCGKEGH	IARNCKAPRK	KGCWKCCKEG	HQMKDCT..E
C_BW_96BW1	GNFKGPRKIP	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCS..E
C_BW_96BW1	SNFKGPKRII	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
C_ET_ETH22	SNFKGPKRAI	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
C_IN_93IN1	SNFKGSKRIV	KCFNCGKEGH	IAKNCRAPRK	KGCWKCCKEG	HQMKDCT..E
C_IN_93IN9	SNFKGSKRII	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
C_IN_93IN9	SNFKGSKRTV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
C_IN_94IN1	SNFKGSKRII	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
C_IN_95IN2	SNFKGSKRIV	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
CRF01_AE_C	GNFKGQKR.I	KCFNCGKEGH	LARNCRAPRK	RGCWKCCKEG	HQMKDCTE..
CRF01_AE_C	GNFKGQKR.I	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCTE..
CRF01_AE_C	GNFKGQKR.I	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCTE..
CRF01_AE_T	GNFKGQKR.I	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCTE..
CRF01_AE_T	GNFKGPRR.I	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCTE..
CRF01_AE_T	GNFKGQTR.I	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCTE..
CRF01_AE_T	GNFKGQKR.I	KCFNCGKEGH	LARNCRALRK	KGCWKCCKEG	HQMKDCTE..
CRF01_AE_T	GNFKGQKR.I	KCFNCGREGH	LARNCRAPRK	QGCWKCCKEG	HQMKDCTE..
CRF01_AE_T	GNFKGQKR.I	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCTE..
CRF02_AG_F	GNFRGQRT.I	KCFNCGKEGH	LARNCKAPRK	KGCWKCCKEG	HQMKDCTE..
CRF02_AG_F	GNFRGQRT.I	KCFNCGKEGH	LARNCKAPRK	KGCWKCCKEG	HQMKDCTE..
CRF02_AG_G	GNFKGQK.RI	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
CRF02_AG_N	GNFRGQRT.I	KCFNCGKEGH	LARNCKAPRK	RGCWKCCKEG	HQMKDCTE..
CRF02_AG_S	GNFRGQRP.I	KCFNCGKEGH	LARNCKAPRK	KGCWKCCKEG	HQMKDCTE..
CRF02_AG_S	GNFRGQRT.I	KCFNCGKEGH	LARNCKAPRK	RGCWKCCKEG	HQMKDCTE..
CRF03_AB_R	SNFRGPKR.I	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCTE..
CRF03_AB_R	SNFRGPKR.I	KCFNCGKDGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCNE..
CRF04_cpx	SKFKGQRRTI	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCTE..
CRF04_cpx	SNFRGQKR.II	KCFNCGKEGH	LARNCRAPRK	RGRWKCCKEG	HQMKDCTE..
CRF04_cpx	SNFKGPRRSI	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCPE..
CRF05_DF_B	GNFKGPRKII	KCFNCGKEGH	IAKNCRAPGK	KGCWKCCKEG	HQMKDCTE..
CRF05_DF_B	GNFKGPRKSI	KCFNCGKEGH	TAKNCRAPRK	RGCWKCCKEG	HQMKDCIE..
CRF06_cpx	SNFKGPKRSI	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCTE..
CRF06_cpx	SNYKGPKRSI	KCFNCGREGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCTE..
CRF06_cpx	SNFKGP.RKI	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCTE..
CRF06_cpx	SNFKGQRKNI	KCFNCGKEGH	TARNCRAPRK	KGCWKCCKEG	HQMKDCTE..
CRF11_cpx	SNFKGQKR.I	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCTE..
CRF11_cpx	GNFKGQKR.I	KCFNCGKEGH	LARNCRAPRK	K.GCKCGKEG	HQMKDCTE..
D_CD_84ZR0	SNFKGTRKIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCTE..
D_CD_ELI_K	GNFKGPRKII	KCFNCGKEGH	IAKNCRAPRK	KGCWRCGREG	HQLKDCTE..
D_CD_NDK_M	GNFKGPRKSI	KCFNCGKEGH	TAKNCRAPRK	KGCWKCCKEG	HQMKDCTE..
D_UG_94UG1	GNFKGPKKII	KCFNCGKEGH	TAKNCRAPRK	KGCWKCCKEG	HQMKDCTE..
F1_BE_VI85	SNFKGQRRVV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
F1_BR_93BR	SNFKGQRRIV	KCFNCGKEGH	IAKNCRAPRK	KGCWKCCKEG	HQMKDCT..E
F1_FI_FIN9	SNFRGQRRIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
F1_FR_MP41	SNYKGPRRFI	KCFNCGKEGH	IAKNCRAPRK	KGCWKCCKEG	HQMKDCT..E
F2_CM_MP25	SNFKGQRRIV	KCFNCGKEGH	IARNCRAPRK	RGCWKCCKEG	HQMKDCT..E
F2KU_BE_VI	GNFKGPRRDV	KCFNCGKEGH	IAKNCRAPRK	KGCWKCCKEG	HQMKDCT..E
G_BE_DRCBL	SNFKGPRRTI	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKECTE..

G_NG_92NG0	SNFKGPRRII	KCFNCGKEGH	LARNCRAPRK	KGCWKCQKEG	HQMKECTE..
G_SE_SE616	SNFKGPRRTI	KCFNCGKEGH	LARNCRAPRK	KGCWKCQKEG	HQMKDCTE..
H_BE_VI991	GNFKGPRRTV	KCSNCGKEGH	IARNCRAPRK	KGCWKCQQEG	HQMKDCT..G
H_BE_VI997	SNFKGPRKIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCQREG	HQMKDCT..E
H_CF_90CF0	GNFKGQRKFV	KCFNCGKEGH	IARNCRAPRK	KGCWKCQREG	HQMKDCT..E
J_SE_SE702	GNFRDHKRIV	KCFNCGKQGH	IAKNCRAPRK	KGCWKCQKEG	HQMKDCT..E
J_SE_SE788	GNFRDHKRIV	KCFNCGKQGH	IAKNCRAPRK	KGCWKCQKEG	HQMKDCT..E
K_CD_EQTB1	GNFKGQRRII	KCFNCGKEGH	LARNCRAPRK	KGCWKCQKEG	HQMKDCS..E
K_CM_MP535	GNFKGHRKIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCQKEG	HQMKDCT..E
N_CM_YBF30	GNFKGIRKPI	KCFNCGKEGH	LARNCKAPRR	GGCWKCQQEG	HQMKDCKNEG
O_CM_ANT70	GQNPIRKGTI	KCFNCGKEGH	IARNCRAPRK	KGCWKCQQEG	HQMKDCRN..G
O_CM_MVP51	GQNPNRKGPI	KCFNCGKEGH	IAKNCRAPRK	RGCWKCQQEG	HQMKDCKN..G
O_SN_99SE_	GQNPSRKGP	KCFNCGKEGH	LARNCRAPRK	KGCWKCQQEG	HQMKDCKN..G
O_SN_99SE_	GQNPGRKGPI	KCFNCGKEGH	LARNCRAPRK	KGCWKCQQEG	HQMKDCRN..G
U_CD___83C	GNFKGPRRIV	KCFNCGKEGH	IAKNCRAPRK	KGCWKCQREG	HQMKDCT..E

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500

00BW0762_1	RQANFLGKIW	PSHKG.RPGN	FLQSR.....	.....PEP	TAPPAESFK.
00BW0768_2	RQANFLGKIW	PSHKG.RPGN	FLQNRPEP..	.....	TAPPAESFK.
00BW0874_2	RQANFLGKIW	PSHKG.RPGN	FLQNRPEPSA	PPAESLRPEP	SAPPAESLR.
00BW1471_2	RQANFLGKIW	PSQKG.RPGN	FLQNRPEP..	.....	SAPPAESFR.
00BW1616_2	RQANFLGKIW	PSHKG.RPGN	FLQSRPEPTA	PP....APVP	TAPPAESFR.
00BW1686_8	RQANFLGKIW	PSHKG.RPGN	FLQNRPEP..	.....	SAPPAESFK.
00BW1759_3	RQANFLGKIW	PSHKG.RPGN	FLQ.....	.....SRPEP	TAPPLESFK.
00BW1773_2	RQANFLGKIW	PSHKG.RPGN	FLQSRPE...	.....P	TAPPAESFR.
00BW1783_5	RQANFLGKIW	PSQKGGRPGN	FLQNRPA...	....ESRLEP	TAPPAESFR.
00BW1795_6	RQANFLGKIW	PSHKG.RPGN	FLQNRPE...	.....P	TAPPAESFR.
00BW1811_3	RQANFLGRIW	PSHKG.RPGN	FLQNRPEPTA	P.....LEP	TAPPAESFR.
00BW1859_5	RQANFLGKIW	PSHKG.RPGN	FLQNRPEP..	.....	TAPPAESFR.
00BW1880_2	RQANFLGKIW	PSHKG.RPGN	FLQSR.....	.....PEP	TAPPAESFK.
00BW1921_1	RQANFLGKIW	PSHKG.RPGN	FLQSRPEP..	.....	TAPPAESFR.
00BW2036_1	RQANFLGKIW	PSNKG.RPGN	FLQNRAPPV	.....EP	TAPPAESFR.
00BW2063_6	RQANFLGKIW	PSHKG.RPGN	FLQSRLE...	.....P	TAPPAESF..
00BW2087_2	RQANFLGKIW	PSHKGGRPGN	FLQSRPEPTA	P.....PAEP	TAPPAESFR.
00BW2127_2	RQANFLGKIW	PSHKG.RPGN	FLQNRPEPTA	P.....RPEP	SAPPAESFR.
00BW2128_3	RQANFLGRIW	PSNKG.RPGN	FLQNRPEPTA	PPAE.NRPEP	TAPPAESFR.
00BW2276_7	RQANFLGKLW	PSNKG.RPGN	FLQNRTEPTA	P.....LEP	TAPPADSFK.
00BW3819_3	RQANFLGKIW	PSHKG.RPGN	FLQNRPE...	P.....TAP	TAPPAESFR.
00BW3842_8	RQANFLGKIW	PSRGG.RPGN	FLQNRTEPTA	P.....PEP	TAPPAESFR.
00BW3871_3	RQANFLGKIW	PSHKG.RPGN	FLQNRPEP..	.....	TAPPAESFR.
00BW3876_9	RQANFLGKIW	PSHKG.RPGN	FLQNRPE...	.....P	TAPPAESFR.
00BW3886_8	RQANFLGKIW	PSHKG.RPGN	FLQNRPEPTA	P.....PAEP	TAPPAESFR.
00BW3891_6	RQANFLGRIW	PSHKG.RPGN	FLQSRPE...	.....P	TAPPAESFR.
00BW3970_2	RQANFLGRFW	PSQKG.RPGN	FLQ.....	.....SRSEP	TAPPAESFR.
00BW5031_1	RQANFLGKIW	PSNKG.RPGN	FLQSRPEPTA	P.....PMP	TAPPAESFR.
96BW01B21	RQANFLGKIW	PSHKG.RPGN	FLQNR.....	.....LEP	SAPPAESFR.
96BW0407	RQANFLGKIW	PSHKG.RPGN	FLQ.....	.....SRPEP	TAPPAESFR.
96BW0502	RQANFLGKIW	PSHKG.RPGN	FLQNRSEPA.	.....APTVP	TAPPAESFR.
96BW06_J4	RQANFLGKIW	PSHKGGRPGN	FLQSRPEP..	.....	TAPPAESFR.
96BW11_06	RQANFLGKIW	PSHKG.RPGN	FLQSRPE...	.....P	TAPPAESL..
96BW1210	GQANFLGKIW	PSHKG.RPGN	FLQSR.....	.....PEP	SAPPAESFR.
96BW15B03	RQANFLGKIW	PSHKG.RPGN	FLQNRTEP..	.....	TAPPAESFK.
96BW16_26	RQADFLGKIW	PSHKG.RPGN	FLQSRPE...	.....P	TAPPAESFR.
96BW17A09	RQANFLGKIW	PSHKGGRPGN	FLQNRPEP..	.....	TAPPAESFR.
96BWM01_5	RQANFLGKIW	PSHKG.RPGN	FLQSRPE...	.....P	TAPPAEIL..
96BWM03_2	RQANFLGKIW	PSHKG.RPGN	FLQSRPEP..	.....	TAPPAERFR.
98BWMC12_2	RQANFLGRLW	PSHKG.RPGN	FPQNR.....	.....VEP	TAPPAESLR.
98BWMC13_4	KQANFLGKIW	PSHKG.RPGN	FLQSRPE...	.....P	TAPPAESL..
98BWMC14_a	RQANFLGKIW	PSHKG.RPGN	FLQSRPEP..	.....	SAPPAESFR.
98BWM014_1	RQANFLGKIW	PSHKGGRPGN	FLQRRPEP..	.....	TAPPAESFR.

98BWM018_d	RQANFLGKIW	PSHKG.RPGN	FIQNRPAPT.	....APPVEP	TAPPAESFR.
98BWM036_a	RQANFLGRIW	PSHKG.RPGN	FLQSRPEPTA	P.....PAEP	TAPPAESFR.
98BWM037_d	RQANFLGKIW	PSHKG.RPGN	FLQ.....	.....KRPEP	TAPPAESFR.
99BW3932_1	RQVNFLGKIW	PSNKG.RPGN	FLQNRTPVPTA	PPAESFRIEP	TAPPAESFR.
99BW4642_4	RQANFLGKIW	PSHKG.RPGN	FFQNRTEP..	.....	TAPPAESFR.
99BW4745_8	RQANFLGKIW	PSNKG.RPGN	FLQNRPEPTA	P.....LEP	TAPPAESFR.
99BW4754_7	RQANFLGKIW	PSNKG.RPGN	FLQSR.....	.....PEP	TAPPAESFK.
99BWMC16_8	RQANFLGKIW	PSNKG.RPGN	FLQNRPEPT.	.....APLEP	TAPPAESFR.
A2_CD_97CD	RQANFLGKIW	PSNKG.RPGN	FPQSRTE...	.....P	TAPPME....
A2_CY_94CY	RQANFLGKIW	PSNKG.RPGN	FPQSRTE...	.....P	TAPPAENLR.
A2D_97KR	RQANFLGKIW	PSHSG.RPGN	FPQSRTE...	.....P	TAPPAEDFG.
A2G_CD_97C	.....	.....	.....	.....	.....
A_BY_97BL0	RQANFLGRIW	PSSKG.RPGN	FPQSRPE...	.....PS	APP.AENFR.
A_KE_Q23_A	RQANFLGKIW	PSRKG.RPGN	FPQNRLE...	.....PT	APP.AETCG.
A_SE_SE659	.....	.....	.....	.....	.....
A_SE_SE725	.....	.....	.....	.....	.....
A_SE_SE753	RQANFLGRIW	PSSKG.RPGN	FPQSRLE...	.....PT	APP.AEIFG.
A_SE_SE853	.....	.....	.....	.....	.....
A_SE_SE889	.....	.....	.....	.....	.....
A_SE_UGSE8	RQANFLGKIW	PSHKG.RPGN	FPQSRPE...	.....PS	APP...AEM.
A_UG_92UG0	RQANFLGKIW	PSSKG.RPGN	FPQSRPE...	.....PT	APPAAEIFG.
A_UG_U455	RQANFLGKIW	PSNKG.RPGN	FPQSRPE...	.....P	TAPPAEIFG.
AC_IN_2130	RQANFLGKIW	PSHKG.RPGN	FLQ.....	.....NRPEP	TAPPAESFR.
AC_RW_92RW	RQANFLGKIW	PSNKG.RPGN	FPQSRL....	.....EP	TAPPA.....
AC_SE_SE94	.....	.....	.....	.....	.....
ACD_SE_SE8	RQANFLGKIW	PSHKG.RPGN	FLQSRPE...	.....PT	APPA.ESFG.
ACG_BE_VI1	RQANFLGKIW	PSNKG.RPGN	FPQSRPEPTA	PP.....AEP	TAPPAESFG.
AD_SE_SE69	RQANFLGKIW	PSSKG.RPGN	FLQSRP....	.....EP	TAPPAESFG.
AD_SE_SE71	.....	.....	.....	.....	.....
ADHK_NO_97	RQANFLGKIW	PSSKG.RPGN	FPQSRPE...	.....PS	APPA.ESFG.
ADK_CD_MAL	RQANFLGKIW	PSHKG.RPGN	FLQSRPE...	.....PT	APPA.ESFG.
AG_BE_VI11	RQANFLGKIW	PSSKG.RPGN	FPQSRLE...	.....PT	APPA.ESLG.
AG_NG_92NG	RQANFLGKIW	PSNKG.RPGN	FLQNRPE...	.....P	TAPPAESFG.
AGHU_GA_VI	RQANFLGKIW	PSNKG.RPGN	FLQNRPE...	.....PT	APPA.ESFG.
AGU_CD_Z32	RQANFLGKIW	PSNKG.RPGN	FLQNRPE...	.....P	TAPPAESFE.
AJ_BW_BW21	RQANFLGKIW	PSNKG.RPGN	FLQSRPE...	.....PT	APPA.ESFG.
B_AU_VH_AF	RQANFLGKIW	PSHKG.RPGN	FLQSRPE...	.....P	TAPPEESFR.
B_CN_RL42_	RQANFLGKIW	PSHKG.RPGN	FLQSRPE...	.....P	TAPPEESFR.
B_DE_D31_U	RQANFLGKIW	PSYKG.RPGN	FLQRRPE...	.....P	TAPPEESFR.
B_DE_HAN_U	RQANFLGKIW	PSHKG.RPGN	FLQSRPE...	.....P	TAPPEESFR.
B_FR_HXB2_	RQANFLGKIW	PSYKG.RPGN	FLQSRPE...	.....P	TAPPEESFR.
B_GA_OYI_	RQANFLGKIW	PSHKG.RPGN	FLQNRPE...	.....P	TAPPAESFG.
B_GB_CAM1_	RQANFLGKIW	PSHKG.RPGN	FLQSRPE...	.....P	TAPPEESFR.
B_GB_GB8_A	RQANFLGKIW	PSHKG.RPGN	FLQSRPEPIA	PP.....EP	TAPPEESFR.
B_GB_MANC_	RQANFLGKIW	PSHKG.RPGN	FLQSRPE...	.....P	TAPPEESFR.
B_KR_WK_AF	RQANFLGKIW	PSHKG.RPGN	FLQSRPE...	.....P	SAPPEESFR.
B_NL_3202A	RQANFLGKIW	PSHKG.RPGN	FLQSRPE...	.....P	TAPPEESFR.
B_TW_TWCYS	RQANFLGKIW	PSHKE.RPGN	FLQSRPE...	.....P	TAPPEESFR.
B_US_BC_L0	RQANFLGKIW	PSHKG.RPGN	FPQSRLE...	.....P	TAPPEESFR.
B_US_DH123	RQANFLGKIW	PSHKE.RPGN	FLQSRPE...	.....P	SAPPEESFR.
B_US_JRCSF	RQANFLGKIW	PSYKG.RPGN	FLQSRPE...	.....P	TAPPEESFR.
B_US_MNCG_	RQANFLGKIW	PSCKG.R.RN	FPQSRTE...	.....P	TAPPEESFR.
B_US_P896_	RQANFLGKIW	PSHKG.RPGN	FLQSRPE...	.....P	TAPPEESFR.
B_US_RF_M1	RQANFLGKIW	PSHKG.RPGN	FLQSRPE...	.....P	TAPPEESFR.
B_US_SF2_K	RQANFLGKIW	PSYKG.RPGN	FLQSRPE...	.....P	TAPPEESFR.
B_US_WEAU1	RQANFLGKIW	SSQKG.RPGN	FPQSRLE...	.....P	TAPPEESFR.
B_US_WR27_	RQAXFLGXIR	PSHXG.RPGX	FLQNRPE...	.....P	SAPPAESFR.
B_US_YU2_M	RQANFLGKIW	PSHKG.RPGN	FLQSRPE...	.....P	TAPSEESVR.
BF1_BR_93B	RQANFLGKIW	PSHKG.RPGN	FLQSRPE...	.....P	TAPPAESFR.
C_BR_92BR0	RQANFLGKIW	PSHRG.RPGN	LLQNRTE...	.....EP	TAPPE.....

C_BW_96BW0	RQANFLGKIW	PSHKG.RPGN	FLQ.....	.....SRPEP	TAPPAESFR.
C_BW_96BW1	RRANFLGKIW	PSHKG.RPGN	FLQSRPE...	.....P	TAPPAESF..
C_BW_96BW1	GQANFLGKIW	PSHKG.RPGN	FLQSR.....	.....PEP	SAPPAESFR.
C_BW_96BW1	RQANFLGKIW	PSHKG.RPGN	FLQNRTEP..	.....	TAPPAESFK.
C_ET'ETH22	RQANFLGRLW	PSNKG.RPGN	FLQSRP....	.....EP	TAPPESLRPE
C_IN_93IN1	RQANFLGKIW	PSHKG.RPGN	FLQ.....	.....SRPEP	TAPPAESFR.
C_IN_93IN9	RQANFLGKIW	PSHKG.RPGN	FLQ.....	.....SRPEP	TAPPAESFR.
C_IN_93IN9	RQANFLGKIW	PSHKG.RPGN	FLQNRPEPTA	PP...ARPEP	TAPPAESFR.
C_IN_94IN1	RQANFLGKIW	PSHKG.RPGN	FLQ.....	.....SRPEP	TAPPAESFR.
C_IN_95IN2	RQANFLGKIW	PSHKG.RPGN	FLQ.....	.....SRPEP	TAPPAESFR.
CRF01_AE_C	RQANFLGKIW	PLNKG.RPGN	FPQSRLE...	.....PT	APPA.ESLG.
CRF01_AE_C	RQANFLGKIW	PSSKG.RPGN	FPQSRPE...	.....PT	APPM.ESLG.
CRF01_AE_C	RQANFLGRIW	PSSKG.RPGN	FPQSRPE...	.....PT	APPA.ESLG.
CRF01_AE_T	RQANFLGKFW	PSNKG.RPGN	FPQSRPE...	.....PT	APPA.ENWG.
CRF01_AE_T	RQANFLGKIW	PSNKG.RPGN	FPQSRPE...	.....PT	APP..AEWG.
CRF01_AE_T	RQANFLGKIW	PSNKG.RPGN	FPQSKPE...	.....PT	APPA.ENWG.
CRF01_AE_T	RQANFLGKIW	PSNKG.RPGN	FPQSRPE...	.....PT	APPA.ENWG.
CRF01_AE_T	RQANFLGKIW	PSNKG.RPGN	FPQSRPE...	.....PT	APPA.ENWG.
CRF01_AE_T	RQANFLGKIW	PSNKG.RPGN	FPQSRPE...	.....PT	APPA.ENWG.
CRF02_AG_F	GQANFLGKIW	PSSKG.RPGN	FPQSRPE...	.....PT	APPA.ESLG.
CRF02_AG_F	RQANFLGKIW	PSSKG.RPGN	FPQSRPE...	.....PT	APPA.ESFG.
CRF02_AG_G	RQANFLGKIW	PSNKG.RPGN	FPQSRPE...	P.....	SAPPAESFG.
CRF02_AG_N	RQANFLGKIW	PSSKG.RPGN	FPQSRPE...	.....PT	APPA.ESFG.
CRF02_AG_S	RQANFLGKIW	PSSKG.RPGN	FPQSRPE...	.....PT	APPA.ESLG.
CRF02_AG_S	RQANFLGKIW	PSSKG.RPGN	FPQSRPE...	.....PT	APPA.ESFG.
CRF03_AB_R	RQANFLGRIW	PSSKG.RPGN	FPQSRPE...	.....PS	APP.AENFG.
CRF03_AB_R	RQANFLGKIW	PSSKG.RPGN	FPQSRPE...	.....PS	APP.AENFG.
CRF04_cpx_	RQANFLGRMW	PSSKG.RPGN	FLQNRPE...	.....PT	APPA.ECLE.
CRF04_cpx_	RQANFLGRMW	PSSKG.RPGN	FLQSRPE...	.....PT	APPA.ESLE.
CRF04_cpx_	RQANSLGRMW	PSSKG.RPGN	FLQSRTE...	.....PT	APPA.ESFE.
CRF05_DF_B	RQANFLGKVV	PSHKG.RPGN	FLQSRP....	.....EP	SAPPAESFR.
CRF05_DF_B	GQANFLGRVW	LSHKG.RPGN	FLQSRP....	.....EP	SAPPAESFG.
CRF06_cpx_	RQANFLGKIW	PSNKG.RPGN	FLQNRPE...	.....P	TAPPIESFG.
CRF06_cpx_	RQANFLGKIW	PSNKG.RPGN	FLQNRPE...	.....P	TAPPAESFG.
CRF06_cpx_	RQANFLGRIW	PSSKG.RPGN	FLQNRPE...	.....P	TAPPAESFG.
CRF06_cpx_	RQANFLGKIW	PSHKG.RPGN	FLQNRPEQNR	P.....EP	SAPPAESFG.
CRF11_cpx_	RQANFLGKIW	PSSKG.RPGN	FLQSRPE...	.....PT	APPA.ESFG.
CRF11_cpx_	RQANFLGKIW	PSSKG.RPGN	FLQSRPE...	.....PT	APPA.ESFG.
D_CD_84ZR0	RQANFLGKIW	PSHKG.RPGN	FLQSRPE...	.....P	TAPPAE.FG.
D_CD_ELI_K	RQANFLGRIW	PSHKG.RPGN	FLQSRP....	.....EP	TAPPAESFG.
D_CD_NDK_M	RQANFLGKIW	PSHKG.RPGN	FLQSRP....	.....EP	TAPPAESFG.
D_UG_94UG1	RQANFLGKIW	PSHNG.RPGN	FLQSRPPA...	.....EP	TAPPAEIFG.
F1_BE_VI85	RQANFLGKIW	PSNKG.RPGN	FLQSRPE...	.....P	TAPPAESFG.
F1_BR_93BR	RQANFLGKIW	PSNKG.RPGN	FIQNRPE...	.....P	SAPPAESFR.
F1_FI_FIN9	RQANFLGKIW	PSNKG.RPGN	FLQSRPE...	.....P	TAPPAESLG.
F1_FR_MP41	RQANFLGKIW	PSNKG.RPGN	FLQNRPE...	.....P	TAPPAESFG.
F2_CM_MP25	RQANFLGKMW	PSNKG.RPGN	FLQNRPE...	.....P	TAPPAESFG.
F2KU_BE_VI	RQANFLGKIW	PSNKG.RPGN	FLQSRPE...	.....P	TAPPAESFG.
G_BE_DRCBL	RQANFLGKIW	PSNKG.RPGN	FLQNRPE...	.....P	TAPPAENFG.
G_NG_92NG0	RQANFLGKIW	PSNKG.RPGN	FLQNRTE...	.....P	TAPPAESFG.
G_SE_SE616	RQANFLGKIW	PSNKG.RPGN	FLQNRTE...	.....P	TAPPAESLG.
H_BE_VI991	RQANFLGKIW	PSSKG.RPGN	FPQKRLE...	.....P	TAPPAESFG.
H_BE_VI997	RQANFLGKIW	PSSKG.RPGN	FLQSRPE...	.....P	TAPPAESFG.
H_CF_90CF0	RQANFLGKIW	PSSKG.RPGN	FLQSRPE...	.....P	TAPPAESFG.
J_SE_SE702	RQANFLGKIW	PSSKG.RPGN	FLQSRPE...	.....P	TAPPAESLG.
J_SE_SE788	RQANFLGKIW	PSSKG.RPGN	FLQSRPE...	.....P	TAPPAESLG.
K_CD_EQTB1	RQANFLGKFW	PLNKE.RPGN	FLQNRPE...	.....P	TAPPAESFG.
K_CM_MP535	RQANFLGKIW	PSHKG.RPGN	FLQSRPE...	.....P	TAPPAESFG.
N_CM_YBF30	RQANFLGKSW	SPFKG.RPGN	FPQTTRK...	.....EP	TAPPLESYG.
O_CM_ANT70	RQANFLGKYW	PP.GGTRPGN	YVQRPAH...	.....P	SAPPMEEVKG

O_CM_MVP51	RQANFLGKYW	PP.GGTRPGN	YVQKQVS...	.....P	SAPPMEEAVK
O_SN_99SE_	RQANFLGKYW	PP.GGTRPGN	YAQRQVS...	.....P	SAPPMTEEMK
O_SN_99SE_	KQANFLGKYW	PP.GGTRPGN	YAQRQVS...	.....P	SAPPMTEEMK
U_CD___83C	RQANFLGKIW	PSNKG.RPGN	FLQNRPE...	.....P	TAPPAESFG.

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550

00BW0762_1	.....FE...	..ETNPTP..	...KQE....	PKDRE.....	PLTSLKSLFG
00BW0768_2	.....FE...	..ETTPAP..	...KQE....	LKDR.....E	PLTALKSLFG
00BW0874_2	.....FE...	..ETTPAL..	...KRE....	LKER.....E	PLISLKSLFG
00BW1471_2	.....FE...	..ETTPAP..	...KQE....	PKDR.....E	PLTSLKSLFG
00BW1616_2	.....F....	..GETTPSP..	...RQE....	AKDRE.....	PLISLKSLFG
00BW1686_8	.....FE...	..ETTPAP..	...KQE....	PKDR.....E	PLTSLKSLFG
00BW1759_3	.....FE...	..ETTPAP..	...KQE....	PKDRE.....	TLTSLRSLFG
00BW1773_2	.....FE...	..ETTPAP..	...KQE....	PKDRE.....	PLTSLKSLFG
00BW1783_5	.....FE...	..ETTPVQ..	...KQE....	TKDRE.....	PLTSLKSLFG
00BW1795_6	.....F....	..EETTPSP..	...KQE....	LKDKE.....	PLTSLKSLFG
00BW1811_3	.....FE...	..ETTPAS..	...KQE....	KKDRE.....	TLTSLRSLFG
00BW1859_5	.....FE...	..ETTPAP..	...KQE....	QKDR.....E	PLTSLKSLFG
00BW1880_2	.....FE...	..ETTPAP..	...KQE....	PKDRE.....	PLTSLKSLFG
00BW1921_1	.....FE...	..ETTPAP..	...KQE....	PKDR.....E	PLTSLKSLFG
00BW2036_1	.....FE...	..ETTPAP..	...KQE....	LKDR.....E	PLISLKSLFG
00BW2063_6	.....FE...	..EETTPAP..	...KQE....	MKDKE.....	PLISLKSLFG
00BW2087_2	.....FE...	..ETTPAS..	...KQD....	LKDRE.....	PLTSLKSLFG
00BW2127_2	.....FE...	..ETTHAP..	...KQE....	LKDRE.....	ALTSLKSLFG
00BW2128_3	.....FE...	..ETTPAP..	...KQE....	PKNRE.....	PLTSLKSLFG
00BW2276_7	.....FE...	..ETTPEL..	...KQG....	PKDR.....E	PLTSLKSLFG
00BW3819_3	.....FE...	..EITPAP..	...KQE....	TKDRE.....	PLTSLKSLFG
00BW3842_8	.....FE...	..ETTPAP..	...KQE....	PKDRGPY.RE	PLISLKSLFG
00BW3871_3	.....FE...	..ETTPVP..	...KQE....	PTDR.....E	PLTSLKSLFG
00BW3876_9	.....FE...	..ETTPTL..	...KQE....	LKDRE.....	PLTSLKSLFG
00BW3886_8	.....FE...	..ETTPVP..	...KQE....	QKDRE.....	ALTSLKSLFG
00BW3891_6	.....FE...	..EITPVP..	...KQE....	PKDR.....E	PLTSLKSLFG
00BW3970_2	.....FE...	..ETTPAP..	...KQE....	PKDRE.....	PLISLKSLFG
00BW5031_1	.....FG...	..ETTPAP..	...KQE....	MKERE.....	PLISLKSLFG
96BW01B21	.....FE...	..ETTPAP..	...KQE....	PKDRE.....	PLTSLRSLFG
96BW0407	.....FE...	..ETTPGQ..	...KQE....	SKDRE.....	TLTSLKSLFG
96BW0502	.....FE...	..ETTPAP..	...KQE....	PKDREPY.RE	PLTALRSLFG
96BW06_J4	.....FE...	..ETTPAL..	...KQE....	PKDK.....E	PLTSLKSPFG
96BW11_06	.....FE...	..EETTPAP..	...KQE....	TKDRE.....	PLISLKSLFG
96BW1210	.....FE...	..ETTPAQ..	...KQE....	PKDREP....	PLASLKSLFG
96BW15B03	.....FE...	..ETTPAP..	...KQE....	PKDR.....E	PLISLKSLFG
96BW16_26	.....FG...	..ETTPAP..	...KQE....	PKDRE.....	PLTSLRSLFG
96BW17A09	.....FE...	..ETTPAP..	...KQE....	PKDR.....E	PLTSFKSLFG
96BWM01_5	.....FE...	..EETTPAP..	...KQE....	MKDKEPY.KE	PLISLRSLFG
96BWM03_2	.....PE...	..PTAPPAE..	...RQE....	SKDR.....E	PLISLKSLFG
98BWMC12_2	.....LE...	..ETTPAS..	...KQE....	MKDR.....E	PLISLKSLFG
98BWMC13_4	.....FE...	..EETTPAP..	...KQE....	PKDKE.....	PLISLKSLFG
98BWMC14_a	.....FE...	..ETTPAP..	...KQE....	QKDR.....E	PLTSLKSLFG
98BWM014_1	.....FESRP	EPTAPPAES.	...FRQE....	PKDR.....E	PLTALKSLFG
98BWM018_d	.....FE...	..ETTPAL..	...KQE....	PKDREA....	PLTSLKSLFG
98BWM036_a	.....FE...	..ETNLAP..	...KQE....	PKDRE.....	PLTSLKSLFG
98BWM037_d	.....FE...	..ETTPAP..	...RQE....	AKDKE.....	PLNSLKSLFG
99BW3932_1	.....FE...	..ETTPAP..	...KQE....	LKDRE.....	ALTSLKSLFG
99BW4642_4	.....FE...	..ETTPAP..	...KQE....	PKDR.....E	PLTSLKSLFG
99BW4745_8	.....FE...	..GATPTP..	...KQE....	PRDR.....E	PLTSLKSLFG
99BW4754_7	.....FE...	..ETTPAQ..	...KQE....	SKDRE.....	PLTSLKSLFG
99BWMC16_8	.....FE...	..ETNPAP..	...KQE....	LKNRE.....	TLTSLRSLFG
A2_CD_97CD	.....FE...	..EEITSSL..	...KQE....	NREPS.....T	PAISLKSLFG
A2_CY_94CY	.....FE...	..MGEEITSSL..	...KQEL...E	TREPY.....N	PAISLKSLFG
A2D___97KR	.....FE...	..MGEEITPLQ..	...KQEL...K	NREQH.....T	PAISLKSLFG



A2G_CD_97C	.....	.....	.....	.....	.....
A_BY_97BL0	.....	MGEET.....	PSLK.Q...E	QKDRE..QYP	PSISLKSLFG
A_KE_Q23_A	.....	MGEETV.....	SPLK.Q...E	QKDRE..QAQ	PLVSLKSLFG
A_SE_SE659	.....	.....	.....	.....	.....
A_SE_SE725	.....	.....	.....	.....	.....
A_SE_SE753	.....	MREEIA.....	SPPK.Q...E	Q..KG..QDP	PLVSLKSLFG
A_SE_SE853	.....	.....	.....	.....	.....
A_SE_SE889	.....	.....	.....	.....	.....
A_SE_UGSE8	.....	MGEETIA.....	SPPK.Q...E	Q.....NNP	PSVSLKSLFG
A_UG_92UG0	.....	MREEIV.....	SPPK.Q...E	QNDRD..QNP	PSVSLKSLFG
A_UG_U455_	.....	.MGEKMTSPA	..KQEL...K	DREQ.....T	PLVSLKSLFG
AC_IN_2130	.....	FE... ..ETTPAL..	..KQE....	QKDRE.....	PLTSLKSLFG
AC_RW_92RW	.....	ENFG MGEETIASPL.	..K.QE....	QKDRE.....	PLISLKSLFG
AC_SE_SE94	.....	.....	.....	.....	.....
ACD_SE_SE8	.....	FGEEITP...	S.QK.Q...E	QKDKE...LY	PLASLKSLFG
ACG_BE_VI1	.....	KEDAIDSS..	..PKQE....	PRDKG..LYP	PLTSLKSLFG
AD_SE_SE69	.....	FGEEIAP...	..SQKQE...Q	KDK....ELY	PLASLKSLFG
AD_SE_SE71	.....	.....	.....	.....	.....
ADHK_NO_97	.....	IGEEIT.....	SYQK.Q...E	QKDRE..PPP	PLVSLKSLFG
ADK_CD_MAL	.....	FGEEIK.....	PSQK.Q...E	QKDKE..L.Y	PLASLKSLFG
AG_BE_VI11	.....	MEEEEIT.....	PSQK.Q...E	PRDTG..LYP	PLTSLKSLFG
AG_NG_92NG	.....	FGEEIAP...	S.LK.Q...E	PREKE..SPP	L.TSLKSLFG
AGHU_CA_VI	.....	FGEEIA.....	PSPR.P...E	PREKE..R.Y	PLTSLKSLFG
AGU_CD_Z32	.....	TKEEITS...	S.PK.Q...E	PRDKG..LYP	PLASLKSLFG
AJ_BW_BW21	.....	FGEETA.....	PSPK.Q...E	GKDKE..L.Y	PLTSLKSLFG
B_AU_VH_AF	.....	FGEETTTTP..	..SQKQE....	PIDK...ELY	PLASLRSLFG
B_CN_RL42_	.....	FGEETTTTP..	..SQKQE....	PIDK...ELY	PLASLKSLFG
B_DE_D31_U	.....	FGEETATP...	..FQKQE....	PIDK...ELY	PLASLRSLFG
B_DE_HAN_U	.....	FGEATAP...	..SQKQE....	PIDK...ELY	PLASLKSLFG
B_FR_HXB2_	.....	SGVETTTTP..	..PQKQE....	PIDK...ELY	PLTSLRSLFG
B_GA_OYI_	.....	FGEETTTTP..	..PQKQE....	PIDK...GLY	PLTSLRSLFG
B_GB_CAM1_	.....	FGEEKTTTP..	..SQKQE....	PIDK...ELY	PLASLRSLFG
B_GB_GB8_A	.....	FGGETTTTP..	..SQKQE....	PINK...EPY	PLASLRSLFG
B_GB_MANC_	.....	FGEEETTTTP..	..AQKQE....	PIDK...ELY	PLASLRPLFG
B_KR_WK_AF	.....	FGEETTTTP..	..SQKQE....	PIDK...ELY	PLASLRSLFG
B_NL_3202A	.....	FGEETTTTP..	..SQKQE....	PRDK...ELY	PLASLRSLFG
B_TW_TWCYS	.....	FGEQTTTP...	..SQKQE....	PIDK...DLY	PLASLESLFG
B_US_BC_L0	.....	FGEETTTTP..	..PQKQERE..	..DK...EMY	PLASLRSLFG
B_US_DH123	.....	FGEETATP...	..SQKQE....	..PK...ELY	PLASLKSLFG
B_US_JRCSF	.....	FGEETATP...	..SQKQEQQQE	PIDK...ELY	PLTSLRSLFG
B_US_MNCG_	.....	FGEETTTTP..	..YQKQEKQKE	TIDK...DLY	PLASLKSLFG
B_US_P896_	.....	FGEETTTTP..	..SQKQE....	PIDK...ELY	PLASLRSLFG
B_US_RF_M1	.....	FGEEETP...	..SQKQE....	KIDK...ELY	PLASLKSLFG
B_US_SF2_K	.....	FGEEKTTTP..	..SQKQE....	PIDK...ELY	PLTSLRSLFG
B_US_WEAU1	.....	FREETTTTP..	..SQKQE....	PIDK...ELY	PLTSLKSLFG
B_US_WR27_	.....	FGXETTTTP..	..SQKQE....	PIDK...ELY	PLASLRSLFV
B_US_YU2_M	.....	FGEETTTTP..	..SQKQE....	PIDK...ELY	PLASLRSLFG
BF1_BR_93B	.....	FGEEVTTTP..	..SQKQE....	PIDK...EMY	PLASLRSLFG
C_BR_92BR0	.....	ESFR FGEETTTTPS.	..RKQE....	TIDKEL....	PLTSLKSLFG
C_BW_96BW0	.....	FE... ..ETTPVP..	..KQE....	PKDRE.....	PLTSLKSLFG
C_BW_96BW1	.....	..EETTPAP...	..KQE....	TKDRE.....	PLISLKSLFG
C_BW_96BW1	.....	FE... ..ETTPAQ..	..KQE....	PKDREP....	PLASLKSLFG
C_BW_96BW1	.....	FE... ..ETTPAP...	..KQE....	PKDR.....E	PLISLKSLFG
C_ET_ETH22	PTAPPPESFR	FEEATPSPK.	..Q..E....	LKDRE.....	ALTSLKSLFG
C_IN_93IN1	.....	FE... ..ETTPAP...	..KQE....	PKDRE.....	PLTSLKSLFG
C_IN_93IN9	.....	FE... ..ETPPAP...	..KQE....	PKDRE.....	PLTSLRSLFG
C_IN_93IN9	.....	FE... ..ETTPAL...	..KQE....	PKDRE.....	PLTSLKSLFG
C_IN_94IN1	.....	FE... ..ETPPAP...	..KQE....	PKERE.....	PLTSLRSLFG
C_IN_95IN2	.....	FE... ..ETTPAP...	..KQE....	PKDRE.....	PLTSLRSLFG
CRF01_AE_C	.....	MGEET.....	SFPK.Q...E	QKDKE..HPS	PLVSLKSLFG

CRF01_AE_C	.....	MGEEIT....	SFPK.Q...E	QKDKK..QPP	PLVSLKSLFG
CRF01_AE_C	.....	MGEEIT....	SFSR.Q...E	QKDRE..HPP	PLVSLKSLFG
CRF01_AE_T	.....	MGEETT....	.SLLKQ...E	QKDKE..HHP	PLVSLKSLFG
CRF01_AE_T	.....	MGEEIT....	SLPK.Q...E	QKDKD..PPP	.LVSLKSLFG
CRF01_AE_T	.....	MGEE.....	.....	QKDKE..HPP	PSVSLKSLFG
CRF01_AE_T	.....	MGEETT....	SSLK.Q...E	QKDKE..PPP	PLISLKSLFG
CRF01_AE_T	.....	MGEEITGEEI	TSLPKQ...E	QKDKE..HPP	PLVSLKSLFG
CRF01_AE_T	.....	MGEEIT....	SFLK.Q...E	QKDKE..HPP	PSVSLKSLFG
CRF02_AG_F	.....	MGEEIT....	SPPK.Q...E	ARDQG..LYP	PLASLKSLFG
CRF02_AG_F	.....	MGEEIT....	SPPK.Q...E	PRDQG..LYP	PLASLKSLFG
CRF02_AG_G	.....	TREEITSS..	.PQQE....	PRDKG..LYP	PLTSLKSLFG
CRF02_AG_N	.....	MGEEIP....	PSPQ.Q...E	PRDKG..LYP	PLTSLKSLFG
CRF02_AG_S	.....	IGEEIT....	SSQK.Q...E	PGDKG..LYP	PLASLKSLFG
CRF02_AG_S	.....	MGEEIT....	SSPK.Q...E	PGDKG..LYP	PLTSLKSLFG
CRF03_AB_R	.....	MGEEIT....	PSLK.Q...E	QKDRE..QHP	PSISLKSLFG
CRF03_AB_R	.....	MGEEIT....	PSLK.Q...E	QKDRG..QHP	PSISLKSLFG
CRF04_cpx_	.....	RKEETTS...S	.LK.Q...E	PRDKE..LYP	.LTSLKSLFG
CRF04_cpx_	.....	MKEETTS...S	.PK.Q...E	PRDKE..LYP	.LTSLKSLFG
CRF04_cpx_	.....	MKEETTS...S	.PK.Q...E	QRDKE..LYP	.ITSLKSLFG
CRF05_DF_B	.....	FGEEIAS...S	.SPKQE...Q	KDEG...LYP	PLASLKSLFG
CRF05_DF_B	.....	FGEEITP...S	.SPKQE...Q	KDEG...KYP	PLASLKSLFG
CRF06_cpx_	.....	FGEEIAP...S	.PK.Q...E	SKEKEEKGLY	PLASLKSLFG
CRF06_cpx_	.....	FGEEIAP...S	.PE.Q...K	PKEKE...LY	PLTSLRSLFG
CRF06_cpx_	.....	FGEEIAP...S	.LK.Q...E	PKEKEKE.LY	PLASLKSLFG
CRF06_cpx_	.....	FGEEIAP...S	.PK.Q...E	PKEKE...LY	PLASLKSLFG
CRF11_cpx_	.....	FGEEIAP...S	.PK.Q...E	PKEKEK.ELY	PLTSLKSLFG
CRF11_cpx_	.....	FGEEITP...S	.PK.Q...E	PKEK...ELY	PITSLKSLFG
D_CD_84ZR0	.....	FGEEITP...S	.SQKQEQK..	DKDK...ELY	PLASLKSLFG
D_CD_ELI_K	.....	FGEEITP...S	.SQKQE...Q	KDK...ELY	PLTSLKSLFG
D_CD_NDK_M	.....	FGEEITP...S	.SQKQE...Q	KDK...ELY	PLASLKSLFG
D_UG_94UG1	.....	LGEEITP...S	.PQKQE...Q	KDK...ELY	PLTSLKSLFG
F1_BE_VI85	.....FG...	.EETPSP...S	...KQE....	QKDGE...YP	PLASLKSLFG
F1_BR_93BR	.....FG...	.EETPSP...S	...KQE....	QKDEGL...YP	PLASLKSLFG
F1_FI_FIN9	.....IR...	.EEVTPSP...S	...RQE....	QKEEGQ...YP	PLASLKSLFG
F1_FR_MP41	.....FK...	.EETPSP...S	...KQE....	QKDEGQGLYP	PLASLKSLFG
F2_CM_MP25	.....FG...	.EEIAPSP...S	...KQE....	QKDKEQ...VP	PLISLKSLFG
F2KU_BE_VI	.....FG...	.EEINPSP...S	...RQE....	TKDKGQ...EP	PLTSLKSLFG
G_BE_DRCBL	.....	FGEEIAP...S	.PK.Q...E	QKEKE...LYP	L.SSLKSLFG
G_NG_92NG0	.....	FGEEIAP...S	.PK.Q...E	PKEKE...LYP	L.TSLKSLFG
G_SE_SE616	.....	FGEEIAP...S	.PK.Q...E	MKEKE...LYP	...SLKSLFG
H_BE_VI991	.....FG...	.EETPSP...S	...RQE....	LKEQE....P	PLTSLRSLFG
H_BE_VI997	.....FG...	.EEMTSP...S	...KQE....	LKDKE....P	PFASLKSLFG
H_CF_90CF0	.....FG...	.EEMTSP...S	...KQE...S	LKDKE....P	PLASLRSLFG
J_SE_SE702	.....FG...	.EEIPSP...S	...KQE....	PKDKE...LY	PLTSLRSLFG
J_SE_SE788	.....LG...	.EEIPSP...S	...KQE....	PKDKE...LY	PLTSLKSLFG
K_CD_EQTB1	.....FG...	.EKITPSL...S	...RQE....	MKDQEQ...GP	PLTSLKSLFG
K_CM_MP535	.....FG...	.EETPSP...S	...RQE....	TKDKEQ...SP	PLTSLKSLFG
N_CM_YBF30	.....FQ...	.EEKSTQ...S	GKEMQE...N	QERTENSLYP	PLTSLRSLFG
O_CM_ANT70	.....	.GQENQEQ...S	...KGG....	PNE....LY	PFASLKSLFG
O_CM_MVP51	.....	.EQENQSQ...S	...KGD....	QEE....LY	PFASLKSLFG
O_SN_99SE_	.....	.GQENQEQ...S	...KED....	QNE....LY	PFASLRSLFG
O_SN_99SE_	.....	.GQENQEQ...S	...KGD....	QNE....LY	PFASLKSLFG
U_CD_83C	.....FG...	.EETPSP...S	...KQE....	PRDKESL.YP	PLTSLKSLFG

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00BW0762_1	SDPLSQ
00BW0768_2	SDPLSQ
00BW0874_2	NDPLSQ
00BW1471_2	SDPLSQ
00BW1616_2	SDPLSQ

00BW1686_8	SDPLSQ
00BW1759_3	SDPLSQ
00BW1773_2	SDPLSQ
00BW1783_5	SDPLSQ
00BW1795_6	SDPLSQ
00BW1811_3	SDPLSQ
00BW1859_5	SDPLSQ
00BW1880_2	NDPLSQ
00BW1921_1	SDPLSQ
00BW2036_1	SDPLSQ
00BW2063_6	NDPLSQ
00BW2087_2	SDPLSQ
00BW2127_2	SDPLSQ
00BW2128_3	SDPWSQ
00BW2276_7	SDPLSQ
00BW3819_3	SDPLSQ
00BW3842_8	SDPLSQ
00BW3871_3	SDPLSQ
00BW3876_9	SDPLSQ
00BW3886_8	SDPLSQ
00BW3891_6	SDPLSQ
00BW3970_2	SDPLSQ
00BW5031_1	SDPLSQ
96BW01B21	SDPLSQ
96BW0407	NDPLSQ
96BW0502	SGPLSQ
96BW06_J4	SDPLSQ
96BW11_06	SDPLSQ
96BW1210	NDPLSQ
96BW15B03	SDPLSQ
96BW16_26	NDPLSQ
96BW17A09	SDPLSQ
96BWMO1_5	SDPLSQ
96BWMO3_2	SDPLSQ
98BWMC12_2	NDPLSQ
98BWMC13_4	SDPLSQ
98BWMC14_a	NDPLSQ
98BWMO14_1	SDPLSQ
98BWMO18_d	SDPLSQ
98BWMO36_a	SDPLSQ
98BWMO37_d	SDPLSQ
99BW3932_1	SDPLSQ
99BW4642_4	SDPLSQ
99BW4745_8	SDPLSQ
99BW4754_7	NDPLSQ
99BWMC16_8	GDPLSQ
A2_CD_97CD	NDLLSQ
A2_CY_94CY	NDPLLQ
A2D___97KR	NDPLLQ
A2G_CD_97C	.....
A_BY_97BL0	NDPLSQ
A_KE_Q23_A	NDLLSQ
A_SE_SE659	.....
A_SE_SE725	.....
A_SE_SE753	NDLLSQ
A_SE_SE853	.....
A_SE_SE889	.....
A_SE_UGSE8	NDLLSQ
A_UG_92UG0	NDLLSQ
A_UG_U455_	NDPLSQ

AC_IN_2130	SDPLSQ
AC_RW_92RW	NDPLSQ
AC_SE_SE94	.....
ACD_SE_SE8	NDP...
ACG_BE_VI1	NDP...
AD_SE_SE69	NDP...
AD_SE_SE71	.....
ADHK_NO_97	NDPLSQ
ADK_CD_MAL	NDQLSQ
AG_BE_VI11	NDP...
AG_NG_92NG	NDP...
AGHU_GA_VI	SDP...
AGU_CD_Z32	SDP...
AJ_BW_BW21	SDP...
B_AU_VH_AF	NDPSSQ
B_CN_RL42	NDPSSQ
B_DE_D31_U	NDPSSQ
B_DE_HAN_U	SDPSSQ
B_FR_HXB2	NDPSSQ
B_GA_OYI	NDPSSQ
B_GB_CAM1	NDPSSQ
B_GB_GB8_A	NDPSSQ
B_GB_MANC	NDPSSQ
B_KR_WK_AF	NDPSSQ
B_NL_3202A	NDPSSQ
B_TW_TWCYS	NDPSSQ
B_US_BC_L0	NDPSSQ
B_US_DH123	NDP...
B_US_JRCSE	NDPSSQ
B_US_MNCG	NDPLSQ
B_US_P896	NDPSSQ
B_US_RF_M1	NDPSSQ
B_US_SF2_K	NDPSSQ
B_US_WEAU1	NDPSSQ
B_US_WR27	NDPSSQ
B_US_YU2_M	SDPSSQ
BF1_BR_93B	NDPSSQ
C_BR_92BR0	SDPLST
C_BW_96BW0	SDPLSQ
C_BW_96BW1	SDPLSQ
C_BW_96BW1	NDPLSQ
C_BW_96BW1	SDPLSQ
C_ET_ETH22	NDHLLQ
C_IN_93IN1	SDLLSQ
C_IN_93IN9	SDPLSQ
C_IN_93IN9	SDPLSQ
C_IN_94IN1	SDPLSQ
C_IN_95IN2	SDPLSQ
CRF01_AE_C	NDPLSQ
CRF01_AE_C	NDPLSQ
CRF01_AE_C	NDPLSQ
CRF01_AE_T	NDPSSQ
CRF01_AE_T	NDPLSQ
CRF01_AE_T	NDPLSQ
CRF01_AE_T	NDPLSQ
CRF01_AE_T	NDPLSQ
CRF01_AE_T	NDPLSQ
CRF02_AG_F	NDP...
CRF02_AG_F	NDP...
CRF02_AG_G	NDP...

CRF02_AG_N	NDP...
CRF02_AG_S	NDP...
CRF02_AG_S	NDPYSQ
CRF03_AB_R	DDPLSQ
CRF03_AB_R	NDPLSQ
CRF04_cpx_	SDPLSQ
CRF04_cpx_	NHPLSQ
CRF04_cpx_	SDPLSR
CRF05_DF_B	NDPLSQ
CRF05_DF_B	NDPLSQ
CRF06_cpx_	SDP...
CRF06_cpx_	NDP...
CRF06_cpx_	NDP...
CRF06_cpx_	SDP...
CRF11_cpx_	SDP...
CRF11_cpx_	SDPLSQ
D_CD_84ZR0	NDPLSQ
D_CD_ELI_K	NDPLSQ
D_CD_NDK_M	NDPSSQ
D_UG_94UG1	NDPLSQ
F1_BE_VI85	NDP...
F1_BR_93BR	NDP...
F1_FI_FIN9	NDP...
F1_FR_MP41	SDP...
F2_CM_MP25	SDQ...
F2KU_BE_VI	SDPLLQ
G_BE_DRCBL	NDQ...
G_NG_92NG0	SDP...
G_SE_SE616	SDP...
H_BE_VI991	NDQ...
H_BE_VI997	NDPLSQ
H_CF_90CF0	SDPLLQ
J_SE_SE702	SDPLSQ
J_SE_SE788	SDPLSQ
K_CD_EQTB1	SDPLSQ
K_CM_MP535	NDPLSQ
N_CM_YBF30	NDPSSQ
O_CM_ANT70	TDQ...
O_CM_MVP51	TDQ...
O_SN_99SE_	TDQ...
O_SN_99SE_	TDQ...
U_CD___83C	SDPSLQ

Table 12. HIV Env Sequence Alignment  
GCG Multiple Sequence File.  
Written by Omiga 1.1

Name: 00BW0762_1	<u>SEQ ID NO: 469</u>	Len: 962	Check: 4645	Weight: 1.00
Name: 00BW0768_2	<u>SEQ ID NO: 470</u>	Len: 962	Check: 9565	Weight: 1.00
Name: 00BW0874_2	<u>SEQ ID NO: 471</u>	Len: 962	Check: 7745	Weight: 1.00
Name: 00BW1471_2	<u>SEQ ID NO: 472</u>	Len: 962	Check: 9593	Weight: 1.00
Name: 00BW1616_2	<u>SEQ ID NO: 473</u>	Len: 962	Check: 792	Weight: 1.00
Name: 00BW1686_8	<u>SEQ ID NO: 474</u>	Len: 962	Check: 3744	Weight: 1.00
Name: 00BW1759_3	<u>SEQ ID NO: 475</u>	Len: 962	Check: 9808	Weight: 1.00
Name: 00BW1773_2	<u>SEQ ID NO: 476</u>	Len: 962	Check: 3500	Weight: 1.00
Name: 00BW1783_5	<u>SEQ ID NO: 477</u>	Len: 962	Check: 9684	Weight: 1.00
Name: 00BW1795_6	<u>SEQ ID NO: 478</u>	Len: 962	Check: 8410	Weight: 1.00
Name: 00BW1811_3	<u>SEQ ID NO: 479</u>	Len: 962	Check: 2068	Weight: 1.00
Name: 00BW1859_5	<u>SEQ ID NO: 480</u>	Len: 962	Check: 5692	Weight: 1.00
Name: 00BW1880_2	<u>SEQ ID NO: 481</u>	Len: 962	Check: 1901	Weight: 1.00
Name: 00BW1921_1	<u>SEQ ID NO: 482</u>	Len: 962	Check: 5923	Weight: 1.00
Name: 00BW2036_1	<u>SEQ ID NO: 483</u>	Len: 962	Check: 7035	Weight: 1.00
Name: 00BW2063_6	<u>SEQ ID NO: 484</u>	Len: 962	Check: 4853	Weight: 1.00
Name: 00BW2087_2	<u>SEQ ID NO: 485</u>	Len: 962	Check: 2085	Weight: 1.00
Name: 00BW2127_2	<u>SEQ ID NO: 486</u>	Len: 962	Check: 4015	Weight: 1.00
Name: 00BW2128_3	<u>SEQ ID NO: 487</u>	Len: 962	Check: 5884	Weight: 1.00
Name: 00BW2276_7	<u>SEQ ID NO: 488</u>	Len: 962	Check: 8913	Weight: 1.00
Name: 00BW3819_3	<u>SEQ ID NO: 489</u>	Len: 962	Check: 9390	Weight: 1.00
Name: 00BW3842_8	<u>SEQ ID NO: 490</u>	Len: 962	Check: 8867	Weight: 1.00
Name: 00BW3871_3	<u>SEQ ID NO: 491</u>	Len: 962	Check: 7069	Weight: 1.00
Name: 00BW3876_9	<u>SEQ ID NO: 492</u>	Len: 962	Check: 4761	Weight: 1.00
Name: 00BW3886_8	<u>SEQ ID NO: 493</u>	Len: 962	Check: 7681	Weight: 1.00
Name: 00BW3891_6	<u>SEQ ID NO: 494</u>	Len: 962	Check: 379	Weight: 1.00
Name: 00BW3970_2	<u>SEQ ID NO: 495</u>	Len: 962	Check: 8001	Weight: 1.00
Name: 00BW5031_1	<u>SEQ ID NO: 496</u>	Len: 962	Check: 4902	Weight: 1.00
Name: 96BW01B21	<u>SEQ ID NO: 497</u>	Len: 962	Check: 5774	Weight: 1.00
Name: 96BW0407	<u>SEQ ID NO: 498</u>	Len: 962	Check: 4260	Weight: 1.00
Name: 96BW0502	<u>SEQ ID NO: 499</u>	Len: 962	Check: 4658	Weight: 1.00
Name: 96BW06_J4	<u>SEQ ID NO: 500</u>	Len: 962	Check: 9749	Weight: 1.00
Name: 96BW11_06	<u>SEQ ID NO: 501</u>	Len: 962	Check: 4328	Weight: 1.00
Name: 96BW1210	<u>SEQ ID NO: 502</u>	Len: 962	Check: 3855	Weight: 1.00
Name: 96BW15B03	<u>SEQ ID NO: 503</u>	Len: 962	Check: 9133	Weight: 1.00
Name: 96BW16_26	<u>SEQ ID NO: 504</u>	Len: 962	Check: 5	Weight: 1.00
Name: 96BW17A09	<u>SEQ ID NO: 505</u>	Len: 962	Check: 6458	Weight: 1.00
Name: 96BWMO1_5	<u>SEQ ID NO: 506</u>	Len: 962	Check: 9487	Weight: 1.00
Name: 96BWMO3_2	<u>SEQ ID NO: 507</u>	Len: 962	Check: 8766	Weight: 1.00
Name: 98BWMC12_2	<u>SEQ ID NO: 508</u>	Len: 962	Check: 2722	Weight: 1.00
Name: 98BWMC13_4	<u>SEQ ID NO: 509</u>	Len: 962	Check: 2526	Weight: 1.00
Name: 98BWMC14_a	<u>SEQ ID NO: 510</u>	Len: 962	Check: 7761	Weight: 1.00
Name: 98BWMO14_1	<u>SEQ ID NO: 511</u>	Len: 962	Check: 93	Weight: 1.00
Name: 98BWMO18_d	<u>SEQ ID NO: 512</u>	Len: 962	Check: 279	Weight: 1.00
Name: 98BWMO36_a	<u>SEQ ID NO: 513</u>	Len: 962	Check: 134	Weight: 1.00
Name: 98BWMO37_d	<u>SEQ ID NO: 514</u>	Len: 962	Check: 9669	Weight: 1.00
Name: 99BW3932_1	<u>SEQ ID NO: 515</u>	Len: 962	Check: 3527	Weight: 1.00
Name: 99BW4642_4	<u>SEQ ID NO: 516</u>	Len: 962	Check: 1175	Weight: 1.00
Name: 99BW4745_8	<u>SEQ ID NO: 517</u>	Len: 962	Check: 8117	Weight: 1.00
Name: 99BW4754_7	<u>SEQ ID NO: 518</u>	Len: 962	Check: 5709	Weight: 1.00
Name: 99BWMC16_8	<u>SEQ ID NO: 519</u>	Len: 962	Check: 285	Weight: 1.00
Name: A2_CD_97CD	<u>SEQ ID NO: 520</u>	Len: 962	Check: 2892	Weight: 1.00
Name: A2_CY_94CY	<u>SEQ ID NO: 521</u>	Len: 962	Check: 8628	Weight: 1.00
Name: A2D_97KR	<u>SEQ ID NO: 522</u>	Len: 962	Check: 471	Weight: 1.00
Name: A2G_CD_97C	<u>SEQ ID NO: 523</u>	Len: 962	Check: 939	Weight: 1.00
Name: A_BY_97BL0	<u>SEQ ID NO: 524</u>	Len: 962	Check: 4291	Weight: 1.00

Name: A_KE_Q23_A	<u>SEQ ID NO: 525</u>	Len: 962	Check: 1190	Weight: 1.00
Name: A_SE_SE659	<u>SEQ ID NO: 526</u>	Len: 962	Check: 6674	Weight: 1.00
Name: A_SE_SE725	<u>SEQ ID NO: 527</u>	Len: 962	Check: 4925	Weight: 1.00
Name: A_SE_SE753	<u>SEQ ID NO: 528</u>	Len: 962	Check: 2482	Weight: 1.00
Name: A_SE_SE853	<u>SEQ ID NO: 529</u>	Len: 962	Check: 1860	Weight: 1.00
Name: A_SE_SE889	<u>SEQ ID NO: 530</u>	Len: 962	Check: 2102	Weight: 1.00
Name: A_SE_UGSE8	<u>SEQ ID NO: 531</u>	Len: 962	Check: 5063	Weight: 1.00
Name: A_UG_92UG0	<u>SEQ ID NO: 532</u>	Len: 962	Check: 6685	Weight: 1.00
Name: A_UG_U455	<u>SEQ ID NO: 533</u>	Len: 962	Check: 8657	Weight: 1.00
Name: AC_IN_2130	<u>SEQ ID NO: 534</u>	Len: 962	Check: 7784	Weight: 1.00
Name: AC_RW_92RW	<u>SEQ ID NO: 535</u>	Len: 962	Check: 4676	Weight: 1.00
Name: AC_SE_SE94	<u>SEQ ID NO: 536</u>	Len: 962	Check: 2949	Weight: 1.00
Name: ACD_SE_SE8	<u>SEQ ID NO: 537</u>	Len: 962	Check: 1464	Weight: 1.00
Name: ACG_BE_VI1	<u>SEQ ID NO: 538</u>	Len: 962	Check: 2980	Weight: 1.00
Name: AD_SE_SE69	<u>SEQ ID NO: 539</u>	Len: 962	Check: 8959	Weight: 1.00
Name: AD_SE_SE71	<u>SEQ ID NO: 540</u>	Len: 962	Check: 7056	Weight: 1.00
Name: ADHK_NO_97	<u>SEQ ID NO: 541</u>	Len: 962	Check: 487	Weight: 1.00
Name: ADK_CD_MAL	<u>SEQ ID NO: 542</u>	Len: 962	Check: 2555	Weight: 1.00
Name: AG_BE_VI11	<u>SEQ ID NO: 543</u>	Len: 962	Check: 6342	Weight: 1.00
Name: AG_NG_92NG	<u>SEQ ID NO: 544</u>	Len: 962	Check: 1272	Weight: 1.00
Name: AGHU_GA_VI	<u>SEQ ID NO: 545</u>	Len: 962	Check: 1974	Weight: 1.00
Name: AGU_CD_Z32	<u>SEQ ID NO: 546</u>	Len: 962	Check: 4356	Weight: 1.00
Name: AJ_BW_BW21	<u>SEQ ID NO: 547</u>	Len: 962	Check: 9995	Weight: 1.00
Name: B_AU_VH_AF	<u>SEQ ID NO: 548</u>	Len: 962	Check: 5833	Weight: 1.00
Name: B_CN_RL42	<u>SEQ ID NO: 549</u>	Len: 962	Check: 4092	Weight: 1.00
Name: B_DE_D31_U	<u>SEQ ID NO: 550</u>	Len: 962	Check: 5486	Weight: 1.00
Name: B_DE_HAN_U	<u>SEQ ID NO: 551</u>	Len: 962	Check: 3480	Weight: 1.00
Name: B_FR_HXB2	<u>SEQ ID NO: 552</u>	Len: 962	Check: 6939	Weight: 1.00
Name: B_GA_OYI	<u>SEQ ID NO: 553</u>	Len: 962	Check: 9780	Weight: 1.00
Name: B_GB_CAM1	<u>SEQ ID NO: 554</u>	Len: 962	Check: 9716	Weight: 1.00
Name: B_GB_GB8_C	<u>SEQ ID NO: 555</u>	Len: 962	Check: 4180	Weight: 1.00
Name: B_GB_MANC	<u>SEQ ID NO: 556</u>	Len: 962	Check: 9762	Weight: 1.00
Name: B_KR_WK_AF	<u>SEQ ID NO: 557</u>	Len: 962	Check: 6641	Weight: 1.00
Name: B_NL_3202A	<u>SEQ ID NO: 558</u>	Len: 962	Check: 7168	Weight: 1.00
Name: B_TW_TWCYS	<u>SEQ ID NO: 559</u>	Len: 962	Check: 3591	Weight: 1.00
Name: B_US_BC_L0	<u>SEQ ID NO: 560</u>	Len: 962	Check: 7266	Weight: 1.00
Name: B_US_DH123	<u>SEQ ID NO: 561</u>	Len: 962	Check: 6905	Weight: 1.00
Name: B_US_JRCFS	<u>SEQ ID NO: 562</u>	Len: 962	Check: 9381	Weight: 1.00
Name: B_US_MNCG	<u>SEQ ID NO: 563</u>	Len: 962	Check: 9951	Weight: 1.00
Name: B_US_P896	<u>SEQ ID NO: 564</u>	Len: 962	Check: 5855	Weight: 1.00
Name: B_US_RF_M1	<u>SEQ ID NO: 565</u>	Len: 962	Check: 6075	Weight: 1.00
Name: B_US_SF2_K	<u>SEQ ID NO: 566</u>	Len: 962	Check: 1434	Weight: 1.00
Name: B_US_WEAU1	<u>SEQ ID NO: 567</u>	Len: 962	Check: 5451	Weight: 1.00
Name: B_US_WR27	<u>SEQ ID NO: 568</u>	Len: 962	Check: 4262	Weight: 1.00
Name: B_US_YU2_M	<u>SEQ ID NO: 569</u>	Len: 962	Check: 5841	Weight: 1.00
Name: BF1_BR_93B	<u>SEQ ID NO: 570</u>	Len: 962	Check: 5506	Weight: 1.00
Name: C_BR_92BR0	<u>SEQ ID NO: 571</u>	Len: 962	Check: 8769	Weight: 1.00
Name: C_BW_96BW0	<u>SEQ ID NO: 572</u>	Len: 962	Check: 6197	Weight: 1.00
Name: C_BW_96BW1	<u>SEQ ID NO: 573</u>	Len: 962	Check: 8144	Weight: 1.00
Name: C_BW_96BW1	<u>SEQ ID NO: 574</u>	Len: 962	Check: 1160	Weight: 1.00
Name: C_BW_96BW1	<u>SEQ ID NO: 575</u>	Len: 962	Check: 2736	Weight: 1.00
Name: C_ET_ETH22	<u>SEQ ID NO: 576</u>	Len: 962	Check: 8219	Weight: 1.00
Name: C_IN_93IN1	<u>SEQ ID NO: 577</u>	Len: 962	Check: 4068	Weight: 1.00
Name: C_IN_93IN9	<u>SEQ ID NO: 578</u>	Len: 962	Check: 3674	Weight: 1.00
Name: C_IN_93IN9	<u>SEQ ID NO: 579</u>	Len: 962	Check: 1581	Weight: 1.00
Name: C_IN_94IN1	<u>SEQ ID NO: 580</u>	Len: 962	Check: 9352	Weight: 1.00
Name: C_IN_95IN2	<u>SEQ ID NO: 581</u>	Len: 962	Check: 6988	Weight: 1.00
Name: CRF01_AE_C	<u>SEQ ID NO: 582</u>	Len: 962	Check: 8684	Weight: 1.00
Name: CRF01_AE_C	<u>SEQ ID NO: 583</u>	Len: 962	Check: 3342	Weight: 1.00
Name: CRF01_AE_C	<u>SEQ ID NO: 584</u>	Len: 962	Check: 5017	Weight: 1.00

Name:	CRF01_AE_T	SEQ ID NO: 585	Len: 962	Check: 9124	Weight: 1.00
Name:	CRF01_AE_T	SEQ ID NO: 586	Len: 962	Check: 2718	Weight: 1.00
Name:	CRF01_AE_T	SEQ ID NO: 587	Len: 962	Check: 2104	Weight: 1.00
Name:	CRF01_AE_T	SEQ ID NO: 588	Len: 962	Check: 8495	Weight: 1.00
Name:	CRF01_AE_T	SEQ ID NO: 589	Len: 962	Check: 4076	Weight: 1.00
Name:	CRF01_AE_T	SEQ ID NO: 590	Len: 962	Check: 948	Weight: 1.00
Name:	CRF02_AG_F	SEQ ID NO: 591	Len: 962	Check: 9298	Weight: 1.00
Name:	CRF02_AG_F	SEQ ID NO: 592	Len: 962	Check: 9278	Weight: 1.00
Name:	CRF02_AG_G	SEQ ID NO: 593	Len: 962	Check: 4373	Weight: 1.00
Name:	CRF02_AG_N	SEQ ID NO: 594	Len: 962	Check: 8955	Weight: 1.00
Name:	CRF02_AG_S	SEQ ID NO: 595	Len: 962	Check: 252	Weight: 1.00
Name:	CRF02_AG_S	SEQ ID NO: 596	Len: 962	Check: 5147	Weight: 1.00
Name:	CRF03_AB_R	SEQ ID NO: 597	Len: 962	Check: 2239	Weight: 1.00
Name:	CRF03_AB_R	SEQ ID NO: 598	Len: 962	Check: 2671	Weight: 1.00
Name:	CRF04_cpx	SEQ ID NO: 599	Len: 962	Check: 4892	Weight: 1.00
Name:	CRF04_cpx	SEQ ID NO: 600	Len: 962	Check: 8070	Weight: 1.00
Name:	CRF04_cpx	SEQ ID NO: 601	Len: 962	Check: 5453	Weight: 1.00
Name:	CRF05_DF_B	SEQ ID NO: 602	Len: 962	Check: 174	Weight: 1.00
Name:	CRF05_DF_B	SEQ ID NO: 603	Len: 962	Check: 2694	Weight: 1.00
Name:	CRF06_cpx	SEQ ID NO: 604	Len: 962	Check: 7351	Weight: 1.00
Name:	CRF06_cpx	SEQ ID NO: 605	Len: 962	Check: 5073	Weight: 1.00
Name:	CRF06_cpx	SEQ ID NO: 606	Len: 962	Check: 661	Weight: 1.00
Name:	CRF06_cpx	SEQ ID NO: 607	Len: 962	Check: 8440	Weight: 1.00
Name:	CRF11_cpx	SEQ ID NO: 608	Len: 962	Check: 2217	Weight: 1.00
Name:	CRF11_cpx	SEQ ID NO: 609	Len: 962	Check: 8216	Weight: 1.00
Name:	D_CD_84ZR0	SEQ ID NO: 610	Len: 962	Check: 4843	Weight: 1.00
Name:	D_CD_ELI_K	SEQ ID NO: 611	Len: 962	Check: 8403	Weight: 1.00
Name:	D_CD_NDK_M	SEQ ID NO: 612	Len: 962	Check: 5813	Weight: 1.00
Name:	D_UG_94UG1	SEQ ID NO: 613	Len: 962	Check: 9407	Weight: 1.00
Name:	F1_BE_VI85	SEQ ID NO: 614	Len: 962	Check: 2982	Weight: 1.00
Name:	F1_BR_93BR	SEQ ID NO: 615	Len: 962	Check: 8919	Weight: 1.00
Name:	F1_FI_FIN9	SEQ ID NO: 616	Len: 962	Check: 6761	Weight: 1.00
Name:	F1_FR_MP41	SEQ ID NO: 617	Len: 962	Check: 478	Weight: 1.00
Name:	F2_CM_MP25	SEQ ID NO: 618	Len: 962	Check: 9292	Weight: 1.00
Name:	F2KU_BE_VI	SEQ ID NO: 619	Len: 962	Check: 567	Weight: 1.00
Name:	G_BE_DRCBL	SEQ ID NO: 620	Len: 962	Check: 6261	Weight: 1.00
Name:	G_NG_92NG0	SEQ ID NO: 621	Len: 962	Check: 4508	Weight: 1.00
Name:	G_SE_SE616	SEQ ID NO: 622	Len: 962	Check: 6733	Weight: 1.00
Name:	H_BE_VI991	SEQ ID NO: 623	Len: 962	Check: 7498	Weight: 1.00
Name:	H_BE_VI997	SEQ ID NO: 624	Len: 962	Check: 8345	Weight: 1.00
Name:	H_CF_90CF0	SEQ ID NO: 625	Len: 962	Check: 2490	Weight: 1.00
Name:	J_SE_SE702	SEQ ID NO: 626	Len: 962	Check: 4446	Weight: 1.00
Name:	J_SE_SE788	SEQ ID NO: 627	Len: 962	Check: 1662	Weight: 1.00
Name:	K_CD_EQTB1	SEQ ID NO: 628	Len: 962	Check: 7406	Weight: 1.00
Name:	K_CM_MP535	SEQ ID NO: 629	Len: 962	Check: 512	Weight: 1.00
Name:	N_CM_YBF30	SEQ ID NO: 630	Len: 962	Check: 1733	Weight: 1.00
Name:	O_CM_ANT70	SEQ ID NO: 631	Len: 962	Check: 75	Weight: 1.00
Name:	O_CM_MVP51	SEQ ID NO: 632	Len: 962	Check: 3290	Weight: 1.00
Name:	O_SN_99SE	SEQ ID NO: 633	Len: 962	Check: 6963	Weight: 1.00
Name:	O_SN_99SE	SEQ ID NO: 634	Len: 962	Check: 6278	Weight: 1.00
Name:	U_CD_83C	SEQ ID NO: 635	Len: 962	Check: 9044	Weight: 1.00

SEQ ID NO	1						50
469	00BW0762_1	...MRVMGI	MRNC.QQWWI	WV.ILGFWML	MVCN.VIGNL	WVTVYYGVPV	
470	00BW0768_2	...MRVREI	LRNC.QQWWT	WG.SLGFWMV	MIYS.VVGEL	WVTVYYGVPV	
471	00BW0874_2	...MRAMGT	QRNC.RQWWI	WG.ILGFWML	MTCS.GVG.E	MVTVYYGVPV	
472	00BW1471_2	...MRVMGI	LRSC.QQWWI	WG.ILGFWML	MICS.VLGNL	WVTVYYGVPV	
473	00BW1616_2	...MRVMGI	QRNC.QRWWI	WG.ILGFWMI	Y.N.VVGNL	WVTVYYGVPV	
474	00BW1686_8	...MRVKGI	QRNW.PQWWI	WG.SLGFWML	MFYS.VMGNL	WVTVYYGVPV	



475	00BW1759_3	....MRVRGI	PRNW.QQWWI	WG.ILGFCMI	ITCK.VVGNL	WVTVYYGVPV
476	00BW1773_2	....MRVREI	LRSY.QHWWM	WS.ILGLWIL	IISN.VVGNL	WVTVYYGVPV
477	00BW1783_5	....MRVMGI	KRNC.PPWWI	WG.ILGFWML	MICN.VMGNL	WVTVYYGVPV
478	00BW1795_6	....TRVMGI	RRNW.QQWWI	WG.ILGFWML	IICN.VMGNM	WVTVYYGVPV
479	00BW1811_3	....MRVRGT	LKNY.QRWWI	WG.ILGLWIL	LINI.VVGNL	WVTVYYGVPV
480	00BW1859_5	....MRVRGI	PRNW.QQWWI	WG.ILGFWIL	MICN.VVGNL	WVTVYYGVPV
481	00BW1880_2	....MRVTGI	MRNC.QQWWI	WV.ILGFWML	MICN.VIGNL	WVTVYYGVPV
482	00BW1921_1	....MRVRGI	QRNW.QQWWI	WG.SLGFWVM	A.CS.VVGNL	WVTVYYGVPV
483	00BW2036_1	....MRVRGI	SRNW.QQWWI	WG.ILGFWMF	MICS.VLGNL	WVTVYYGVPV
484	00BW2063_6	....MRVMGI	MRNW.PPWWI	WG.ILGFWML	MICN.VMGNL	WVTVYYGVPV
485	00BW2087_2	....MRVTGM	WKNC.QQWWI	WG.ILGFWML	MICS.VLGNL	WVTVYYGVPV
486	00BW2127_2	....MRVRGI	PRNW.QQWWI	WG.ILGFW..	MIYS.MMGNL	WVTVYYGVPV
487	00BW2128_3	....MRVRGI	LKNC.QQWWI	WI.ILGFWLL	IITN.VVGKL	WVTVYYGVPV
488	00BW2276_7	....MRVRGI	LRNW.QQWWI	WG.ILGFWMV	MICS.VWGNL	WVTVYYGVPV
489	00BW3819_3	....MRVRGI	LRNW.QQWWI	WG.ILSFVVL	MICS.RGEDR	WVTVYYGVPV
490	00BW3842_8	....MRVRGI	LRNW.QQWWI	WV.ILGFW..	.IYS.VAGNL	WVTVYYGVPV
491	00BW3871_3	....MRVRGI	QRNW.QQWWI	WG.SLGFWML	MIYN.VMGSL	WVTVYYGVPV
492	00BW3876_9	....MRVREI	LRNW.KQLWT	WG.ILGFVVL	IICS.AGGNL	WVTVYYGVPV
493	00BW3886_8	....MRVRGI	LRIW.QWWWI	WA.SLGFWML	IICN.EKGKL	WVTVYYGVPV
494	00BW3891_6	....MRVRGI	LRNY.QQWWI	WG.ILGFWML	MMCN.VMGDL	WVTVYYGVPV
495	00BW3970_2	....MRVKGI	MRNC.QQWWI	WG.ILGFWML	LICN.GEGNL	WVTVYYGVPV
496	00BW5031_1	....MRVMGT	QRNC.QQWWI	WG.ILGFWML	MIYN.VGGNL	WVTVYYGVPV
497	96BW01B21	....MRVRGI	LRNY.PQWWI	WG.ILGFWMI	MLCN.VMGNL	WVTVYYGVPV
498	96BW0407	....MRVMGI	QRNC.QQWWI	WG.ILGFWMI	FNGM.GSW..	VT.VYYGVPV
499	96BW0502	....MRVMGI	LKNY.QQWWM	WG.ILGFWML	IISS.VVGNL	WVTVYYGVPV
500	96BW06_J4	....MRVKGI	PRNW.QQWWI	WG.SLGFWII	C..S.VMGNL	WVTVYYGVPV
501	96BW11_06	....MRVMEI	MRNC.QQWWI	WG.ILGFWML	MICN.VMGKS	WVTVYYGVPV
502	96BW1210	....MRVRGI	LRNY.LQWWI	WG.ILGFWML	MVCS.K.ENM	WVTVYG.VPV
503	96BW15B03	....MRVRGI	LRSW.QQWWI	WG.TLGFW..	.ICS.GLGNL	WVTVDGVPV
504	96BW16_26	....MIVRGI	LKTC.QQWWI	WI.ILGFWIL	IINN.VVGHL	WVTVDGVPV
505	96BW17A09	....MRVMGI	LRNC.QQWWI	WG.ILGFWML	MICS.VLGNL	WVTVYYGVPV
506	96BWM01_5	....MRVMGI	KKNW.QPWWI	WG.VLGFWTL	MICS.VMGNL	WVTVYYGVPV
507	96BWM03_2	....MRVRGT	QRNW.QRWWI	WS.ILAFWIL	INCN.GEEKL	WVTVYYGVPV
508	98BWMC12_2	....MRVMGI	QKNC.QRWWI	WG.ILGFWMI	MSYS.VLGNL	WVTVYYGVPV
509	98BWMC13_4	....MRVMGI	KMNW.QQWWI	WG.ILGFWML	MICS.VMGNL	WVTVYYGVPV
510	98BWMC14_a	....MRVKGI	LRNW.LQWWI	WG.SLGFWML	C..S.VMGNM	WVTVYYGVPV
511	98BWM014_1	....MRVMGT	LRNC.QQWWT	WG.ILGFWML	MICS.VGGNL	WVTVYYGVPV
512	98BWM018_d	....MRVMGI	QKNC.QHWWI	WG.ILGFWML	MICN.GK.DL	WVTVYYGVPV
513	98BWM036_a	....MRVRGI	LRNC.PQWWI	WG.ILGFWML	MTCN.MEGNL	WVTVYYGVPV
514	98BWM037_d	....MRVRGI	LRNY.QQWWI	WG.ILGFWML	MICN.VVGNL	WVTVYYGVPV
515	99BW3932_1	....MRVRGI	PRNW.QQWWI	WS.ILG....	.FCS.VVGQL	WVTVYYGVPV
516	99BW4642_4	....MRVKGI	LRNW.QQWWI	WG.ILGFWML	MICN.VVGNL	WVTVYYGVPV
517	99BW4745_8	....MRVRGI	LRDY.QQWWI	WS.ILGFWM.	.ICN.GMGNL	WVTVYYGVPV
518	99BW4754_7	....MRVMGI	KRNC.QQWWI	WG.ILGFWML	MI...CNGNL	WVTVYYGVPV
519	99BWMC16_8	....MRVMEI	WRNC.PPWWI	WG.ILGFWML	MICN.GG.NR	WVTVYYGVPV
520	A2_CD_97CD	....TRVMGT	QRNC.QKWE	WG.ILVFGMI	MMCK.AAD.L	WVTVYYGVPV
521	A2_CY_94CY	....MRVMGT	QRNY.QHLWR	GG.ILILGML	IMCK.ATD.L	WVTVYYGVPV
522	A2D__97KR	....MRVRGI	QRNY.QHLWK	WG.ILILGML	MISK.ATEDL	WVTVYYGVPV
523	A2G_CD_97C	....MRVKGM	QRNW.QNLWK	WG.ALILGLV	IICS.ASNNL	WVTVYYGVPV
524	A_BY_97BL0	....MKARGM	XRNY.QHLWR	XG.TMLFWM	IMCK.AAEDL	VX.VYXXVPV
525	A_KE_Q23_A	....MRVMGI	QRNC.QHLLT	WG.IMILGTI	IFCS.AVENL	WVTVYYGVPV
526	A_SE_SE659	....MRVMGI	QRNC.QHLLR	WG.TIILGLI	IICS.VADKL	WVTVYYGVPV

527	A_SE_SE725	...MRVMGT	QMNW.QHLLR	WG.TIILGMI	MICS.TADNL	WVTVYYGVPV
528	A_SE_SE753	...MRAMGI	QRNC.QHLLR	WG.TMILGLV	IICS.VAGNL	WVTVYYGVPV
529	A_SE_SE853	...MRVKGI	QRNS.QHLLR	WG.TMILGMI	IICS.TADKL	WVTVYYGVPV
530	A_SE_SE889	...MRVMGT	QMNW.QNLWR	WG.TMILGII	IICS.AAENL	WVTVYYGIPV
531	A_SE_UGSE8	...MRVMGT	QRNC.QHLLN	WG.IMILGMI	IICS.TAENL	WVTVYYGVPV
532	A_UG_92UG0	...MRVMGI	ERNY.PCWWT	WG.IMILGMI	IICN.TAENL	WVTVYYGVPI
533	A_UG_U455_	...MRVMGI	QRNY.PCLWR	WG.TMILGLI	IICN..AQQL	WVTVYYGVPV
534	AC_IN_2130	...MRVRGI	LRNY.QQWWI	WG.SLGFWML	MVCN.VVGNL	WVTVYYGVPV
535	AC_RW_92RW	...MRVMGT	LMNY.QNLWG	WG.TMILGML	TICS.AANNL	WVTVYYGVPV
536	AC_SE_SE94	...MRVTGT	QRSC.QPWWI	WG.ILGFWML	IICS.ATDKL	WVTVYYGVPV
537	ACD_SE_SE8	...MRVMGI	QRNW.QHLLR	WG.TMILGMI	LICS.AVDKL	WVTVYYGVPV
538	ACG_BE_VI1	...MRVKGI	QRNY.QQWWT	WG.SLGLWML	LICN.VMGNL	WVTVYYGVPV
539	AD_SE_SE69	...MRVRGI	EMN.YQNLWR	WG.TLLLGLM	MT.CSVTGRL	WVTVYYGVPV
540	AD_SE_SE71	...MRVMGI	QRNC.QNLLT	WG.TMILGMI	IICS.VAENL	WVTVYYGVPV
541	ADHK_NO_97	...MKVMGT	QRN.YPNWWR	WG.VLILGML	LICS.TTGNL	WVTVYYGVPV
542	ADK_CD_MAL	...MRVREI	QRN.YQNWWR	WG.MMLLGML	MT.CSIAEDL	WVTVYYGVPV
543	AG_BE_VI11	...MRVRGT	QMSWP.HLWN	GG.ILILGLV	IICS.ASNNL	WVTVYYGVPV
544	AG_NG_92NG	...MRVKGT	QRNWQ.HLWT	WW.TLILGLV	IICS.ASNNL	WVTVYYGVPV
545	AGHU_GA_VI	...MRVMET	QRN.YPRLWR	WG.TIILGML	MICN.AKENL	WITVYYGVPV
546	AGU_CD_Z32	...MKVKGI	QRNC.QHLWK	WG.TFILGLV	IICS.AAENL	WVTVYYGVPV
547	AJ_BW_BW21	...MRVMET	LMNCT.NLWR	WG.LMIFGML	MTCS.ATGNM	WVTVYYGVPV
548	B_AU_VH_AF	...MKVKET	KRN.WQRLWR	WG.IMLLGML	MICS.ATEKL	WVTVYYGVPV
549	B_CN_RL42_	...MRVTGI	RKN.YQHLWR	WG.TMLLGML	MICN.AAENL	WVTVYYGVPV
550	B_DE_D31_U	...MKVKEI	RKN.YQHLWR	WG.TMLLGML	MICS.ATEKL	WVTVYYGVPV
551	B_DE_HAN_U	...MKVKET	RKN.YQRLWR	GG.TLLLGLM	MISS.VAGNL	WVTVYYGVPV
552	B_FR_HXB2_	...MRVKEK	YQHLWRWGWR	WG.TMLLGML	MICS.ATEKL	WVTVYYGVPV
553	B_GA_OYI_	...MTARGT	RKN.YQRLWR	WG.TMLLGML	MICS.AAENL	WVTVYYGVPV
554	B_GB_CAM1_	...MRAKGI	RKN.CQRLWR	WG.TMLLGML	MICS.AADKL	WVTVYYGVPV
555	B_GB_GB8_C	...MKAKGT	RKN.YQHLWK	WG.IMLLGML	MICS.ATEKL	WVTVYYGVPV
556	B_GB_MANC_	...MKVKEI	RKN.YQNLWR	WG.TLFLGML	MICS.AEEKL	WVTVYYGVPV
557	B_KR_WK_AF	...MRVKGI	RKN.YQHWWR	WG.IMLLGMW	MICS.AAEKL	WVTVYYGVPV
558	B_NL_3202A	...MKVKET	RKN.YQHLWR	WG.TMLLGML	MICS.AAEQL	WVTVYYGVPV
559	B_TW_TWCYS	...MRVRGT	RMN.CQHLWR	WG.TMLLGML	MISS.AAENL	WVTVYYGVPV
560	B_US_BC_LO	...MRVKEI	RKN.YQHLWR	WG.TMLFGIL	MIYS.AAGNL	WVTVYYGVPV
561	B_US_DH123	...MRVMGI	RKN.YQHLWK	GG.TLLLGIL	MICS.AAEQL	WVTVYYGVPV
562	B_US_JRCSF	...MRVKGI	RKN.YQHLWK	GG.ILLGTL	MICS.AVEKL	WVTVYYGVPV
563	B_US_MNCG_	...MRVKGI	RRN.YQHWWG	WG.TMLLGLL	MICS.ATEKL	WVTVYYGVPV
564	B_US_P896_	...MRVKEI	RKN.WQHLR.	GG.ILLGML	MICSAAKEKT	WVTIYYGVPV
565	B_US_RF_M1	...MRVMEM	RKN.CQHLWK	WG.TMLLGML	MICS.AAEDL	WVTVYYGVPV
566	B_US_SF2_K	...MKVKGT	RRN.YQHLWR	WG.TLLLGLM	MICS.ATEKL	WVTVYYGVPV
567	B_US_WEAU1	...MRVKGI	RKN.YQHLWK	WG.IMLLGIL	MICS.AAENL	WVTVYYGVPV
568	B_US_WR27_	...MRVKGI	RKN.CQHLWR	WG.IMLLGML	MICN.ATEQL	WVTVYYGVPV
569	B_US_YU2_M	...MRATEI	RKN.YQHLWK	GG.TLLLGLM	MICS.AAEQL	WVTVYYGVPV
570	BF1_BR_93B	...MRVRGM	QRN.WQHLGK	WG.LLFLGIL	IICN..AENL	WVTVYYGVPV
571	C_BR_92BR0	...MRVEGI	QRNW.KQWWI	WG.ILGFWMV	MIYN.VRGNL	WVTVYYGVPV
572	C_BW_96BW0	...MRVMGI	QRNC.QQWWI	WG.ILGFWMI	INGM.GSW..	VT.VYYGVPV
573	C_BW_96BW1	...MRVMGI	MRNC.QPWWI	WG.ILGFWML	MICN.VMGKS	WVTVYYGVPV
574	C_BW_96BW1	...MRVRGI	LRNY.LQWWI	WG.ILGFWML	MVCS.K.ENM	WVTVYG.VPV
575	C_BW_96BW1	...MRVRGI	LRSW.QQWWI	WG.TLGFW..	.ICS.GLGNL	WVTVYDGVVPV
576	C_ET_ETH22	...MKVMGI	QRNC.QQWWI	WG.ILGFWML	MICN.GMGNL	WVTVYYGVPV
577	C_IN_93IN1	...MRVRGT	LRNY.QQWWI	WG.VLGFWML	MICN.GGGNL	WVTVYYGVPV
578	C_IN_93IN9	...MRVRGT	LRNY.QQWWI	WG.VLGFWML	MICN.VGGNL	WVTVYYGVPV

579	C_IN_93IN9	...	MRVRGI	LRNY.QQWWI	WG.ILGFWML	MICN.VVGNL	WVTVYYGVPV
580	C_IN_94IN1	...	MRVRGT	LRNY.QQWWI	WG.VLGFWML	MICN.GGKDL	WVTVYYGVPV
581	C_IN_95IN2	...	MRVRGI	LRNY.QQWWI	WG.VLGFWML	MICN.VVGNL	WVTVYYGVPV
582	CRF01_AE_C	...	MGVKGT	QMNW.PHLWK	WG.TLILGLV	IICS.ASDTL	WVTVYYGVPV
583	CRF01_AE_C	...	MRVKGT	RRNW.PNLWK	WG.TLILGLV	IICS.ASDNL	WVTVYYGVPV
584	CRF01_AE_C	...	MRVKGT	QMNW.PNLWK	WG.TLILGLV	IMCS.ASDNL	WVTVYG.VPV
585	CRF01_AE_T	...	MRVKET	QMNW.PNLWK	WG.TLILGLV	IICS.ASDNL	WVTVYYGVPV
586	CRF01_AE_T	...	MRVKET	QMN..PNLWK	WG.TLILGLV	IICS.ASDDL	WVTVYYGVPV
587	CRF01_AE_T	...	MRVKET	QINW.PNLWK	WG.TLILGLV	IMCS.ASNNL	WVTVYYGVPV
588	CRF01_AE_T	...	MRVKET	QMSW.PNLWK	WR.TLILGLV	IICS.ASDNL	WVTVYYGVPV
589	CRF01_AE_T	...	MRVKET	QMNW.PNLWK	WG.TLILGLV	IICS.ASDNL	WVTVYYGVPV
590	CRF01_AE_T	...	MRVKET	QMNW.PNLWK	WG.TLILGLV	IICS.ASENL	WVTVYYGVPV
591	CRF02_AG_F	...	MRVMGM	QRNY.PLLWK	WG.TIIFWIM	IICN..AEKL	WVTVYYGVPV
592	CRF02_AG_F	...	MRVMGI	QRNY.PLFWK	WG.MIIFWIM	IICN..AEKL	WVTVYYGVPV
593	CRF02_AG_G	...	MRVRGM	QRNC.QNLWR	WA..HDFWIL	IICN.AAENL	WVTVYYGVPV
594	CRF02_AG_N	...	MRVMGI	QKNY.PLLWR	WG.TNIFWIM	IICN..AEQL	WVTVYYGVPV
595	CRF02_AG_S	...	MRVMGI	QKNY.PLLWR	WG.MIIFWIM	TICS..AGNL	WVTVYYGVPV
596	CRF02_AG_S	...	MRVMGI	LKSC.PPFWR	WGMIMLLWIL	IICN..AENL	WVTVYYGVPV
597	CRF03_AB_R	...	MRVKEI	RKH....LWR	WG.TLFLGML	MICS.ATENL	WVTVYYGVPV
598	CRF03_AB_R	...	MRVKEI	RKH....LWR	WG.TLLLGLM	MICS.ATENL	WVTVYYGVPV
599	CRF04_cpx_	...	MRVMGM	QRN.YPHLWE	WG.TLILGLV	IICS.ASNNL	WVTVYYGVPV
600	CRF04_cpx_	...	MRVMGI	QRN.YPHLWE	WG.TLILGLV	IMCS.ASKDM	WVTVYYGVPV
601	CRF04_cpx_	...	MTVMGT	QRN.CPRLWT	WG.TFILWL	IICS.ASNNL	WVTVYYGVPV
602	CRF05_DF_B	...	MRVRGM	QRN.WPHLGK	WG.LLFLGIL	IICS.ATDKF	WVTVYYGVPV
603	CRF05_DF_B	...	MRVRGM	QRN.WQHLGK	WG.LLFLGIL	IICS.AADNL	WVTVYYGVPV
604	CRF06_cpx_	...	MRVKGI	QTSWQ.HLWK	WG.TLILGLV	IICS.ASKNM	WVTVYYGVPV
605	CRF06_cpx_	...	MRVRGI	QKNWQ.HLWK	WG.TLILGLV	IICS.ASNNL	WVTVYYGVPV
606	CRF06_cpx_	...	MRVKGI	QMNWQ.HLWK	WG.TLILGLA	IICS.ATSNL	WVTVYYGVPV
607	CRF06_cpx_	...	MTVKGI	QRNWQ.HLWK	WG.TLILGLV	IICS.ASQNM	WVTVYYGVPV
608	CRF11_cpx_	...	MRARGT	QKNWH.DLWR	WG.LMISGML	MICN.ATDNL	WVTVYYGVPV
609	CRF11_cpx_	...	MRVKET	QRNWH.NLWR	WG.LMIFGML	MICN.AEK.M	WVTVYYGVPV
610	D_CD_84ZR0	...	MRVKGI	KRN.YQPLWK	WG.IMLLGML	MMTYSAADNL	WVTVYYGVPV
611	D_CD_ELI_K	...	MRARGI	ERN.CQNWWK	WG.IMLLGIL	MT.CSAADNL	WVTVYYGVPV
612	D_CD_NDK_M	...	MRAREK	ERN.CQNLWK	WG.IMLLGML	MT.CSAAEDL	WVTVYYGVPV
613	D_UG_94UG1	...	MRVRET	KRN.YQHLWK	WG.TMLLGML	MI.CSVTGKS	WVTVYYGVPV
614	F1_BE_VI85	...	MRVRGM	QRN.WQHLGK	WG.LLFLGIL	IICN.AADNL	WVTVYYGVPV
615	F1_BR_93BR	...	MRVRGM	QRN.WQHLGK	WG.LLFLGTL	IICN.AAENL	WVTVYYGVPV
616	F1_FI_FIN9	...	MRVRGM	QRN.WQHLGK	WG.LLFLGML	IICK.AADDL	WVTIYYGVPV
617	F1_FR_MP41	...	MRVRVM	QRN.WQHLGK	WG.LLFLGIL	IICS.AADNL	WVTVYYGVPV
618	F2_CM_MP25	...	MRVREM	QRN.WQHLGR	WG.LLFLGIL	IICS.AADKL	WVTVYYGVPV
619	F2KU_BE_VI	...	MRVRER	RRN.WQPLGR	WG.ILFLGIF	IICN.AAEDL	WVTVYYGVPV
620	G_BE_DRCBL	...	MRVKGI	QRNWQ.HLWN	WG.ILILGLV	IICS.AEK.L	WVTVYYGVPV
621	G_NG_92NG0	...	MRVKGI	QRNWQ.HLWK	WG.TLILGLV	IICS.ASDNL	WVTVYYGVPV
622	G_SE_SE616	...	MRVTGI	QRNW..HLWK	WG.TLILGLV	IICS.ASNNL	WVTVYYGVPV
623	H_BE_VI991	...	TRVMET	QRN.YPSLWR	WG.TLILGML	LICS.VVGNL	WVTVYYGVPV
624	H_BE_VI997	.....	TRV	MRN.YPQWR	GG.ILLGML	LIYS.AAGNL	WVTVYYGVPV
625	H_CF_90CF0	...	TRVMET	QRN.YPSLWR	WG.TLILGML	LICS.AAQN	WVTVYYGVPV
626	J_SE_SE702	...	TRVMET	QTSWL.SLWR	WG.LMIFGML	MICS.AREN	WVTVYYGVPV
627	J_SE_SE788	...	TRVMET	QKNWQ.TLWR	GG.LMIFGML	MICK.AKEDL	WVTVYYGVPV
628	K_CD_EQTB1	...	MRAREI	QRN.WQHLGK	RG.ILFLGIL	IICS.AANNL	WVTVYYGVPV
629	K_CM_MP535	...	MRVRGM	QRN.WQTLGN	WG.ILFLGIL	IICS.NADKL	WVTVYYGVPV
630	N_CM_YBF30	...	MKVMGM	QSGWMGMKSG	WLLFYLLVSL	IKVIG.SEQH	WVTVYYGVPV

<u>631</u>	O_CM_ANT70	....MKAMEK	RNK...K..L	WTLYLAMALI	TPCLSLR.QL	YATVYAGVPV
<u>632</u>	O_CM_MVP51	....MKVMKK	NNR...K..S	WSLYIAMALL	IPCLSYSKQL	YATVYSGVPV
<u>633</u>	O_SN_99SE_	MTVTMKVMEQ	RNR...K..L	GILCIVMALI	TPCLSYN.QH	YATVYAGVPV
<u>634</u>	O_SN_99SE_	MTVTMKVMEK	RNR...K..L	GILCMVMALI	TPCLSHN.QH	YATVYAGVPV
<u>635</u>	U_CD___83C	....MRVKEI	QRN.YQHLWK	WS.LIILGMI	MICK.AIEKS	WVTVYYGVPV

00BW0762_1	WREAKTTTLFC	ASDAKAYDRE	VHNVWATHAC	VPTDPNPQEL	VLENVTFNFN
00BW0768_2	WKEAKTTTLFC	ASDAKAYEKE	VHNVWATHAC	VPTDPNPQEI	VLGNVTENFN
00BW0874_2	WKEAKTTTLFC	ASDAKAYERE	VHNVWATHAC	VPTDPDPQEM	VLENVTFNFN
00BW1471_2	WREAKTTTLFC	ASDAKAYEKE	VHNVWATHAC	VPTDPNPQEM	YLVNVTFNFN
00BW1616_2	WKEAKTTTLFC	ASDAKAYDRE	VHNVWATHAC	VPTDPNPQEI	GLENVTFNFN
00BW1686_8	WKEAKTTTLFC	ASDAKAYEKE	VHNIWATHAC	VPTDPNPQEI	VLENVTFNFN
00BW1759_3	WRETKTTTLFC	ASDAKAYDKE	VHNVWATHAC	VPTDPNPQEL	VLGNVTESFN
00BW1773_2	WKEAKTTTLFC	ASDAKAYEKE	VHNVWATHAC	VPTDPNPQEI	PLKNVTENFN
00BW1783_5	WKEAKTTTLFC	ASDAKAYEKE	AHNIWATHAC	VPTDPNPREM	FLENVTQNFN
00BW1795_6	WREAKAPLFC	ASDAKAYDRE	VHNVWATHAC	VPTDPNPQEM	VLKNVTENFN
00BW1811_3	WKEAKTTTLFC	ASDAKGYDRE	VHNVWATHAC	VPTDPNPQEL	VLGNVTENFN
00BW1859_5	WKEAKTTTLFC	ASDAKAYERE	VHNVWATHAC	VPTDPNPQEI	VLENVTFNFN
00BW1880_2	WKEAKATLFC	ASEAKAYESE	VHNVWATHAC	VPTDPNPQEI	VLENVTFNFN
00BW1921_1	WKEAKTTTLFC	ASDAKAYETE	VHNVWATHAC	VPTDPNPQEM	ALENVTFNFN
00BW2036_1	WREAKTTTLFC	ASDAKAYETE	VHNIWATHAC	VPTDPNPQEI	VLGNVTENFN
00BW2063_6	WREAKATLFC	ASDAKAYERE	VHNVWATHAC	VPTDPNPQEI	VLENVTFNFN
00BW2087_2	WKEAKTTTLFC	ASDAKAYERE	VHNVWATHAC	VPTDPNPQEM	ELKNVTENFN
00BW2127_2	WKEAKAPLFC	ASDAKAYEKE	AHNVWATHAC	VPTDPNPQEI	ELKNVTENFN
00BW2128_3	WKEAKTTTLFC	ASDAKAYEKE	VHNVWATHAC	VPTDPNPQEM	VLENVTFNFN
00BW2276_7	WKEAKTTTLFC	ASDAKAYEKE	VHNVWATHAC	VPTDPNPQEL	VLENVTFNFN
00BW3819_3	WREAKATLFC	ASDAKAHERE	VHNVWATHAC	VPTDPNPQEM	VMENVTFNFN
00BW3842_8	WKEAKTTTLFC	ASDAKGYETE	VHNVWATHAC	VPTDPDPQEM	VLGNVTENFN
00BW3871_3	WREAKTTTLFC	ASDAKAYERE	VHNVWATHAC	VPTDPNPQEM	LLKNVTENFN
00BW3876_9	WKEAKTTTLFC	ASDAKVYEKE	VHNVWATHAC	VPTDPNPQEM	VLDNVTFNFN
00BW3886_8	WKEAKTTTLFC	ASDAKAYERE	VHNVWATHAC	VPTDPNPQEI	VLGGVTENFN
00BW3891_6	WREAKTTTLFC	ASDAKGYEKE	VHNVWATHAC	VPTDPDPQEM	VLENVTFNFN
00BW3970_2	WKEAKTTTLFC	ASDAKGYERE	VHNIWATHAC	VPTDPNPQEM	FLHNVTFNFN
00BW5031_1	WKEAKTTTLFC	ASDAKAYEKE	VHNVWATHAC	VPTDPSQEI	VLENVTTTFN
96BW01B21	WKEAKTTTLFC	ASDAKAYEKG	VHNVWATHAC	VPTDPNPQEV	FLENVTFNFN
96BW0407	WKEAKATLFC	ASDARAYDRE	VHNVWATHAC	VPTDPNPQEV	ILENVTFNFN
96BW0502	WKEAKTTTLFC	TSDAKAYETE	VHNVWATHAC	VPTDPNPQEI	VLENVTFNFN
96BW06_J4	WKEAKTTTLFC	ASDAKAYEKE	VHNVWATHAC	VPTDPSQEI	VLGNVTENFN
96BW11_06	WREAKATLFC	ASDAKAYEKE	VHNVWATHAC	VPTDPNPQEV	VLENVTFNFN
96BW1210	WKEAKTTTLFC	ASDAKAYEGE	VHNVWATHAC	VPTDPNPQEL	VLGNVTENFN
96BW15B03	WREASNTLFC	ASYAKAYEKE	VHNVWATHAC	VPTDPNPQEI	ELDNVTENFN
96BW16_26	WKEAKTTTLFC	ASDAKAYDKE	VHNVWATHAC	VPTDPNPQEI	ILKNVTENFN
96BW17A09	WREAKTTTLFC	ASDAKAFESE	VHNVWATHAC	VPTDPNPQEM	VLENVTFNFN
96BWM01_5	WREAKTTTLFC	ASDAKAYEAE	VHNVWATHAC	VPTDPNPQEI	ELKNVTENFN
96BWM03_2	WKEAKTTTLFC	ASDAKAYERE	VHNVWATHAC	VPTDPNPQEM	VLENVTFNFN
98BWMC12_2	WREAKTTTLFC	ASDAKAYERE	VHNIWATHAC	VPTDPNPQEM	VLENVTFNFN
98BWMC13_4	WKEAKAPLFC	ASDAKVYEKE	VHNVWATHAC	VPTDPNPQEL	VLENVTFNFN
98BWMC14_a	WREATTTTLFC	ASDAKAYEKE	VHNVWATHAC	VPTDPNPQEI	VLGNVTENFN
98BWM014_1	WKEAKTTTLFC	ASDAKAYDKE	VHNVWATHAC	VPTDPSQEM	FLANVTENFN
98BWM018_d	WREAKATLFC	ASNAKAYEKE	VHNVWATHAC	VPTDPNPQEM	VLENVTFNFN
98BWM036_a	WKEAKATLFC	ASDAKAYDKE	VHNVWATHAC	VPTDPDPQEI	VLENVTFESFN
98BWM037_d	WKEAKTTTLFC	ASDAKAYDKE	VHNVWATHAC	VPTDPNPQEM	VLENVTFNFN
99BW3932_1	WKEAKATLFC	ASDAKAYEKE	VHNVWATHAC	VPTDPNPQKL	VLGNVTENFN
99BW4642_4	WKEAKTTTLFC	ASDAKAYDKE	VHNVWATHAC	VPTDPNPQEI	VLENVTFNFN
99BW4745_8	WREAKTTTLFC	ASDAKAYEKE	VHNVWATHAC	VPTDPNPQEL	VLKNVTENFN
99BW4754_7	WREAKTTTLFC	ASDAKAYDKE	VHNVWATHAC	VPTDPNPQEI	VLENVTFNFN
99BWMC16_8	WREAKATLFC	ASDAKAYERE	VHNVWATHAC	VPTDPDPQEI	ALENVTFNFN
A2_CD_97CD	WRDADTTTLFC	ASDAKAYATE	KHNVWATHAC	VPTDPNPQEV	NLANVTEDFN
A2_CY_94CY	WKDADTILFC	ASDAKAYDTE	VHNVWATHAC	VPTDPNPQEI	NLENVTFNFN
A2D_97KR	WRDAETTLFC	ASDAKAYDTE	AHNVWATHAC	VPTDPNPQEI	NLENVTFNFN
A2G_CD_97C	WEDANTPLFC	ASDAKSYSTE	RHNVWATHAC	VPTDPNPQEM	ILENVTFESFN
A_BY_97BL0	XXDAATTLFC	ASDAKAXDKE	VHNVWATHAC	VPTDPDPQEI	ILGNVTEKFD
A_KE_Q23_A	WRDADTTTLFC	ASDAKAYETE	KHNVWATHAC	VPTDPNPQEI	HLDNVTEKFN
A_SE_SE659	WKDAETTLFC	ASDAKAYDPE	VHNVWATHAC	VPTDPNPQEM	HLENVTEESFN
A_SE_SE725	WKDAETTLFC	ASDAQAYKTE	MHNVWATHAC	VPTDPNPQEL	HLKNVTEEFN

A_SE_SE753	WKDAETTLFC	ASDAKAYETE	KHNVWATHAC	VPTDPNPQEI	HLKNVTEKFN
A_SE_SE853	WKDAETTLFC	ASDAKAYDTE	VHNVWATHAC	VPTDPNPQEL	HLANVTEEFN
A_SE_SE889	WRDAETTLFC	ASDAKAYDTE	VHNVWATHAC	VPTDPNPQEI	NLENVTEEFN
A_SE_UGSE8	WKDAETTLFC	ASDAKAYEKE	VHNVWATHAC	VPTDPNPQEL	YLENVTEDFN
A_UG_92UG0	WKDANTTLFC	ASDAKAYDTE	VHNVWATHAC	VPTDPSPQEL	KMENVTEEFN
A_UG_U455_	WKDAVTTLFC	ASDAKAYDAE	VHNVWATHAC	VPTDPNPQEI	DLVNVTEEFN
AC_IN_2130	WKDAETTLFC	ASDAKAYETE	KHNVWATHAC	VPTDPNPQEI	HLENVTEDFN
AC_RW_92RW	WKDAETTLFC	ASDAKAYDPE	KHNVWATHAC	VPIDPDPQEI	HLENVTEEFN
AC_SE_SE94	WKEAKTTLFC	ASDAKAYEAE	VHNVWATHAC	VPTDPNPHEI	NLENVTENFN
ACD_SE_SE8	WKDAETTLFC	ASDAKAYDTE	VHNVWATHAC	VPTDPNPQEV	LLGNVTEDFN
ACG_BE_VI1	WKEAKTTLFC	ASDAKAYETE	AHNVWATHAC	VPTDPSPQEI	ELKNVTENFN
AD_SE_SE69	WRDAETTLFC	ASDAKAYDAE	VHNVWATHAC	VPTDPNPQEI	NLENVTEEFN
AD_SE_SE71	WKDAETTLFC	ASDAKAYETE	KHNVWATHAC	VPTDPNPQEI	HLENVTENFN
ADHK_NO_97	WKEAKTTLFC	ASDAKAYDTE	MHNVWATHAC	VPTDPSPQEI	VLENVTENFN
ADK_CD_MAL	WKEATTTLFC	ASDAKSYETE	VHNIWATHAC	VPTDPNPQEI	ELENVTEGFN
AG_BE_VI11	WEDADTTLFC	ASDAKAYSTE	SHNVWATHAC	VPTDSNPQEI	PLENVTENFN
AG_NG_92NG	WEDADTPLFC	ASDAKAYSTE	RHNVWATHAC	VPTDPNPQEI	TLENVTETFN
AGHU_GA_VI	WRDAKTSLFC	ASDAKSYSTE	SHNVWATHAC	VPTDPNPQEI	NLENVTENFN
AGU_CD_Z32	WKDAETTLFC	ASDAKAYDTE	KHNVWATHAC	VPTDPNPQEL	SLGNVTEKFN
AJ_BW_BW21	WKEAKTTLFC	ASNAKAYSTE	GHNIWATHAC	VPTDPNPQEI	ILENVTENFN
B_AU_VH_AF	WKEATTTLFC	ASDAKAYDKE	VHNVWATHAC	VPTDPNPQEI	LLENVTEEFN
B_CN_RL42	WKEATTTLFC	ASDAKAYDTE	VHNVWATHAC	VPTDPNPQEV	VLGNVTENFN
B_DE_D31_U	WKEATTTLFC	ASDAKAYDKE	VHNVWATHAC	VPTDPPQEV	VLENVTEDFN
B_DE_HAN_U	WKEATTTLFC	ASDAKAYDTE	VHNVWATHAC	VPTDPNPQEV	VMGNVTENFN
B_FR_HXB2_	WKEATTTLFC	ASDAKAYDTE	VHNVWATHAC	VPTDPNPQEV	VLVNVTENFN
B_GA_OYI_	WKEATTTLFC	ASDARAYATE	VHNVWATHAC	VPTDPNPQEV	VLGNVTENFD
B_GB_CAM1_	WKEATTTLFC	ASDAKAYDTE	VHNVWATHAC	VPTDPNPQEV	VLENVTENFN
B_GB_GB8_C	WKEATTTLFC	ASDAKAYDTE	KHNVWATHAC	VPTDPNPQEV	VLGNVTENFN
B_GB_MANC_	WKEATTTLFC	ASDAKAHGE	VHNVWATHAC	VPTDPNPQEI	VLENVTEYFD
B_KR_WK_AF	WKEATTTLFC	ASDAKAYDTE	VHNVWATHAC	VPIDPNPQEV	FLENVTENFN
B_NL_3202A	WKEATTTLFC	ASDAKASDTE	VHNVWATHAC	VPTDPNPQEV	ALENVTEDFD
B_TW_TWCYS	WKEATTTLFC	ASDAKTYDTE	VHNVWATHAC	VPTDPNPQEV	TLGNVTENFN
B_US_BC10	WKEATTTLFC	ASDAKAYDTE	VHNVWATHAC	IPTDPNPQEI	VLENVTEDFN
B_US_DH123	WKEANTTLFC	ASDAKAYDTE	VHNVWATHAC	VPTDPNPQEI	LLENVTEDFN
B_US_JRCSF	WKETTTTLFC	ASDAKAYDTE	VHNVWATHAC	VPTDPNPQEV	VLENVTEDFN
B_US_MNCG_	WKEATTTLFC	ASDAKAYDTE	VHNVWATHAC	VPTDPNPQEV	ELVNVTENFN
B_US_P896_	WREATTTLFC	ASDAKAYDTE	VHNVWATHAC	VPTDPNPQEV	VLGNVTENFN
B_US_RF_M1	WKEATTTLFC	ASEAKAYKTE	VHNVWATHAC	VPTDPNPQEV	LLENVTENFN
B_US_SF2_K	WKEATTTLFC	ASDARAYDTE	VHNVWATHAC	VPTDPNPQEV	VLGNVTENFN
B_US_WEAU1	WKEATTTLFC	ASDAKAYDTE	VHNVWATHAC	VPTDPNPQEV	VLENVTENFN
B_US_WR27_	WKEATTTLFC	ASDAKAYDTE	VHNVWATHAC	VPTDPNPQEV	RLENVTEDFN
B_US_YU2_M	WKEATTTLFC	ASDAKAYDTE	VHNVWATHAC	VPTDPNPQEV	KLENVTENFN
BF1_BR_93B	WKEATTTLFC	ASDAKAYEKE	AHNVWATHAC	VPTDPNPQEV	VLENVTENFD
C_BR_92BR0	WKEAKTTLFC	ASDAKAYDAE	VHNVWATHAC	VPTDPNPQEM	VLENVTENFN
C_BW_96BW0	WKEAKATLFC	ASDARAYDRE	VHNVWATHAC	VPTDPNPQEV	NLENVTENFN
C_BW_96BW1	WREAKATLFC	ASDAKAYERE	VHNVWATHAC	VPTDPNPQEV	VLENVTENFN
C_BW_96BW1	WKEAKTTLFC	ASDAKAYEGE	VHNVWATHAC	VPTDPNPQEL	VLGNVTENFN
C_BW_96BW1	WREASNTLFC	ASYAKAYEKE	VHNVWATHAC	VPTDPNPQEI	ELDNVTENFN
C_ET_ETH22	WKDASPTLFC	ASDAKAYDTE	VHNVWGTFC	VPTDPSPQEL	GLENVTENFN
C_IN_93IN1	WKEAKTTLFC	ASDAKAYERE	VHNVWATHAC	VPTDPNPQEI	VLGNVTENFN
C_IN_93IN9	WKEAKTTLFC	ASDAKAYEKE	VHNVWATHAC	VPTDPNPQEI	PLGNVTENFN
C_IN_93IN9	WKEAKTTLFC	ASDAKAYEKE	VHNVWATHAC	VPTDPNPQEM	VLENVTENFN
C_IN_94IN1	WKEAKTTLFC	ASDAKAYGKE	VHNVWATHAC	VPTDPNPQEI	SLENVTENFN
C_IN_95IN2	WKEANTTLFC	ASDAKAYEKE	VHNVWATHAC	VPTDPNPQEI	VMENVTENFN
CRF01_AE_C	WRDADTTLFC	ASDANAQETE	VHNVWATHVC	VPTDPNPQEI	HLENVTENFD
CRF01_AE_C	WRDADTILFC	ASDAKAHVTE	VHNVWATHAC	VPTDPNPQEI	YLENVTENFD
CRF01_AE_C	WRDADTTLFC	ASDAKAHETE	VHNIWATHAC	VPTDPNPQEI	DLENVTENFN
CRF01_AE_T	WKDADTTLFC	ASDAKAHETE	VHNVWTHAC	VPTDP . PQEI	HLENVTENFN
CRF01_AE_T	WRDADTTLFC	ASDAKAHETE	VHNVWATHAC	VPTDPNPQEI	HLENVTENFN
CRF01_AE_T	WRDADTTLFC	ASDAKAHETE	VHNVWATHAC	IPTDPNPQEM	HLENVTENFN

CRF01_AE_T	WRDADTTLFC	ASDAKAHEAE	VHNVWATHAC	VPTDPNPQEI	HLENVTENFN
CRF01_AE_T	WRDADTTLFC	ASDAKAHETE	VHNVWATHAC	VPTDPNPQEI	HLENVTENFN
CRF01_AE_T	WRDADTTLFC	ASDAKAHETE	VHNVWATHAC	VPTDPNPQEI	HMENVTENFN
CRF02_AG_F	WRNAETTLFC	ASDAKAYDAE	VHNVWATHAC	VPTDPNPQEI	HLKNVTEKFN
CRF02_AG_F	WRDAETTLFC	ASDAKAYDVE	VHNVWATHAC	VPTDPNPQEI	HLKNVTEKFN
CRF02_AG_G	WKTADTTLFC	ASDAKAYDTE	VHNVWATHAC	VPTDPNPQEI	HLENVTEEFN
CRF02_AG_N	WKTAETTLFC	ASDAKAYDTE	VHNVWATHAC	VPTDPNPQEI	HLENVTEKFN
CRF02_AG_S	WRDAETTLFC	ASDAKAYDTE	VHNVWATHAC	VPTDPNPQEI	HLGNVTEDFN
CRF02_AG_S	RRDAETTLFC	ASDAKAYETE	VHNVWATHAC	VPTDPSPQEM	HLENVTENFN
CRF03_AB_R	WKEATTTLFC	ASDAKAYSKE	VHNVWATYAC	VPTDPSPQEI	PLKNVTENFN
CRF03_AB_R	WKEATTTLFC	ASDAKAYSKE	VHNVWATYAC	VPTDPSPQEI	PLENVTENFN
CRF04_cpx_	WRDAETTLFC	ASEAKAYEKE	VHNIWATHAC	VPTDPNPQEV	ALINVTENFN
CRF04_cpx_	WRDAETKPCX	ASDAKAYDKE	IHNIWATHAC	VPTDPNPQEL	ALTNVTEFN
CRF04_cpx_	WRDAETSPFC	ASDAKAYDKE	VHNIWATHAC	VPTDPNPQEI	FLKNVTEDFN
CRF05_DF_B	WREAKTTLFC	ASDAKGYDKE	VHNVWATHAC	VPTDPNPQEV	VLGNVTENFN
CRF05_DF_B	WKEANTTLFC	ASDAKGYEKE	AHNVWATHAC	VPTDPNPQEL	ALENVTENFN
CRF06_cpx_	WEDADTILFC	ASDAKAYSPD	KHNVWATHAC	VPTDPNPQEI	SLKNVTENFN
CRF06_cpx_	WEDADTILFC	ASDAKAYSAE	KHNVWATHAC	VPTDPNPQEI	PLKNVTENFN
CRF06_cpx_	WEDADTILFC	ASDAKAYSAE	KHNVWATHAC	VPTDPNPQEI	PLENVTENFN
CRF06_cpx_	WEDADTILFC	ASDAKAYSAE	KHNVWATHAC	VPTDPNPQEI	KLENVTENFN
CRF11_cpx_	WKDANTTLFC	ASDAQAYSPE	KHNVWATHYC	VPTDPNPQEI	LLGNVTENFN
CRF11_cpx_	WRDADTILFC	ASDARTYSTE	KHNVWATHSC	VPTDPNPREL	SLENVTENFN
D_CD_84ZR0	WKEATTTLFC	ASDAKSYKTE	AHNIWATHAC	VPTDPNPQEI	ELKNVTENFN
D_CD_ELI_K	WKEATTTLFC	ASDAKSYETE	AHNIWATHAC	VPTDPNPQEI	ALENVTENFN
D_CD_NDK_M	WKEATTTLFC	ASDAKAYKKE	AHNIWATHAC	VPTDPNPQEI	ELENVTENFN
D_UG_94UG1	WKEATTTLFC	ASDAKAYKAE	AHNIWATHAC	VPTDPNPQEI	KLENVTENFN
F1_BE_VI85	WKEATTTLFC	ASDAKAYERE	AHNVWATHAC	VPTDPNPQEV	FLKNVTENFD
F1_BR_93BR	WKEATTTLFC	ASDAKSYEKE	AHNVWATHAC	VPTDPNPQEV	VLENVTERFN
F1_FI_FIN9	WKEANTTLFC	ASDAKSYEKE	VHNVWATHAC	VPTDPNPQEV	ALN.VTENFN
F1_FR_MP41	WKEATTTLFC	ASDAKGYERE	VHNVWATHAC	VPTDPNPQEI	WLKNVTENFD
F2_CM_MP25	WKEATTTLFC	ASDAKAYERE	VHNVWATYAC	VPTDPSPQEL	VLGNVSEKFN
F2KU_BE_VI	WKEANTTLFC	ASDAKPYDTE	VHNVWVTHAC	VPTDPNPQEV	FLQNVTENFN
G_BE_DRCBL	WEDANAPLFC	ASDAKAHSTE	SHNIWATHAC	VPTDPSPQEI	NMRNVTENFN
G_NG_92NG0	WEDADTPLFC	ASDAKSYSSE	KHNVWATHAC	VPTDPNPQEI	AIENVTENFN
G_SE_SE616	WEDADTTLFC	ASDAKSYSAE	SHNVWATHAC	VPTDPNPQEI	IMENVTEYFN
H_BE_VI991	WKEAKTTLFC	ASDAKAYDTE	RHNVWATHAC	VPTDPNPQEM	VLENVTETFN
H_BE_VI997	WKEAKTTLFC	ASDAKAYEPE	KHNVWATHAC	VPTDPSPQEM	VLANVTENFN
H_CF_90CF0	WKEAKTTLFC	ASDAKAYETE	KHNVWATHAC	VPTDPNPQEM	VMENVTESFN
J_SE_SE702	WRDAKTTLFC	ASDAKAYSTE	KHNVWATHAC	VPTDPNPQEM	SLPNVTENFN
J_SE_SE788	WKDAKTTLFC	ASDAKAYSTE	KHNVWATHAC	VPTDPSPQEM	NLPNVTENFN
K_CD_EQTB1	WKEATTTLFC	ASDAKAYETE	VHNVWATHAC	VPTDPNPQEV	VLENVTENFN
K_CM_MP535	WKEATPTLFC	ASDAKAYEKE	VHNVWATHAC	VPTDPNPQEV	EMENVTENFN
N_CM_YBF30	WREAETTLFC	ASDAKAHSTE	AHNIWATQAC	VPTDPNPQEV	LLPNVTEKFN
O_CM_ANT70	WEDATPVLFC	ASDANLTSTE	KHNIWASQAC	VPTDPTPYEY	PLHNVTDDEFN
O_CM_MVP51	WEEAAPVLFC	ASDANLTSTE	QHNIWASQAC	VPTDPNPHEF	PLGNVTDNFD
O_SN_99SE_	WEEATPVLFC	ASDANLTSTE	QHNIWASQAC	VPTDPSPYEY	PLTKVTDNFN
O_SN_99SE_	WEEATPVLFC	ASDVNLTSTE	QHNIWASQAC	VPTDPSPYEY	PLKNVTDNFN
U_CD___83C	WKDAETTLFC	ASDAKAYEKE	SHNVWATHAC	VPTDPSPQEL	VLGNVTENFN

00BW0762_1	MWKNYMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCINV	TN.....
00BW0768_2	MWKNDMVDQM	HEDVISLWDQ	SLKPCVKLTP	LCITLNCTSI	NG.....
00BW0874_2	MWKNDMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCTNY	NN.....
00BW1471_2	MWKNDMVDQM	HEDIISIWDQ	SLKPCVKLTP	LCVTLYCTNV	TKR.....
00BW1616_2	MWKNDMVNQM	HEDIISLWDQ	SLKPCVRLTP	LCVTLNCNNV	TT.....
00BW1686_8	MWKNDVVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLQCSNV	S.....
00BW1759_3	MWKNDMVDQM	HEDIISLWDQ	SLNPCVKLTP	LCVTLKCSNV	N.....
00BW1773_2	MWKNDMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLECEDA	N.....
00BW1783_5	MWKNDMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLTCSNL	NI.....
00BW1795_6	MWKNDMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLDCTNA	TI.....
00BW1811_3	MWKNDMVDQM	HEDIISLWDE	SLKPCVKLTP	LCVTLNCINA	TN.....
00BW1859_5	MWKNDMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLTCKDY	N.....
00BW1880_2	MWENG MVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCSNA	KA.....
00BW1921_1	MWKNDMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLKCSDA	K.....
00BW2036_1	MWKNDMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCTNA	NV.....
00BW2063_6	MWENDMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLKCRNA	NN.....
00BW2087_2	MWKNDMVDQM	HEDIISLWDE	SLKPCVKLTP	LCVTLNCVTV	NCT.....
00BW2127_2	MWKNDMVEQM	HEDIIRLWDE	SLKPCVRLTP	LCVTLRCSNA	GSG.....
00BW2128_3	MWKNDMVDQM	HEDIISLWDE	SLKPCVKLTP	LCVTLSCNAT	N.....
00BW2276_7	MWKNDMVDQM	HEDIISLWDE	SLKPCVKLTP	LCVTLNCSIV	N.....
00BW3819_3	MWKNDMVDQM	HEDIISLWDE	SLKPCVKLTQ	LCVTLECSNV	N.....
00BW3842_8	MWENDMVDQM	HEDVISLWDE	SLKPCVKLTP	LCVTLNCTNY	NG.....
00BW3871_3	MWKNDMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLMCSNV	T.....
00BW3876_9	MWENDMVDQM	HEDIISLWDQ	SPKPCVKLTP	LCVTLKCTDA	T.....
00BW3886_8	MWKNDMVDQM	HEDVISLWDE	SLKPCVKLTP	LCVTLKCGNV	NN.....
00BW3891_6	MWKNDMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLKCVSI	N.....
00BW3970_2	MWKNDMVDQM	HEDIISLWDE	SLKPCVKLTP	LCVTLECKNV	TTN.....
00BW5031_1	MWKNDMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCSAA	NN.....
96BW01B21	MWKNDMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLKCSTY	N.....
96BW0407	MWKNDMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCTKV	NGT.....
96BW0502	MWKNDMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLKCRNV	N.....
96BW06_J4	MWKNDMVDQM	HEDIISLWDQ	SLKPCVKLTS	LCVTLHCSNV	N.....
96BW11_06	MWENDMVNQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCT..	.....
96BW1210	MWKNDMVDQM	HEDIISLWDE	SLKPCVKLTP	LCVTLNCSNN	VTR.....
96BW15B03	MWKNDMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLKCTNY	ST.....
96BW16_26	MWKNDMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLDCTNV	T.....
96BW17A09	MWKNDMVDQM	HEDIISLRDQ	SLKPCVKLTP	LCVTLNCTNA	TN.....
96BWM01_5	MWENDMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCKNV	TS.....
96BWM03_2	MWKNDMADQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCTEA	KV.....
98BWMC12_2	MWKNDMVDQM	HEDIIRLWDQ	SLKPCVKMTP	LCVTLNCANF	NAS.....
98BWMC13_4	MWKNDMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLKCSNV	TV.....
98BWMC14_a	MWRNDMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLDCTNV	T.....
98BWM014_1	MWENDMVDQM	HQDIISLWDE	SLKPCVKLTP	LCVTLNCRNA	NLN.....
98BWM018_d	MWKNDMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLTCTNA	TKNVTN....
98BWM036_a	MWKNDMVDQM	HEDVISIWDQ	SLKPCVKLTP	LCVTLNCSNV	N.....
98BWM037_d	MRDNDMVDQM	HEDIINLWDQ	SLKPCVRLTP	LCVTLNCKDA	SVN.....
99BW3932_1	MWKNDMVDQM	HEDMIRLWDQ	SLKPCVKLTP	LCVTLKCREV	N.....
99BW4642_4	MWKNDMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLKCTNV	N.....
99BW4745_8	MWKNDMVDQM	HEDVISLWDQ	SLKPCVKLTP	LCVTLICSNV	I.....
99BW4754_7	MWKNDMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCKNV	TV.....
99BWMC16_8	MWKNDMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCSNV	TKNVTK....
A2_CD_97CD	MWKNNMVEQM	HADIISLWDQ	SLKPCVKLTP	LCVTLNCSNA	NTTNT.....
A2_CY_94CY	MWKNNMVEQM	QEDIISLWDQ	SLKPCVKLTP	LCVILNCSNA	NTSTH.....
A2D_97KR	MWKNGMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCSR	KNTIS.....
A2G_CD_97C	MWKNDMVEQM	HVDIISLWDQ	SLKPCVKLTP	FCVTLNCTNA	TFPNA.....
A_BY_97BL0	MXKNNXVEQM	QTDIISL.DQ	SLKPCVKLTP	LCVTLNCAEP	NSTRS.....
A_KE_Q23_A	MWKNNMVEQM	HTDIISLWDQ	SLKPCVKLTP	LCVTLHCTNV	TSV.....
A_SE_SE659	MWKNNMVEQM	HTDIISLWDQ	SLKPCVKLTP	LCVTLNCTNV	.....
A_SE_SE725	MWKNSMVEQM	HTDIISLWDE	SLKPCVKLTP	LCVTLNCTNA	.....



A_SE_SE753	MWKNYMVEQM	HTDIISLWDQ	SLEPCVKLTP	LCVTLECHYN	ITV.....
A_SE_SE853	MWKNSMVEQM	HTDIISLWDQ	SLIPCCKLTP	LCVTLECN DY	NYN.....
A_SE_SE889	MWKNNMVEQM	HTDIISLWDQ	SLKPCVKLTP	LCVTLNCSSV	TN.....
A_SE_UGSE8	MWKNNMVEQM	HTDIISLWDQ	SLKPCVQLTP	LCVTLNCSSN	VT.....
A_UG_92UG0	MWKNNMVEQM	HTDIISLWDQ	SLKPCVQLTP	LCVTLD CSYN	ITN.....
A_UG_U455_	MWKNNMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLDCHNI	TIN.....
AC_IN_2130	MWKNSMVEQM	HTDIISLWDQ	SLKPCVKLTP	LCVTLNCSSN	NG.....
AC_RW_92RW	MWKNNMVEQM	HTDIISLWDQ	SLKPCVKLTP	LCVTLECN NI	TNVNN.....
AC_SE_SE94	IWKNYMVEQM	HQDIISLWDQ	SLKPCVKLTP	LCVTLNC RDA	TV.....
ACD_SE_SE8	MWKNNMVEQM	HTDIISLWDQ	SLQPCVKLTP	LCVTLNCTNV	TIT.....
ACG_BE_VI1	MWKNDMVDQM	HQDIISLWDE	SLKPCVKLTP	LCVTLNCSSN	TAIN.....
AD_SE_SE69	MWKNNMVEQM	HTDIISLWDQ	SLKPCVQLTP	LCVTLNCNNV	TNKN.....
AD_SE_SE71	MWKNNMVKQM	HTDIISLWDQ	SLQPCVKLTP	LCVTLHCNDT	.N.....
ADHK_NO_97	MWENNMDVQM	HTDIISLWDQ	SLKPCVKLTP	LCVTLNCTDP	AN.....
ADK_CD_MAL	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCTNV	NGTAVNG.TN
AG_BE_VI11	MWKNNMVDQM	HEDIISLWDE	SLKPCVKLTP	LCVTLTCTNV	NCTNN.....
AG_NG_92NG	MWKNNMVEQM	HEDIISLWDE	SLKPCVKLTP	LCVTLNCTNV	NCNSN...VT
AGHU_GA_VI	MWKNNMVEQM	HTDIISLWDQ	SLKPCVQITP	LCVTLECSKI	N.....
AGU_CD_Z32	MWKNNMVEQM	HEDVISLWDQ	SLKPCVKLTP	LCVTLSCSDI	R.....
AJ_BW_BW21	IWKNDMVEQM	QEDIISVWDE	SLKPCVKLTP	LCVTLNCTNA	TVSNT.....
B_AU_VH_AF	MWKNNMVEQM	HEDIISLWDQ	SLKPCVQLTP	LCVTLNCTDE	LT.....
B_CN_RL42_	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCTNL	K.....
B_DE_D31_U	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCTDL	K.....
B_DE_HAN_U	MWKNDMVEQM	QEDIISLWDQ	SLKPCVKLTP	LCVTLKCTDY	N.....
B_FR_HXB2_	MWKNDMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVSLKCTDL	K.....
B_GA_OYI_	MWKNNMVEQM	QEDIISLWDQ	SLKPCVKLTP	LCVTLDCTDV	NTTSSS....
B_GB_CAM1_	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLIC TNV	NN.....
B_GB_GB8_C	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCTDL	R.....
B_GB_MANC_	MWKNNMVEQM	QEDVISLWDQ	SLKPCVKLTP	LCVTLDCTDY	VG.....
B_KR_WK_AF	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLKCTDL	NDTNTN....
B_NL_3202A	MWKNNMVEQM	HEDIINLWDQ	SLKPCVKLTP	LCVTLNCTDF	G.....
B_TW_TWCYS	MWKNNMADQM	QEDIISLWDE	SLKPCVELTP	LCVTLKCN DT	.....
B_US_BC_L0	MWKNNMVEQM	QEDIISLWDQ	SLKPCVKLTP	LCVTLNCTDE	LKNA.....
B_US_DH123	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLHCTDL	K.....
B_US_JRCSF	MWKNNMVEQM	QEDVINLWDQ	SLKPCVKLTP	LCVTLNCKDV	.....
B_US_MNCG_	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCTDL	R.....
B_US_P896_	MWKNNMVDQM	HEDIISLWDE	SLKPCVKLTP	LCVTLNCTNL	.....
B_US_RF_M1	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCTDA	NLN.....
B_US_SF2_K	MWKNNMVEQM	QEDIISLWDQ	SLKPCVKLTP	LCVTLNCTDL	G.....
B_US_WEAU1	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCTNV	NVTN.....
B_US_WR27_	MWKNNMXEQM	HEDIIXLWDQ	SLKPCVKLTP	LCVTLNCTDV	.....
B_US_YU2_M	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCTDL	.....
BF1_BR_93B	MWKNNMVEQM	HTDIISLWDQ	SLKPCVKLTP	LCVTLRCSNA	TT.....
C_BR_92BR0	MWENDMVEQM	HQDIISLWDQ	SLKPCVKLTP	LCVTLHCSNR	T.....
C_BW_96BW0	MWKNDMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCTEV	NGTSDSS...
C_BW_96BW1	MWENDMVNQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCTNV	TV.....
C_BW_96BW1	MWKNDMVDQM	HEDIISLWDE	SLKPCVKLTP	LCVTLNCSSN	VTR.....
C_BW_96BW1	MWKNDMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLKCTNY	ST.....
C_ET_ETH22	MWKNDMVEQM	HQDIISLWDQ	GLKPCVKLTP	LCVTLNCNAI	KNNTKVT...
C_IN_93IN1	MWKNDMVDQM	HEDVISLWDQ	SLKPCVKLTP	LCVTLECRNV	S.....
C_IN_93IN9	MWKNDMVNQM	HEDVISLWDQ	SLKPCVKLTP	LCVTLECKNV	K.....
C_IN_93IN9	MWKNDMVNQM	HEDVISLWDQ	SLKPCVKLTP	LCVTLECSY	NGTSKAN...
C_IN_94IN1	MWKSDMVNQM	HEDVISLWDQ	SLKPCVKLTP	LCVTLECGNV	T.....
C_IN_95IN2	MWKNDMVNQM	HEDVISLWDQ	SLKPCVKLTP	LCVTLECRNV	NST.....
CRF01_AE_C	MWKNNMVEQM	QEDVISLWDQ	SLKPCVKLTP	LCVTLHCTKA	KLNDTYN...
CRF01_AE_C	MWKNNMVEQM	QEDVISLWDQ	SLQPCVKLTP	LCVTLHCTKA	SFTNATS...
CRF01_AE_C	MWKNNMVEQM	QEDVISL.DQ	SLKPCVKLTP	LCVTLDCTKA	DFYTTKF...
CRF01_AE_T	MWKNNMVEQM	QEDVISLWDQ	SLQPCVKLTP	LCVTLHCTTA	KLTNVTN...
CRF01_AE_T	MWKNNMVEQM	QEDVISLWDQ	SLKPCVKLTP	LCVTLNCTNA	NLTNVNN...
CRF01_AE_T	MWKNNMVEQM	QEDVISLWDQ	SLKPCVKLTP	LCVTLNCTNA	NWTNANV...

CRF01_AE_T	MWKNNMVEQM	QEDVISLWDQ	SLKPCVKLTP	LCVTLNCTTA	NFTNFNL...
CRF01_AE_T	MWKNNMVEQM	QEDVISLWDQ	SLKPCVKLTP	LCVTLNCTNA	NLTNGSS...
CRF01_AE_T	MWKNNMAEQM	QEDVISLWDQ	SLKPCVKLTP	LCVTLNCTNV	NATNVS...
CRF02_AG_F	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLDCHNV	NSS.....
CRF02_AG_F	MWKNNMVEQM	HEDIISLWDQ	SLKPCVELTP	LCVTLDCHNV	SS.....
CRF02_AG_G	MWKNNMVEQM	HVDIISLWDQ	SLKPCVKLTP	LCVTLDCHNV	KN.....
CRF02_AG_N	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLDCHNF	NN.....
CRF02_AG_S	MWKNSMVEQM	HEDIISLWDQ	SLKPCVQLTP	LCVTLHCQDN	LT.....
CRF02_AG_S	MWKNNMVEQM	HVDIISLWDQ	SLKPCVKLTP	LCVTLECHNY	NYT.....
CRF03_AB_R	MGKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCTDL	KK.....
CRF03_AB_R	MGKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCTEV	KT.....
CRF04_cpx_	MWKNDMVEQM	HEDIISLWNE	GLKPCAKLTS	LCVTFTCINA	T.....
CRF04_cpx_	MWENSTVEQM	HEDIISLWDE	GLKPCVKLTP	LCVALNCSNA	TIINS....
CRF04_cpx_	MWKNNMVEQM	HEDIISLWEE	GLKPCVKLTP	LCVALNCGDA	TIK.....
CRF05_DF_B	MWKNDMVEQM	HTDIISLWDQ	SLKPCVKLTP	LCVTLNCTDF	KA.....
CRF05_DF_B	MWKNNMVEQM	HADIISLWDQ	SLKSCVKLTP	LCVTLNCTDA	TS.....
CRF06_cpx_	MWKNNMVDQM	HEDIISLWDE	SLKPCVKLTP	LCVTLTCTNA	TLGNKTLGNN
CRF06_cpx_	MWENHMVEQM	HEDIISLWDE	SLKPCVKLTP	LCVTLICITNI	NITSTNS...
CRF06_cpx_	MWKNNMVEQM	HEDIISLWDE	SLKPCVKLTP	LCVTLNCTNV	TDHGIN....
CRF06_cpx_	MWKNNMVEQM	HEDIISLWEE	SLKPCVKLTP	LCVTLNCTNV	NAT.....K
CRF11_cpx_	MWKNNMVEQM	HEDIISLWDE	SLKPCVKLTP	LCVTLNCAEV	TS.....
CRF11_cpx_	MWKNNMVEQM	HEDVISLWDE	SLKPCVKLTP	LCVALNCTDA	R.....
D_CD_84ZR0	MWKNNMVDQM	HEDIISLWDQ	SLKPCVKLTP	RCVTLNCTDA	SRN.....S
D_CD_ELI_K	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCSDE	LRNNG....T
D_CD_NDK_M	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCTDE	LRN.....S
D_UG_94UG1	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCTNW	VTD.....
F1_BE_VI85	MWKNNMVEQM	HTDIISLWDQ	SLKPCVKLTP	LCVTLNCTNA	TN.....
F1_BR_93BR	MWENNMVEQM	HTDIISLWDQ	SLKPCVKLTP	LCVTLDCHNV	AT.....
F1_FI_FIN9	MWENDMVEQM	HKDIISLWDQ	SLKPCVKLTP	LCVTLNCTNA	TT.....
F1_FR_MP41	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLHCSDV	NI.....
F2_CM_MP25	MWKNNMVDQM	HEDIISLWDE	SLKPCVKLTP	LCVTLNCTKA	II.....
F2KU_BE_VI	MWKNNMVEQM	HADIISLWDQ	GLQPCVKLTP	LCVTLNCSSEK	IN.....
G_BE_DRCBL	MWKNNMVEQM	HEDIISLWDE	SLKPCVKLTP	LCVTLNCTEI	N...N....
G_NG_92NG0	MWKNNMVEQM	QEDIISLWEE	SLKPCVKLTP	LCITLNCTNV	N.....
G_SE_SE616	MWKNNMVEQM	HEDIISLWDE	SLKPCVKLTP	LCVTLNCTDV	TNKGNGR.NN
H_BE_VI991	MWVNDMVEQM	HTDIISLWDQ	SLKPCVKLTP	LCVTLDCHNV	NA.....
H_BE_VI997	MWDNDMVEQM	QTDIISLWDQ	SLKPCVKLTP	LCVTLDCHNV	TR.....
H_CF_90CF0	MWENNMVEQM	HTDIISLWDQ	SLKPCVKLTP	LCVTLNCTNV	RN.....
J_SE_SE702	MWKNDMVDQM	QEDIISVWDE	SLKPCVKITP	LCVTLNCSDV	NSNNS.....
J_SE_SE788	MWKNDMVDQM	QEDIISVWDE	SLKPCVKITP	LCVTLNCSNI	TSNSN.....
K_CD_EQTB1	MWKNNMVEQM	HTDIISLWDE	SLKPCVKLTP	LCVTLTCTNV	TN.....
K_CM_MP535	MWKNNMVEQM	HTDIISLWDE	SLKPCVELTP	LCVTLNCTDY	KG.....
N_CM_YBF30	MWENKMADQM	QEDIISLWEQ	SLKPCVKLTP	LCVTMLCNDN	YGEER.....
O_CM_ANT70	IWKNYMVEQM	QEDIISLWDQ	SLKPCVQMTF	LCVQMECTN.	.....
O_CM_MVP51	IWKNYMVDQM	HEDIISLWEQ	SLKPCVQMTF	LCVQMNCTNY	.....
O_SN_99SE_	IWKNYMVEQM	QEDIISLWEQ	SLKPCVQMTF	LCVQMNCTNY	VQ.....
O_SN_99SE_	IWENYMVEQM	QEDIISLWEQ	SLKPCVQMTF	LCVQMNCTN.	.....
U_CD___83C	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTF	LCVTLNCTDV	KN.....

00BW0762_1	.....ATNVT	N.....	A.....	DYKNCSFNIT	TELDRKRRKE
00BW0768_2	.....THK	V.....	TNDTLYG...	EIKNCSFNVT	TEIRDKKRKE
00BW0874_2	.....T	E.....	GNTTYGG...	EMRNCSFNIT	TELDRKKRQE
00BW1471_2	.....VI	T.....	YNNNMTE...	EMKNCSFNIT	TELDRKKTKKE
00BW1616_2	.....YNGTY	S.....	D.....	GMKSCSFNIT	TELDRKRRKE
00BW1686_8	..RDATSSSS	E.....	GMREGMR...	EIKNCSFNVT	TELDRKRRKNV
00BW1759_3	....KT.NFT	D.....	TTNG.....	EIKNCSFNIT	TEVRDRKKNE
00BW1773_2	....NGS...	.....	...VTQG...	EIKNCSFNVT	TELDRKIQKV
00BW1783_5	.TNSTAFNTT	I.....	K.....E...	EMKNCSFNMT	TEIRDKRKE
00BW1795_6	.TDNTIDEGM	G.....	N.....	EIKNCSFNIT	TELDRKKKRE
00BW1811_3	.....SN	T.....	YNNSIKE...	EMKNCSFNIT	TEIRDKKKQV
00BW1859_5	.....KN	I.....	TYD..NN...	EIKNCSFNIT	TELDRKRRKNV
00BW1880_2	.....NSNAS	M.....	EG.....	EIENCSFNIT	TELDRKKRQE
00BW1921_1	..GNGN....	.....	...RTG...	EIKNCSFNVT	TELDRKRRQV
00BW2036_1	.TYHNVTY..	.....	...NNTD...	EVKNCSFNMT	TELDRKKQNV
00BW2063_6	.NASNTYQVT	T.....	PT..PPD...	IMKNCSFNIP	TELDRKSKKE
00BW2087_2	....NNVTSC	L.....	CNNTICE...	QMRNCSFNAT	TEIRDKKQKV
00BW2127_2	....NATANR	A.....	THNPMEG...	EIKNCSFNAT	TEIKDRKKQV
00BW2128_3	....KSNSTN	V.....	TSENKEG...	EMKNCSFNIT	TELINKKQRE
00BW2276_7	.....GT	.....	.....	DMTNCTFNAT	TEIKDKRRKV
00BW3819_3	....VTSSV	N.....	ITKNMMD...	EIKNCSFNVT	TEVRDKKKQV
00BW3842_8	.TKNNDTK..	I.....	YNDTMYG...	EIKNCSFNMT	TELDRKKKEM
00BW3871_3	..RNQTKNQ	N.....	YTYEGIG...	EIKNCSFNMT	TELDRKKKNV
00BW3876_9	.....VND	T.....	VNHSME...	ETKNCSFNAT	TEIRDKKRRKV
00BW3886_8	.DTEN.....	.....	...MKE...	EMRNCTFNIT	TEIRDKEKQM
00BW3891_6	....AT.SNG	T.....	VTIN..G...	EIKNCSFNVT	TELDRKRRKE
00BW3970_2	.....VTINN	V.....	TANNNTS...	DMKNCSFNAT	TEVTDKIRKE
00BW5031_1	.....	.....	TVAEMKG...	EIKNCSFNAT	TEMRDKRQKE
96BW01B21	....G..TYT	D.....	N...YQE...	KIKNCSFNIT	TEIRDKKQSG
96BW0407	....NGTSN	N.....	SSVPMEE...	EMKNCSFNIT	TELDRKKQQG
96BW0502	....ATNNIM	I.....	D.NSNKG...	EMKNCSFNVT	TELDRKRRQV
96BW06_J4	..GSNN.ANS	S.....	YSNDMKE...	EIKNCSFNMT	TELDRKKQKV
96BW11_06	.NDTLHQNL	T.....	.....	..MKNCSFNVT	TELDRKKRKE
96BW1210	....N.....	.....	YNNKNNG...	EIKNCSFNAT	TEIRDKKQKV
96BW15B03	.NYSNTMN..	S.....	YNNNTTE...	EIKNCTFNMT	TELDRKKQV
96BW16_26	....SNATMG	N.....	TLENGGG...	EMKNCSFNMT	TEIRDKKKQV
96BW17A09	.....TN	N.....	VTSSMIG...	GMKNCSFNIT	TELDRKRRKE
96BWM01_5	.KDINTSNAE	M.....	K.....A...	EMKNCSFNIT	TELDRKKKQE
96BWM03_2	.NMKKDT...	.....	...MKE...	EIKNCSFKNV	TELKDKKHKE
98BWM12_2	.....STS	T.....	GTNSMNG...	QIKNCSFNIT	TELDRKRRQE
98BWM13_4	.NTTYNNAID	G.....	ET..IDK...	EMKNCSFNIT	TELDRKKKQE
98BWM14_a	..VDANSTYV	I.....	HVGNIIT...	EMKNCSFNMT	TELDRKRRKNV
98BWM014_1	....STRKS.	.....	..NPSMQG...	DIKNCSFNIT	TELDRKRRKV
98BWM018_d	.....N	N.....	DTTYNIE...	EMRNCSFNIT	TEIRDKRRQE
98BWM036_a	.....N.	T.....	IDGAMKE...	GMKNCSFNIT	TEVRDKKKNQ
98BWM037_d	....YTNA	G.....	WPTETE...	KLQNCNFNVT	TVIRDKHHKE
99BW3932_1	.....ATK	N.....	GNITMKG...	EIKNCSFNAT	TEIKHKKKEM
99BW4642_4	.....AT	N.....	VNRTMTE...	EIKNCSFNIT	MELDRKRRQV
99BW4745_8	....TI.TNT	T.....	IYKYTTS...	DIRNCPFNVT	TELKDKRRKE
99BW4754_7	....NTTVT	V.....	TNNTMDT...	VMKNCSFNVT	TELDRKRRQE
99BWM16_8	.....N	.....	LNNNMKE...	EIKNCSFNIT	TELDRKKQNV
A2_CD_97CD	..NS.....	.....	.....TE	EIKNCSYNMP	TELKDKTKQV
A2_CY_94CY	...SNSSSTQ	S.....	.....PINE	EIKNCSYNIT	TILDRKTKQV
A2D_97KR	...STQS...	.....	.....PDSN	NTMNCSEFTT	TELDRKKQKV
A2G_CD_97C	...TGNN...	S.....	.....IFTE	EMKNCSYNIT	TELDRKTKTV
A_BY_97BL0	...NNSSVNS	N.....	SSDSLFX...	XMKNCSFNMT	TELDRKRRKT
A_KE_Q23_A	...NTTGDR.	.....	.....E	GLKNCSFNMT	TELDRKRRQV
A_SE_SE659	...NS..TRV	V.....	NITDKE...	EIKNCSFNMT	TELVDRKQV
A_SE_SE725	...NG..TQN	V.....	NITN.V...	GMRNCSFNMT	TELDRKKQKG

A_SE_SE753	...KNITVSS	N.....	NNISISNSTE	DMRNCSFNMT	TELRDKQQKV
A_SE_SE853	...VTNSSHS	Y.....	NVTNMQ....	EMKNCSFNVT	TELRDKRQKV
A_SE_SE889	.....SSVT	N.....	ITSDMAG...	EIKNCSFNMT	TEIRDKRQKV
A_SE_UGSE8	...NTNSTSA	N.....	LTDsvKG...	EMRNCSFNIT	TELRDKKKKV
A_UG_92UG0	...NITNSIT	N.....	SSVNMRE...	EIKNCSFNMT	TELRDKNRKV
A_UG_U455_	...NTN.NNT	N.....	ITDgVR...E	EMKNCSFNMT	TELRDKKQKV
AC_IN_2130	...NSTGWGK	.....	.....E	EIKNCSFNIT	TELRDKRQKV
AC_RW_92RW	...TVN....	.....	ITDDMKG...	EIKNCSFNMT	TELRDKKQRV
AC_SE_SE94	...TPNNATH	N.....	DSM..V...G	DMKNCPFNMT	TELRDKRRKE
ACD_SE_SE8	...TNATDSN	N.....	..ASLQDMAK	EMTNCSFNMT	TELRDKKQRV
ACG_BE_VI1	....SNGTAI	N.....	ITESIKG...	EMKNCSFKAT	TEIKDKKKKE
AD_SE_SE69	....ETSMN	G.....	.....	EIKNCSFNMT	TELRDKEQQV
AD_SE_SE71	...VTNATNI	T.....	NANTITG...	EMKNCSFNMT	TELRDCKRKV
ADHK_NO_97	...HTDTTNN	.....	...TSIQPSQ	PSANCSFNVT	TAIRDKQQKV
ADK_CD_MAL	AGSNRTNAEL	KM.....	.....EIG	EVKNCSFNIT	PVGSDKR.QE
AG_BE_VI11	.STREIRGKN	CSLD.....	.....TEVG	ELKNCSFNIT	TELRDKKKTE
AG_NG_92NG	STGNSAGTNA	TCNI.....	.....EEAN	NLKNCSFNIT	TEIRDKKKTE
AGHU_GA_VI	...ITNNSTD	KANV.....	...TNN..DA	EMRNCSFNIT	TEIRDKRKKE
AGU_CD_Z32	.....NSTES	N.....	ITAEMQG...	EIKNCSYNMT	TELRDKQRKI
AJ_BW_BW21	.....GCTNN	NCT.....	.....VS	EMKECHFNT	GGGR..RKKE
B_AU_VH_AF	...NVFTFNS	RHVTNS...	.SYVGSMEKG	EMKNCSFNIT	TSIRDKRHKE
B_CN_RL42_	...NATNTSS	T.....	.....MEGG	EIKNCSFNIT	TSIKTKVK.D
B_DE_D31_U	...NATNTNN	SSWT.....	...MTGEMKG	EIKNCSFNIT	TSIRDKVQKE
B_DE_HAN_U	...NATNSS.	.....	...WGRMEKG	EIQNCSFKVT	TNIRDKVQKE
B_FR_HXB2_	...NDTNTNS	SS.G.....	...RMIMEKG	EIKNCSFNIS	TSIRGKVQKE
B_GA_OYI_	.LRNATNTTS	SS.....	...WETMEKG	ELKNCSFNIT	TSIRDKMQEQ
B_GB_CAM1_	...TRTNSSD	WDRR.....	...EGEKMKG	EIKNCSFNVT	TSIRNKVRKE
B_GB_GB8_C	...NDTNTNN	SIME.....	.....GG	EMKNCSFNIT	TSIRDKMQKE
B_GB_MANC_	...NATNTTS	TNNTAS...	.GSWGAMR.G	EIKNCSFNIT	TNIRDKVHKE
B_KR_WK_AF	.N.SSTSENN	TNPTIS...	..GGEGMGEG	EMKNCSFNVT	TNIRDKVQKE
B_NL_3202A	...NATNTTS	S..S.....	...GVIEKG	EIKNCSFKIN	TNMKDKAQIE
B_TW_TWCYS	...TMSKNDS	N.....	...TLTMEKG	EIKNCSFNVT	TSLRNKVQKE
B_US_BC_L0	.TNTTSTNTP	SGS.....	...WKKMERG	EIKNCSFNVL	G...DKKQKA
B_US_DH123	...NGTNLKN	GTK.....	..IIGKSMRG	EIKNCSFNVT	KNIIDKVQKE
B_US_JRCSF	...NATNTTS	.....	.SSEGMMERG	EIKNCSFNIT	KSIRDKVQKE
B_US_MNCG_	...NTTNTNN	STANN.NS..	.NSEGTIKGG	EMKNCSFNIT	TSIRDKMQKE
B_US_P896_	...NITKNTT	N....PTS..	.SSWGMMEKG	EIKNCSFYIT	TSIRNKVKKE
B_US_RF_M1	....GTNVTS	SSG.....	...GTMMENG	EIKNCSFQVT	TSRRDKTQKK
B_US_SF2_K	...KATNTNS	SN.....	...WKEEIKG	EIKNCSFNIT	TSIRDKIQKE
B_US_WEAU1	.LKNETNTNS	SSG.....	...GEKMEEG	EMKNCSFNVT	TLIRNKRKTE
B_US_WR27_	...WNATSTS	KNTTITNS..	.SNERPMEKG	EMKNCSFSIT	TSIRDKVQKE
B_US_YU2_M	.R.NATNTTS	SS.....	...WETMEKG	EIKNCSFNIT	TSIRDKVQKE
BF1_BR_93B	...IDT....	.QND.....	...TLKEEPG	AIQNCSFNMT	TEVRDKQLKV
C_BR_92BR0	....NDYN..	N.....	RTDNMGG...	EIKNCSFNMT	TEVRDKREKV
C_BW_96BW0	V..PANGTSN	.....	SSVSMKE...	EMRNCSFNIT	TELRDKNKQE
C_BW_96BW1	.NDTLHQNFT	D.....	.....	.MKNCSFNVT	TELRDKRKHE
C_BW_96BW1	....NS..NA	T.....	YNNKNNG...	EIKNCSFNAT	TEIRDKQQKV
C_BW_96BW1	.NYSNTMNAT	S.....	YNNNTTE...	EIKNCTFNMT	TELRDKKQQV
C_ET_ETH22	.....N	N.....	SINSAND...	EMKNCSFNIT	TELRDKKRKA
C_IN_93IN1	....RNVSSY	N.....	TYNGSVE...	EIKNCSFNAT	PEVRDRKQRM
C_IN_93IN9	...NDSTHN	E.....	TYTESVK...	EIKNCSFNAT	TEIRDKQTV
C_IN_93IN9	ATNNVNATSN	G.....	NATSNGE...	EIQQCFFNVT	TEMRDKKQRV
C_IN_94IN1	....QNGTYN	D.....	...ESNK...	EITNCTFNIT	TEIRGRKQKV
C_IN_95IN2	....GNGTHS	K.....	TYNESMK...	EIKNCSFNAT	TVIKDKKQTV
CRF01_AE_C	GTAKL....N	.....	....DTIGD	EVNCSFNVT	TELRDKKQEV
CRF01_AE_C	DRIK.....	.....	.....MED	AVRNCSFNMT	TELQDKKQEV
CRF01_AE_C	NTTEK....P	E.....	..IEISEMQK	EVSNCPFNIT	TELRDKEQEV
CRF01_AE_T	I.....TNVP	N.....	..IG..NITD	EVNCSFNMT	TEIRDKKQKV
CRF01_AE_T	.....NVS	N.....	..IIG.NITD	EVNCSFNMT	TELRDKKQQV
CRF01_AE_T	TNVN..NNVT	N.....	..IVG.NITE	EVNCSFNMT	TELIDKKQKV

CRF01_AE_T	TKADNMTNVS	N.....	..ITIGNITD	EVNCTFNMT	TDLIDKKQKV
CRF01_AE_T	K.....TNVS	N.....	..IIG.NITD	EVNCTFNMT	TELTDKKQKV
CRF01_AE_T	T.....TEAP	N.....	..IV...GTD	EVKNCSFNVT	TELRDKTQQV
CRF02_AG_F	...NSSTSNS	SNSSTPINRT	IDSDMQE...	EIKNCSFNMT	TELRDKKQKV
CRF02_AG_F	...NSSISVK	S.....	ISRDMQG...	EIKNCSFNMT	TELRDKKQKV
CRF02_AG_G	.....	.....	ISDGSNS...	EIKNCSFNMT	TELRDKKQKV
CRF02_AG_N	....SYSNSS	N.....	LTSDMNG...	EIKNCSFNIT	TEVRDKKKKM
CRF02_AG_S	....SS.GN.	.....	ISENMQG...	EIKNCSFNMT	TELRDKKQKV
CRF02_AG_S	...RNN....	.....	SKINEVQ...	EMKNCSFNMT	TVLKDKKKKM
CRF03_AB_R	...EVTSTNT	S.....	.....SIKMM	EMKNCSFNIT	TDLRDKVKKE
CRF03_AB_R	...NDTSTNA	S.....	.....GIEMM	KN..CSFNIT	TDLRDKVKKE
CRF04_cpx	....TTNSTN	GTVI.....	...K.....E	GIKNCSFDIT	TEIRDKKKKE
CRF04_cpx	TNNSTTNSTG	NSTV.....	...KS...TA	EIKNCSFNIT	TEVRDKQKKE
CRF04_cpx	....STNSTP	NVTT.....	...T....N	EMKNCSFNIT	TEIRDKKKKA
CRF05_DF_B	...NSTANST	TNST.....	...TLKEETG	AVQNCSFNMT	TEVNDKKLKV
CRF05_DF_B	...ATTTSKN	ISATPTSN..	PNDTLKEEQG	AIQNCTFNIT	TEVKDKNKR
CRF06_cpx	STNSTLGNNS	TIVD.....	.....DISK	EIKNCSFNIT	TEIRDKTKKE
CRF06_cpx	.....T.KNI	TVES.....	.....GE	EIKNCSFNVT	TEIRDKQKEE
CRF06_cpx	.....NNN	TVEG.....	.....KE	EIKNCSFNVT	TEIKDKKKKE
CRF06_cpx	YSNETVGKSL	TVKD.....	.....RE	EIKNCSFNIT	TEVRDQKKTE
CRF11_cpx	.....	.....	.....YNTT	EMKNCSFNVT	TELIDRRKQE
CRF11_cpx	.....	.....	.....DNAT	DIKNCTFNIT	TELEDKKKNE
D_CD_84ZR0	TDNNSTLPTV	KP.....	.....GE.	.MKNCSFNIT	TVVTDKKRQV
D_CD_ELI_K	MGNNVTTEEK	G.....	.....	.MKNCSFNVT	TVLKDKKQKV
D_CD_NDK_M	KGNGKVEEEE	K.....	.....	.RKNCSFNVR	...DKREQV
D_UG_94UG1	....TTNTT	G.....	.....	.MANCSFNIT	TEIRDKKKQV
F1_BE_VI85	...NSQ....	.....	...EK...PG	AMQNCSFNMT	TEVRDKKLKL
F1_BR_93BR	...NGTNDTI	AIND.....	...TLKEDPE	AIQNCSFNIT	TEIRDKQLKV
F1_FI_FIN9	...TNDTLS.	DQSS.....	...TLKEEPG	AIQNCSFNMT	TEVEDKKQKV
F1_FR_MP41	...TSNATTT	NDTS.....	...TP.EESG	AIQNCSFNMT	TEVKDKKLKV
F2_CM_MP25	...NVTSSNN	TTLA.....	...PNVTISE	EMKNCSFNIT	TEIRDKQKKE
F2KU_BE_VI	...INSTDLT	NWANKTNNWA	NETTLLNITT	GMRNCSFNIT	TMLKDKKKKQ
G_BE_DRCBL	.....NS	TRNI.....	.....TEEY	RMTNCSFNMT	TELRDKKKAE
G_NG_92NG0	.SANHTEANN	..TV.....	.....ENKE	EIKNCSFKIT	TERGGKKKEE
G_SE_SE616	STDNSTETNN	S.TV.....	.....DNPG	EIKNCSFNVT	TEIRDKKKKE
H_BE_VI991	...TNVTKSN	NSTD.....	...INIGELQ	EQRNCSFNVT	TAIRDKNQKV
H_BE_VI997	...NDTNSSS	TVNA.....	...TSSPSAN	ELTNCSFNVT	TVIRDKQQRV
H_CF_90CF0	...NTSNSTS	SMEA.....	...GG.....	ELTNCSFNVT	TVLRDKQQKV
J_SE_SE702	....TDSNS	SASN.....	.....NSPE	IMKNCSFNVT	TEIRNKRKQE
J_SE_SE788	....TTSNS	SVS.....	.....SPD	IMTNCSFNIT	TEIRNKRKQE
K_CD_EQTB1	...NRTNANK	NDT.....	NINATVTSTD	EIKNCSFNIT	TELKDKKKRV
K_CM_MP535	...TNSTN..	.....	NATSTVVSPA	EIKNCSFNIT	TEIKDKKKKE
N_CM_YBF30	...NNTNMTT	R.....	...EPDIGYK	QMKNCSFNAT	TELTDKKKQV
O_CM_ANT70	....IAG...	.....	....TTNEN	LMKKCEFNTV	TVIKDKKEKK
O_CM_MVP51	...LQTNKTG	.....	LLN...ETIN	EMRNCSFNVT	TVLTDKKEQK
O_SN_99SE	..GNYTNSSS	.....	INNDTSSPEN	LVKQCEFNTV	TVVKDKKEKK
O_SN_99SE	..VNDETNS	.....	VKNDTSSSEN	LMKKCEFNTV	TVLKDKEQKQ
U_CD___83C	.....STNN	N.....	.....TEEA	TITNCSFKVP	TELKDKTETV

	201			250
00BW0762_1	YALFYRLDIV	QLGE.....	NNAN SE.....	YRLI
00BW0768_2	HALFYRLDIV	PLDEKDK...	SSN SN.....	YRLI
00BW0874_2	SALFYRLDIV	PLNGS.....	ERNK SE.....	YRLI
00BW1471_2	RALFYRLDIV	PLNESDN...	NSY RE.....	YRLI
00BW1616_2	YAIFHSLDIV	PLEN.....	SEN SE.....	YRLI
00BW1686_8	YALFYKLDIV	PLEE.....	NDI ST.....	YRLI
00BW1759_3	HALFYRLDIV	PLEGE.....	NNTN NE.....	YRLI
00BW1773_2	HALFYRLDIV	QLD.....	N SS.....	YRLI
00BW1783_5	YALFYKLDIV	PLEGNNS...	E.. ..	YRLI
00BW1795_6	YALFYRLDIV	SLDNENN...	KT. AE.....	YRLI
00BW1811_3	YALFYKPDIV	PLDGS.....	NS SE.....	YRLI
00BW1859_5	YALFYKIDIV	PLND....N.	NSN.N SM.....	YRLI
00BW1880_2	YALFYRLDVV	PLDSPS....	NATN SR.....	YRLI
00BW1921_1	YALFYRLDVV	QLN.....	SE.....	YRLI
00BW2036_1	YALFYKLDIV	PLNGNSG...	SE.....	YRLI
00BW2063_6	YALFYKLDIV	PLGNTNG...	T.. .E.....	YRLI
00BW2087_2	YALFYKLDIV	SLDD.....	NN S.....	YRLI
00BW2127_2	YALFYRLDVV	PLDND.....	SA TN.....	YRLI
00BW2128_3	YALFYKLDIV	PLNNS.....	SDNSS GE.....	YRLI
00BW2276_7	QALFYKLDIV	PLNSTGE...	NNN TE.....	YRLI
00BW3819_3	YALFYRLDVV	PLNGK.....	NS SS.....	YRLI
00BW3842_8	HALFYRLDIV	PLEDNSG...	NSS SN.....	YRLI
00BW3871_3	YALFYKLDIV	PLND.....	N.. NE.....	YRLI
00BW3876_9	NALFYKLDVV	PLHE.....	GN S.....	YRLI
00BW3886_8	YALFYRLDIV	PLHDSSS...	DG. SE.....	YVLI
00BW3891_6	HALFYRLDIV	PLNG.....	KNQS NE.....	YRLI
00BW3970_2	NALFYTLDIV	PLDENQ....	N.....	YRLI
00BW5031_1	FALFNILDIV	PLNNEN....	NTKN SD.....	YRLI
96BW01B21	YALFYKFDVV	PLN.....	GNNT SE.....	YILI
96BW0407	RALFYSLDIV	QPNN.....	S TE.....	YRLI
96BW0502	HALFYRLDVV	PLQG.....	NN NE.....	YRLI
96BW06_J4	YALFYRLDVV	PLGD.....	N.. SS.....	YRLI
96BW11_06	YALFYRLDIV	PLNNKNE...	S.. SE.....	YRLI
96BW1210	YALFYRLDIV	PLDN.....	NS SE.....	YRLI
96BW15B03	YALFYKLDIV	PLNSNS....	SE.....	YRLI
96BW16_26	YALFYRLDVV	PLNGE.....	NSNSS GE.....	YRLI
96BW17A09	SALFYRLDIV	PLNENNS...	SSN SE.....	YRLI
96BWM01_5	YALFYKLDIV	PLTNDAS...	EN. SE.....	YRLI
96BWM03_2	YALFYKLDIV	PLDGNNE...	DGN KQ.....	YRWI
98BWMC12_2	SALFYRLDIV	PLK.....	ENS SE.....	YRLI
98BWMC13_4	QALFYRLDIV	PLDNANG...	T.. SE.....	YRLI
98BWMC14_a	YALFYRLDIV	PLGE.....	D.. SS.....	YRLI
98BWM014_1	YALFYKLDIV	ELDG.....	NS SN.....	YVLI
98BWM018_d	SALFYKLDIV	PLD.....	NSS SK.....	YILI
98BWM036_a	YVLFYKLDIV	PLNGNG....	SN SE.....	YRLI
98BWM037_d	YALFYRPDIV	PLNEG.....	N.....	YRLI
99BW3932_1	YALFYRLDIV	PLKN.....	S SE.....	YRLI
99BW4642_4	NALFYKLDIV	PLNE....K.	ANNSY SY.....	YRLI
99BW4745_8	YALFYRIDIV	PLDE.....	NNNS SE.....	YRLI
99BW4754_7	HALFYRLDIV	PLETK.....	NSNE SA.....	YRLI
99BWMC16_8	YALFYKVIV	PLSE.....	NST SE.....	YRLI
A2_CD_97CD	YSLFYELDVV	LLNRSKN...	SSY ST.....	YRLI
A2_CY_94CY	YSLFYRLDVV	QLDESENKNT	SGSN TL.....	YRLI
A2D_97KR	QALFYELDIV	QLNSSDSND.	TLN RQ.....	YRLI
A2G_CD_97C	RSLFYTLDIV	QINKDNN...	T.....	YRLI
A_BY_97BL0	HSLFYKLDIV	STSNNDXS...	.Q.....	YRLI
A_KE_Q23_A	YSLFYRLDIV	PINEN.....	QG..... SE.....	YRLI
A_SE_SE659	HSLFYRLDIV	QMNE.....	RGNSSNSSY NE.....	YRLI
A_SE_SE725	YSLFYKLDIV	QINDN.....	GNNSNNS.. SE.....	YRLI

A_SE_SE753	YSLFYRLDLV	KIDEN.....	.KSN...SSN	SK.....	.....YRLI
A_SE_SE853	TSLFYKLDVV	PIGGN.....	.....DTNS	TQ.....	.....YRLI
A_SE_SE889	HALFYRLDVV	PMDN.....	.....NNS	.L.....	.....YRLI
A_SE_UGSE8	YSLFYKLDIV	KINKNKSFGR	.KNSSGNSSS	DR.....	.....YRLI
A_UG_92UG0	YSLFYKLDVV	QINNG.....	.....NNSS	NL.....	.....YRLI
A_UG_U455_	YSLFYRLDIV	QINKTD....	.....N	NS.....	.....YRLI
AC_IN_2130	YSLFYRLDVV	PIEEGQGNS.	.....SNSGY	KE.....	.....YRLI
AC_RW_92RW	YSLFYRLDIV	QINSNSN...	.....NSSH	NQ.....	.....YRLI
AC_SE_SE94	HALFYRLDIV	PLDEGNSNSN	....ESNNNY	SD.....	.....YRLI
ACD_SE_SE8	YSLFYKLDVV	QINSN.....	.....QNNS	SQ.....	.....YRLI
ACG_BE_VI1	YALFYRLDIL	PLNKENK...	.....GSS	GK.....	.....YRLI
AD_SE_SE69	HSLFYKLDVV	QMGNSNS...	.....	SQ.....	.....YRLI
AD_SE_SE71	YSLFYKLDVV	QINENQ....	..YNSSNNSN	KE.....	.....YRLI
ADHK_NO_97	HALFYRVDLV	SIDN.....	.....NDNN	TQ.....	.....YRLI
ADK_CD_MAL	YATFYNLDLV	QIDDSDN...	.....S	S.....	.....YRLI
AG_BE_VI11	HALFYRPDVV	PINNDN....	.....	.....	.....SSYMLI
AG_NG_92NG	YALFYRLDVV	PIDGNNNV..	.....	.S.....	.....NNYRLI
AGHU_GA_VI	YALFYKHDLV	PITN.....	.....ET	KT.....	.....FILI
AGU_CD_Z32	YSLFYRLDIV	PIEENSNG.	.....N..S	SE.....	.....YRLI
AJ_BW_BW21	YALFYKEDIA	LIKDRPN...	.....NS	NY.....	.....SEYILV
B_AU_VH_AF	FALFYKLDVV	QIDGS.....	.....N	TS.....	.....YRLI
B_CN_RL42_	YALFYKVDVV	PIGND.....	.....S	TS.....	.....YRLI
B_DE_D31_U	YAHFYKLDVV	PIDND.....	.....N	TS.....	.....YRLI
B_DE_HAN_U	SALFYKTDVV	PIDNNKTS..	....NRDNT	TS.....	.....YMLI
B_FR_HXB2_	YAFFYKLDII	PIDND.....	.....T	TS.....	.....YKLT
B_GA_OYI_	YALFYKLDVL	PIDKN.....	.....D	TK.....	.....FRLI
B_GB_CAM1_	YALFYKLDVV	PIDKAN....	.....	TS.....	.....YTLI
B_GB_GB8_C	YALLYKLDIV	SIGSD.....	.....N	TS.....	.....YILT
B_GB_MANC_	YALFYKLDVV	PIEKK.....	.....N	TS.....	.....FRLI
B_KR_WK_AF	YALFYKLDII	PIDN.....	.....	TS.....	.....YALR
B_NL_3202A	YALFYKLDVV	PIDNN..N..	.....TNTSY	TS.....	.....YRLI
B_TW_TWCYS	YASFYRLDLV	QTDEN.....	.....S	TS.....	.....YRLI
B_US_BC_L0	YALFYKLDVV	PIDNDKNS..	.....	TK.....	.....YRLI
B_US_DH123	YALFYRHDVV	PIDRN.....	.....I	TS.....	.....YRLI
B_US_JRCSF	YALFYKLDVV	PID.....	.....NKNN	TK.....	.....YRLI
B_US_MNCG_	YALLYKLDIV	SIDND.....	.....S	TS.....	.....YRLI
B_US_P896_	YALFNRLDVV	PIE.....	.....NTNN	TK.....	.....YRLI
B_US_RF_M1	YALFYKLDVV	PIEKGNI SPK	N.NTSNNTSY	GN.....	.....YTLI
B_US_SF2_K	NALFRNLDVV	PIDN..AS..	.....TTTNY	TN.....	.....YRLI
B_US_WEAU1	YALFYKLDVM	PIDHDNTS..	.....	.....	.....YTLI
B_US_WR27_	HALFYRLDVV	PIDK.....	.....NNTN	TS.....	.....YRLI
B_US_YU2_M	YALFYNLDDV	PIDN.....	.....	AS.....	.....YRLI
BF1_BR_93B	HALFYRLDIV	PISNDNSSND	.....NSS	RE.....	.....YRLI
C_BR_92BR0	HALFYRLDIV	PLKNE.....	.....SSNTS	GD.....	.....YRLI
C_BW_96BW0	RARFYRLDIV	QLNNN.....	.....SNS	NE.....	.....YRLI
C_BW_96BW1	YALFYRLDIV	PLNNKNE...	.....SN.	SE.....	.....YRLI
C_BW_96BW1	YALFYRLDIV	PLDN.....	.....NS	SE.....	.....YRLI
C_BW_96BW1	YALFYKLDIV	PLNSNS....	.....	SE.....	.....YRLI
C_ET_ETH22	YALFYKLDIV	PLN.....	.....NGS	TD.....	.....YRLI
C_IN_93IN1	YALFYGLDIV	PLN...KKN.	.....SSENS	SE.....	.....YRLI
C_IN_93IN9	YALFYRLDIV	QLN...SDD.	.....KKNSS	EY.....	.....YRLI
C_IN_93IN9	HALFYRLDLV	PLDNENKSS.	.....FSNSS	KT.....	.....YRLI
C_IN_94IN1	YALFYKLDIV	PIS...ETS.	.....NQS..	.....	.....RLI
C_IN_95IN2	YALFYKLDIV	PLDNEEQEN.	.....DSNSS	GY.....	.....YRLI
CRF01_AE_C	HALFYVPDIV	RIG....EK.	..NKNSSGNS	SE.....	.....YILI
CRF01_AE_C	HALFYTSDDV	QISSSVQNNN	NSNTSGQNNS	HK.....	.....FRLI
CRF01_AE_C	YALFYRSDLV	PIE.....	..RNSGENNG	SS.....	.....YRLI
CRF01_AE_T	HALFYKLDIV	QIEDK.....	.....NDS	SK.....	.....YGLI
CRF01_AE_T	HALFYKLDIV	QMN.....	.....KNS	SE.....	.....YRLI
CRF01_AE_T	YALFYKLDIV	QMN.....	.....SNS	SE.....	.....YRLI

CRF01_AE_T	YALFYKLDTI	PIG.....	.....NNN	NM.....	.....YRLI
CRF01_AE_T	HALFYKLDIV	QIEDK.....	.....KTS	SE.....	.....YRLI
CRF01_AE_T	QALFYKLDIV	QMGG.....	.....NDS	GE.....	.....YRLI
CRF02_AG_F	SALFYRLDVV	QINES.....	.....GN	SQ.....	.....YRLI
CRF02_AG_F	SALFYRLDVV	QINES.....	.....SN	SQ.....	.....YRLI
CRF02_AG_G	NALFYRVDVV	QMNS.....	.....Q	.....	.....YRLI
CRF02_AG_N	HALFYRLDVV	QINEN.....	.....NG	SQ.....	.....YRLI
CRF02_AG_S	YALFYRYDVV	QINETG....	.....DN	IQ.....	.....YRLI
CRF02_AG_S	AALFYKIDIV	PIDKN.....	.....A	TY.....	.....YRLI
CRF03_AB_R	YALFYKLDVV	QIDND.....	.....S	.....	.....YRLI
CRF03_AB_R	HALFYKLDVV	QIDND.....	.....S	.....	.....YRLI
CRF04_cpx_	YALFYRIDIV	PINARVPING	...SNRNNST	EE.....	.....YMLI
CRF04_cpx_	HALFYRLDVV	PINNNVPINN	...TSNTSEY	RE.....	.....YRLM
CRF04_cpx_	YALFYRLDIV	PIDNNSTN.	...SRRSSNT	SD.....	.....YMLI
CRF05_DF_B	HALFYRLDIV	PISSD....D	.....SSN	SS.....	.....YRLI
CRF05_DF_B	HALFYRLDIV	SINS.....	.....SRK	E.....	.....YRLI
CRF06_cpx_	YALFYRPDIV	PIGDD.....	.....S	NN.....	.....SDYRLI
CRF06_cpx_	YALFYRLDVV	PINDG.....	.....S	NN.....	.....NSYRLI
CRF06_cpx_	RALFYTLDVV	PINDN.....	.....G	NN.....	.....STYRLI
CRF06_cpx_	YALFYRPDVM	QVDG.....	.....K	NS.....	.....STYRLI
CRF11_cpx_	YALFYKLDIV	PINDNNN...	.....SS	NV.....	.....SDYRLI
CRF11_cpx_	RALFYRLDVV	PINDS.....	.....SS	NI.....	.....GQYRLI
D_CD_84ZR0	HALFYRLDVV	QIDNEGKNE.	.....INDTY	GT.....	.....YRLI
D_CD_ELI_K	YALFYRLDIV	PIDNDSS...	.....TNS	TN.....	.....YRLI
D_CD_NDK_M	YALFYKLDIV	PIDNNNR...	.....TNS	TN.....	.....YRLI
D_UG_94UG1	QALFYKLDVV	KINDNDS...	.....DN	TS.....	.....YRLI
F1_BE_VI85	SALFYRLDIV	PIGNN...N.	.....S	SE.....	.....YRLI
F1_BR_93BR	HALFYKLDIV	QINKD..DN.	.....RT	.....	.....YRLI
F1_FI_FIN9	HALFYRLDIE	PISNN...N.	.....SR	EE.....	.....YRLI
F1_FR_MP41	NALFYKLDII	PINNS.....	.....SS	SD.....	.....YRLI
F2_CM_MP25	YALFYKLDVV	QINNS.....	.....NTS	.....	.....YRLI
F2KU_BE_VI	YALFYREDIV	PINIKKNNKT	.....NSN	SKKNNNTSNN	SIENSKYRLI
G_BE_DRCBL	YALFYRTDVV	PINEMNNENN	.....GT	NS.....	.....TWYRLT
G_NG_92NG0	YALFYKLDVV	PISNGN....	.....K	.....	.....TSYRLI
G_SE_SE616	YAFFYRLDVV	PINN.....	.....A	.....	.....TNYRLT
H_BE_VI991	HALFYRADIV	QIDEGER...	.....NKSD	NH.....	.....YRLI
H_BE_VI997	HALFYRLDVV	PIDETSNNN.	.....NSNS	TK.....	.....YRLI
H_CF_90CF0	HALFYRLDVV	PIDNNS....	.....TQ	.....	.....YRLI
J_SE_SE702	YALFYRQDVV	PIN.....	.....S	DN.....	.....KSYILI
J_SE_SE788	YALFYRQDVV	PID.....	.....S	NN.....	.....KNYILI
K_CD_EQTB1	SALFYKLDIV	QIKQSEINQS	.....ESE	.....	.....DRLI
K_CM_MP535	SALFYRLDVL	PLN.GEGNNS	.....STE	.....	.....YRLI
N_CM_YBF30	YSLFYVEDVV	PINAYN....	.....	.....	.....KTYRLI
O_CM_ANT70	QALFYVSDLM	ELNETSSTNK	.....T	NS.....	.....KMYTLT
O_CM_MVP51	QALFYVSDLS	KVNDNAVN.	.....G	.....	.....TTYMLT
O_SN_99SE_	QALFYVSDLM	KINEANDT..	.....K	.....	.....DMYTLI
O_SN_99SE_	QALFYVSDLM	KVNENND...	.....	.....	.....TMYTLI
U_CD___83C	HTLFYKLDVV	PLNVTN....	.....N	SS.....	.....ISSTYRLI



	251				300
00BW0762_1	NCNTSTITQA	CPKVNFDPIP	IHYCAPAGYA	ILKCNKTFTD	GTGPCTNVST
00BW0768_2	NCNTSAVTQA	CPKVSFEPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNNVST
00BW0874_2	NCNTSAITQA	CPKVSFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNNVST
00BW1471_2	NCNTSTITQA	CPKVTFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNNVST
00BW1616_2	KCNTSTITQA	CPKVNFDPIP	IHYCAPAGYA	ILKCRNKTFN	GTGPCNNVST
00BW1686_8	NCNTSSISQA	CPKVSFGPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCQNVST
00BW1759_3	NCNTSAVTQA	CPKVTFDPIP	VHYCAPAGYA	ILKCNNKTFN	GAGPCNNVST
00BW1773_2	NCNTSAITQA	CPKVSFDPIP	IHYCTPAGYA	ILKCNNQTFN	GTGPCNDVSS
00BW1783_5	NCNTSAITQA	CPKVSFEPIP	IHFCAPAGYA	ILKCNNKTFN	GTGPCNNVST
00BW1795_6	NCNTSTITQA	CPKVSFDPIP	IHYCAPAGYA	ILKCNNKTFN	GKGPCNNVST
00BW1811_3	NCNTSALTQA	CPKVSFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCTNVST
00BW1859_5	NCNTSAITQA	CPKVSFDPIP	IHYCAPAGYA	ILKCNDKTFN	GTGPCQNVST
00BW1880_2	NCNTSAITQA	CPKINFDDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNNVST
00BW1921_1	NCNTSAITQA	CPKVTFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNNVST
00BW2036_1	NCNTSAITQA	CPKVSFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCQNVST
00BW2063_6	NCNTSTITQS	CPKVTFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNNVST
00BW2087_2	NCNTSAITQA	CPKVSFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNNVSI
00BW2127_2	NCNTSAITQA	CPKISFDPIP	IHYCAPTGYA	ILKCNNKTFN	GTGPCNNVST
00BW2128_3	NGNTSALTQA	CPKVSFDPIP	IHYCTPAGYA	ILKCNNKTFN	GTGPCNNVST
00BW2276_7	NCNTSAITQA	CPKITFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCQNVSP
00BW3819_3	NCNTSAVTQS	CPKISFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNNVST
00BW3842_8	NCNTSAITQA	CPKVSFDPIP	IHYCAPAGYA	ILKCNNKTFN	GIGPCQNISI
00BW3871_3	NCNTSAISQA	CPKVSFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCQNVST
00BW3876_9	HCNTSTITQA	CPKVSFEPIP	IHYCAPAGYA	ILKCNDKTFS	GTGPCLNVST
00BW3886_8	NCNTSTITQA	CPKVSFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCQNVST
00BW3891_6	NCNTSAITQA	CPKVSFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNNVST
00BW3970_2	NCNTSKVTQA	CPKVSFDPIP	LHYCAPAGYA	ILKCNNKTFN	GTGPCNNVST
00BW5031_1	SCNTSTITQA	CPKVSWDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNNVST
96BW01B21	NCNTSAISQA	CPKVSFDPIP	IHYCTPAGFA	ILKCNNKTFN	GTGPCNNVST
96BW0407	NCNTSTITQA	CPKVSFDPIP	IHYCAPAGYA	ILKCNNKTFN	GLGPRNNVST
96BW0502	NCNTSAITQA	CPKVSFDPIP	IHYCTPAGYA	ILKCNNQTFN	GTGPCNNVSS
96BW06_J4	NCNTSTISQA	CPKISFDPIP	IHYCAPGGYA	ILKCNNKTFN	GTGPCQNVST
96BW11_06	NCNTSTITQS	CPKVSFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNNVST
96BW1210	NCNTSTITQA	CPKVSFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCTNVST
96BW15B03	NCNTSAITQA	CPKVSFDPIP	IHYCAPAGYA	ILKCKNNTFN	GTGPCQNVST
96BW16_26	NCNTSALTQA	CPKVTFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNNVST
96BW17A09	NCNTSTITQA	CPKVSFDPIP	IHYCAPAGYA	ILECNNKTFN	GTGPCTNVST
96BWM01_5	NCDTSTITQS	CPKVTFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNNVST
96BWM03_2	NCNTSSITQA	CPKVSFDPIP	IHYCAPAGFA	ILKCNNKTFN	GTGPCQNVST
98BWMC12_2	NCNTSAITQA	CPKVSFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNNVST
98BWMC13_4	NCNTSTITQS	CPKVSFDPIP	IHYCAPAGYA	ILKCNNKTFN	GIGPCNNVST
98BWMC14_a	NCNTSAISQA	CPKISFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCQNVST
98BWM014_1	NCNTSTVKQA	CPKVTFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNNVST
98BWM018_d	NCNTSVITQA	CPKVTFEPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNNVST
98BWM036_a	NCNTSTLTQA	CPKVSFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNNVST
98BWM037_d	NCNTSTVTQA	CPKVSFDPIP	IHYCTPAGYA	ILKCNNKTFN	GKGPCNNVST
99BW3932_1	NCYTSAIAQT	CPKISFDPIP	IHYCAPAGYA	ILKCYNKTFN	GTGPCKNVST
99BW4642_4	NCNTSAITQA	CPKVSFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCQNVST
99BW4745_8	NCNTSAVTQA	CPKVSFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNNVST
99BW4754_7	NCNTSAITQA	CPKVTFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTRPCNNVST
99BWMC16_8	NCNTSAITQA	CPKVSFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNDVST
A2_CD_97CD	SCNTSVITQA	CPKVSFEPIP	IHYCAPAGYA	ILKCKDKEFN	GKGSCSNVSS
A2_CY_94CY	NCNTSTITQA	CPKVTFEPIP	IHYCAPAGFA	ILKCKDPRFN	GTGSCKNVSS
A2D_97KR	HCDTSTITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCKDPEFN	GTGPCKNVSS
A2G_CD_97C	KCNTSTITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCKDPKFN	GTGPCENVSS
A_BY_97BL0	NCNTSAMTQA	CPXVTFEPIP	IYYCAPAGFA	ILKCXDTNFT	RTXPCKNVST
A_KE_Q23_A	NCNTSAITQA	CPKVSFEPIP	IHYCTPAGFA	ILKCKDEGFN	GTGLCKNVST
A_SE_SE659	NCNTSAITQA	CPKVTFEPIP	IHYCAPAGFA	ILKCKDDAFN	GTGRCKNVST
A_SE_SE725	NCNTSAITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCRDKEFN	GTGPCNNVST

A_SE_SE753	NCNTSAITQA	CPKVTFEPIP	IHYCAPAGFA	ILKCNDKEFN	GTGLCNNVST
A_SE_SE853	NCNTSAITQA	CPKVTFEPIP	IHYCAPAGFA	ILKCRDENFN	GTGPCKNVST
A_SE_SE889	NCNTSAITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCNDKEFN	GTGPCKNVSS
A_SE_UGSE8	NCNTSAITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCNEDEFN	GTGTCRNVST
A_UG_92UG0	NCNTSALTQA	RPKVTFEPIP	IHYCAPAGYA	ILKCNDKEFN	GTGLCKNVST
A_UG_U455_	NCNTSTITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCKDPEFN	GKGPCRNVST
AC_IN_2130	NCNTSAITQA	CPKVTFNPIP	IHYCTPAGYA	ILKCNEETFN	GTGPCKNVST
AC_RW_92RW	NCNTSAITQA	CPKVSFEPIP	INYCAPAGFA	ILKCKDKKFN	GTGPCKNVST
AC_SE_SE94	NCNTSAITQA	CPKVSFDPIP	IHYCAPGFA	ILKCKDAKFN	GIGPCNNVST
ACD_SE_SE8	NCNTSAITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCNNKEFN	GTGPCKNVST
ACG_BE_VI1	NCNTSAITQA	CPKVSFDPIP	IHYCAPAGFA	ILKCNNKTFN	GTGPCNNVST
AD_SE_SE69	NCNTSAIKQA	CPKVTFEPIP	IHYCAPAGFA	ILKCKDTEFN	GTGPCKNVST
AD_SE_SE71	NCNTSAITQA	CPKVTFEPIP	IHYCAPAGFA	ILKCKDEKFN	GTGPCKNVST
ADHK_NO_97	NCNTSVITQA	CPKVTFEPIP	IHYCAPAGFA	ILKCNNKTFN	GTGPCKNVST
ADK_CD_MAL	NCNTSVITQA	CPKVSFDPIP	IHYCAPAGFA	ILKCNDKKFN	GTEICKNVST
AG_BE_VI11	NCNSSTIKQA	CPKVSFEPIP	IHYCAPAGFA	ILRCRDKKFN	GTEPCKNVST
AG_NG_92NG	NCNVSTIKQA	CPKVSFDPLP	IHYCAPAGFA	ILKCRGKNFT	GTGQCKNVSS
AGHU_GA_VI	HCNTSTITQA	CPKVSFDPIP	IHYCAPAGFA	ILKCKDKAFN	GTGPCKNVST
AGU_CD_Z32	NCNTSAITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCRDEEFE	GKGPCRNVST
AJ_BW_BW21	KCNTTVIKQA	CPKVSFQPIP	IHYCAPAGFA	ILQCNDKKFN	GTGPCKNVST
B_AU_VH_AF	NCNTSVITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCNNKTFN	GKGPCANIST
B_CN_RL42_	NCNTSVITQA	CPKVSFEPIP	IHYCTPAGFA	ILKCNNKKFN	GTGPCTNVST
B_DE_D31_U	SCNTSVITQA	CPKVSFEPIP	IHYCTPAGFA	MLKCKDKRFN	GKGQCKNVST
B_DE_HAN_U	HCNRSVITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCNDKKFN	GKGPCKNVST
B_FR_HXB2_	SCNTSVITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCNNKTFN	GTGPCTNVST
B_GA_OYI_	HCNTSTITQA	CPKISFEPIP	MHYCTPAGFA	ILKCNDKKFN	GTGPCTNVST
B_GB_CAM1_	HCNTSVITQA	CPKVSFEPIP	IHYCTPAGFA	ILKCNDKKFN	GKGPCCTNVST
B_GB_GB8_C	ECNASVITQA	CPKISFEPIP	IHFCAAGFA	ILKCNNKTFD	GKGPCCTNVST
B_GB_MANC_	SCNTSTITQA	CPKVSFEPIP	IHYCTPAGFA	ILKCNNKKFD	GKGQCTNVST
B_KR_WK_AF	HCNTSVITQA	CPKVSFEPIP	IHYCAPAGFA	ILQCNDKKFN	GTGPCTNVST
B_NL_3202A	SCNTSVITQA	CPKVSFEPIP	IHFCTPAGFA	LLKCNDKKFN	GTGPCKNVST
B_TW_TWCYS	SCNASVIKQA	CPKVSFEPIP	IHYCTPAGFA	ILKCNNKTFN	GTGTCTNVST
B_US_BC_L0	SCNTSVITQA	CPKISFEPIP	IHYCAPAGFA	ILKCKDKKFN	GTGPCTNVST
B_US_DH123	SCNTSVITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCKDKKFN	GTGPCTNVST
B_US_JRCSF	SCNTSVITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCNNKTFN	GKGQCKNVST
B_US_MNCG_	SCNTSVITQA	CPKISFEPIP	IHYCAPAGFA	ILKCNDKKFS	GKGSCKNVST
B_US_P896_	SCNTSVITQA	CPKVSFQPIP	IHYCVPAGFA	MLKCNNKTFN	GSGPCTNVST
B_US_RF_M1	HCNSSVITQA	CPKVSFEPIP	IHYCTPAGFA	ILKCNDKKFN	GTGPCKNVST
B_US_SF2_K	HCNRSVITQA	CPKVSFEPIP	IHYCTPAGFA	ILKCNNKTFN	GKGPCCTNVST
B_US_WEAU1	NCKSSTITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCNDKKFN	GKGPCCKNVST
B_US_WR27_	HCNTSTITQA	CPKVSFEPIP	IHYCTPAGFA	ILKCNDKKFN	GTGQCKNVST
B_US_YU2_M	SCNTSVITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCNDKKFN	GTGPCTNVST
BF1_BR_93B	NCNTSTLTQA	CPKVSFDPPIP	IHYCAPAGYA	ILKCNDKKFN	GTGPCRNVST
C_BR_92BR0	NCNTSAITQA	CPKVSFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNNVST
C_BW_96BW0	NCNTSTITQA	CPKVSFDPIP	IHYCAPAGYA	ILKCNNKTFN	GSGPCNNVST
C_BW_96BW1	NCNTSTITQS	CPKVSFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNNVST
C_BW_96BW1	NCNTSTITQA	CPKVSFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCTNVST
C_BW_96BW1	NCNTSAITQA	CPKVSFDPIP	IHYCAPAGYA	ILKCKNNTFN	GTGPQNVST
C_ET_ETH22	NCNTSTITQA	CPKVSFDPIP	IHYCAPAGYA	ILKCRDKTFT	GTGPCHNVST
C_IN_93IN1	NCNTSAITQA	CPKVSFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNNVST
C_IN_93IN9	NCNTSAITQA	CPKVSFDPIP	IHYCTPAGYA	ILKCKDKTFN	GTGPCHNVST
C_IN_93IN9	NCNTSAITQA	CPKVSFDPIP	IHYCTPAGYA	ILKCNEKTFN	GTGLCQNVST
C_IN_94IN1	SCNTSVITQA	CPKVSFDPIP	IHYCTPAGYA	ILKCNDKTFN	GTGPCRNVST
C_IN_95IN2	NCNTSALTQA	CPKVSFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCHNVST
CRF01_AE_C	HCNTSVIKQA	CPKVSFDPIP	IHYCTPAGYA	ILKCNEKNFN	GTGPCKNVSS
CRF01_AE_C	HCNTSVIKQA	CPKVSFDPIP	IHYCAPAGYA	ILKCNDKNFN	GTGPCKNVSS
CRF01_AE_C	HCNTSVIKQA	CPKVSFDPIP	IHYCAPAGYA	ILKCNDKNFN	GTGPCKNVSS
CRF01_AE_T	NCNTSVIKQA	CPKISFDPIP	IHYCTPAGYV	ILKCNDKNFN	GTGPCKNVSS
CRF01_AE_T	NCNTSVIKQA	CPKISFDPIP	IHYCTPAGYA	ILKCNDKNFN	GTGPCKNVSS
CRF01_AE_T	NCNTSVIKQA	CPKVSFDPIP	IHYCTPAGYA	ILKCNDKNFN	GTGPCKNVSS

CRF01_AE_T	NCNDSVIKQA	CPKISFDPIP	IHYCTPAGYA	MLKCNDKNFN	GTGPCKNVSS
CRF01_AE_T	NCNTSVIKQA	CPKISFDPIP	IHYCTPAGYA	ILKCNDKNFN	GTGPCKNVSS
CRF01_AE_T	NCNTSVIKQA	CPKVSFDPIP	IHYCTPAGYA	ILKCNDKNFN	GTGPCKNVSS
CRF02_AG_F	NCHTSAITKA	CPRVTLLEPI	IHYCAPAGLA	ILKCNDKKFN	GTGLCKNVST
CRF02_AG_F	NCNTSAIKQA	CPKVTFEPIP	IHYCAPAGFA	ILKCNDKKFN	GTGPCKNVST
CRF02_AG_G	NCNTSAITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCKDRNFN	GTGPQCNVST
CRF02_AG_N	NCNTSAITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCKDKGFN	GTGPCKNVST
CRF02_AG_S	NCNTSAITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCNDKDFN	GTGPCKNVST
CRF02_AG_S	NCNTSAITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCNEKDFS	GTGSCKNVST
CRF03_AB_R	SCNTSVVTQA	CPKISFEPIP	IHYCAPAGFA	ILKCNDKKFN	GTGPCTNVST
CRF03_AB_R	SCNTSVVTQA	CPKISFEPIP	IHYCAPAGFA	ILKCNDKKFN	GTGPCTNVST
CRF04_cpx_	NCNASTIKQA	CPKVSFEPIP	IHYCAPAGFA	ILKCNEKNFT	GLGPCTNVSS
CRF04_cpx_	SCNTSNHKQA	CPKVTLEPNS	HTLLCPGWFC	DLKCNDKNSP	GLGSCTNVSP
CRF04_cpx_	NCNVSSITQA	CPKIKFEPIP	IHYCAPAGFA	ILQCNEKRFN	SGSPCKNVSS
CRF05_DF_B	NCNTSTIKQA	CPKVSWDPIP	IHYCAPAGYA	ILKCNEKKFS	GTGPCKNVST
CRF05_DF_B	NCNTSTIKQA	CPKVCWDPIP	IHYCAPAGYA	ILKCKEKRFN	GTGPCKNVST
CRF06_cpx_	NCNVSTIKQA	CPKVSFEPIP	IHYCAPAGFA	ILKCRDKDFN	GTGPCKNVST
CRF06_cpx_	NCNASTIKQA	CPKVTFEPIP	IHYCAPAGFA	ILKCRDKNFN	GTGPCKNVST
CRF06_cpx_	NCNTSTIKQA	CPKVSFEPIP	IHYCAPAGFA	ILKCRDKNFN	GTGPCKNVST
CRF06_cpx_	NCNASTIKQA	CPKVSFEPIP	IHYCAPAGFA	ILKCRDKNFN	GTGACKNVST
CRF11_cpx_	NCNVSTIKQA	CPKVTFEPIP	IHYCAPAGFA	ILKCRDKEFN	GTGPCKNVST
CRF11_cpx_	NCNVSAVKQA	CSKVTFEPIP	IHYCAPAGFA	ILKCRDKEFN	GTGPCKNVST
D_CD_84ZR0	NCNTSAITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCNDKRFN	GTGPCKNVSS
D_CD_ELI_K	NCNTSAITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCRDKKFN	GTGPCTNVST
D_CD_NDK_M	NCNTSTITQA	CPKISFEPIP	IHYCAPAGFA	ILKCRDKKFN	GTGPCS NVST
D_UG_94UG1	NCNTSAITQA	CPKMTFEPIP	IHYCAPAGFA	ILKCNEKKFN	GTGPCKNVST
F1_BE_VI85	NCNTSTITQA	CPKVSWDPIP	IHYCAPAGYA	ILKCNDKRFN	GTGPCKNVST
F1_BR_93BR	NCDASTITQA	CPKVSWDPIP	IHYCAPAGYA	ILKCNEKNFT	GTGSCKNVST
F1_FI_FIN9	TCNTSTITQA	CPKVSWDPIP	IHYCAPAGYA	ILKCKDKRFN	GTGPCKNVST
F1_FR_MP41	NCNTSTIKQA	CPKVSWDPIP	IHYCAPAGYA	ILKCRDPRFN	GTGPCKNVST
F2_CM_MP25	NCNTSTLTQA	CPKVSFDPIP	IHYCAPAGFA	ILKCNNKTFN	GTGLCRNVST
F2KU_BE_VI	NCNTSAITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCNEKEFN	GTGPCKNVST
G_BE_DRCBL	NCNVSTIKQA	CPKVTFEPIP	IHYCAPAGFA	ILKCVDKKFN	GTGTCTNVST
G_NG_92NG0	HCVNSTIKQA	CPKVNFDPIP	IHYCAPAGFA	ILKCRDKEYN	GTGPCKNVST
G_SE_SE616	HCVNSTIKQA	CPKVTFDPIP	IHYCAPTGFA	ILKCRDKEFN	GTGPCKNVST
H_BE_VI991	NCNTSVIKQA	CPKVSFEPIP	IHYCAPAGFA	ILKCNGKKFN	GTGPCTNVST
H_BE_VI997	NCNTSVITQA	CPKVSFDPIP	IHYCAPAGFA	ILKCNNKTFN	GTGPCTNVST
H_CF_90CF0	NCNTSVITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCNNKTFN	GTGLCTNVST
J_SE_SE702	NCNTSVIKQA	CPKVSFQPIP	IHYCAPAGFA	ILKCNNKTFN	GTGPCKNVST
J_SE_SE788	NCNTSVIKQA	CPKVSFQPIP	IHYCAPAGFA	ILKCNDKNFN	GTGSCKNVST
K_CD_EQTB1	NCNTSTVTQA	CPKVSFEPIP	IHYCAPAGFA	ILKCNNNTCN	GTGPCTNVST
K_CM_MP535	NCNTSTITQT	CPKVTFEPIP	IHYCAPAGFA	ILKCKDKRFN	GTGPCKNVST
N_CM_YBF30	NCNTTAVTQA	CPKTSFEPIP	IHYCAPPGFA	IMKCNEGNFS	GNGSCTNVST
O_CM_ANT70	NCNSTTITQA	CPKVSFEPIP	IHYCAPAGYA	IFKCNSTEFN	GTGTCRNITV
O_CM_MVP51	NCNSTIIKQA	CPKVSFEPIP	IHYCAPTGFA	IFKCNDDTFN	GTGLCHNISV
O_SN_99SE_	NCNSTTIKQA	CPKVSFEPIP	IHYCAPAGYA	IFKCNSTEFN	GTGPCNNITA
O_SN_99SE_	NCNSTTIKQT	CPKVSFEAIP	IHYCAPAGYA	IFKCNNTGFN	GTGPCTNVTV
U_CD___83C	NCNTSTITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCNDKKFN	GTGPCKNVST

00BW0762_1	VQCTHGIKPV	VSTQLLLLNGS	LSEE.GIVIR	SENITNNAKT	IIVHLNESVE
00BW0768_2	VQCTHGIKPV	VPTQLLLLNGS	LAEE.EIIIR	SEALTNNAKT	IIARLNKSVE
00BW0874_2	VQCTHGIKPV	VSTQLLLLNGS	LAEE.EIIIR	SENLAKNDKT	IIVHLNESVE
00BW1471_2	VLCTHGIKPV	VSTQLLLLNGS	LSEG.EIMIR	SENLTDNAKT	IIVQLNKPVE
00BW1616_2	VQCTHGIKPV	VSTQLLLLNGS	LAEE.EIVIR	SENITNNAKI	IIVHLNETVD
00BW1686_8	VQCTHGIKPV	VSTQLLLLNGS	LAEG.EIIIR	SENMTDNVKT	IIVHLNESVE
00BW1759_3	VQCTHEIKPV	VSTQLLLLNGS	LAEE.QIIIR	SENMTNNAKT	IIVHLKKPVQ
00BW1773_2	VQCTHGIKPV	VSTQLLLLNGS	LAEK.EIIIR	SENLTNNAKI	IIVHLKDPVN
00BW1783_5	VQCTHGIKPV	VSTQLLLLNGS	LAEE.EIIIR	SENLTNNVKT	IIVHLNESIQ
00BW1795_6	VQCTHGIKPV	VSTQLLLLNGS	LAEG.EIIIR	SKNLTDNART	IIVHLNESVQ
00BW1811_3	VQCTHGIKPV	VSTQLLLLNGS	LAEE.DIIIR	SENLTDNVKT	IIVHLNESVE
00BW1859_5	VQCPHGIKPV	VSTQLLLLNGS	LAEE.EIIIR	SENIEDNVKT	IIVHLNESIE
00BW1880_2	VQCTHGIKPV	VATQLLLLNGS	LAEE.EIVIR	FKNITNNAKI	IIVQLNTSVG
00BW1921_1	VQCTHGIKPV	VSTQLLLLNGS	LAEE.GIIIR	SENLTDNAKT	ITVQLDQAVE
00BW2036_1	VQCTHGIRPV	VSTQLLLLNGS	LAEG.EIIIR	SENLAADNAKT	IIVHFNESVE
00BW2063_6	VQCTHGIKPV	VSTQLLLLNGS	LAEK.EIIIR	SKNITDNVKT	IIVHLNEAVE
00BW2087_2	VQCTHGIKPV	VSTQLLLLNGS	LAEE.EIIIR	SENLTNNAKT	IIVHLNDSVE
00BW2127_2	VQCTHGIKPL	VSTQLLLLNGS	LAQQ.QIMIT	SENLTNNAKI	IIVHLKEAIN
00BW2128_3	VQCTHGIKPV	VSTQLLLLNGS	LAEE.IIIR.	SENLTNNAKT	IIVQLKEPVK
00BW2276_7	VQCTHGIKPV	VSTQLLLLNGS	LAEE.EIIIR	SENLTNNVKT	IIVHLNKSVE
00BW3819_3	VQCTHGIKPV	VSTQLLLLNGG	LAEK.EIIIR	SENLTNNVKT	IIVHLNESVE
00BW3842_8	VQCTHGIKPV	VSTQLLLLNGS	LAEG.EIIIR	SKNLSDNAKI	IIVHLNESVG
00BW3871_3	VQCTHGIKPV	VSTQLLLLNGS	IAEG.EIIIR	SENLTNNAKT	IIVHLNESVK
00BW3876_9	IQCTHGIKPV	VSTQLLLLNGS	LAEK.DIIIR	SENLTNNIKT	IIVHLNDSVQ
00BW3886_8	VQCTHGIKPV	VSTQLLLLNGS	LAEG.EIIIR	SENLTNNAKT	IIVHLNESIE
00BW3891_6	VQCTHGIKPV	VSTQLLSNGS	LSEK.EIIIR	SENLTNNVKT	IIVHLNESVE
00BW3970_2	IQCTHGIKPV	VSTQLLLLNGS	RAEK.EIIIR	SENMTNNAKT	IIVHLNESIE
00BW5031_1	VQCTHGIKPV	VSTQLLLLNGS	LA.E.EIVIR	SENISDNAKT	IIVHLNESVE
96BW01B21	VQCTHGIKPV	VSTQLLLLNGS	LAEE.DIIIR	SENLTDNVKT	IIVHLNESIE
96BW0407	VQCTHGIKPV	VSTQLLLLNGS	LAEE.EIIIR	SENLTDNAKI	IIVHLNESVR
96BW0502	VQCAHGIKPV	VSTQLLLLNGS	VAKG.EIIIR	SENLTNNAKI	IIVQLNKPVK
96BW06_J4	VQCTHGIKPV	VSTQLLLLNGS	LAEE.KIIIR	SGNVTNNAKT	IIVHLNESVE
96BW11_06	VQCTHGIKPV	VSTQLLLLNGS	LAEK.EIIIR	FKNITNNAKT	IIVHLNESVE
96BW1210	VQCTHGIKPV	VSTQLLLLNGS	LAEE.EIIIR	SENITDNVKT	IIVHLNKSVE
96BW15B03	VQCTHGIKPV	VSTQLLLLNGS	LAEG.EIIIR	SKNLSNNAYT	IIVHLNDSVE
96BW16_26	VQCTHGIKPV	VSTQLLLLNGS	LAEE.EIIIR	SENLTNNAKT	IIVHLNESVE
96BW17A09	VQCTHGIKPV	VSTRLLLLNGS	LAEE.EIIIR	SENLTNNAKI	IMVQLNESIE
96BWM01_5	VQCTHGIKPV	VSTQLLLLNGS	LAEK.EIIIR	SKNITDNVKT	IIVHLNESVE
96BWM03_2	VQCTHGIKPV	VSTQLLLLNGS	LAEE.EIIIR	SENLTDNAKT	IIVHFNESVQ
98BWMC12_2	VQCTHGIKPV	VSTQLLLLNGS	LAEE.EIIIR	SENLTNNVKT	IIVHLNESVE
98BWMC13_4	VQCTHGIKPV	VSTQLLLLNGS	LAEK.EIVIR	SENLTDNVKT	IIVHLNQSVQ
98BWMC14_a	VQCTHGIKPV	VSTQLLLLNGS	LAEE.EVVIR	SENLTNNAKT	IIVQLKEPVK
98BWM014_1	VQCTHGIKPV	VSTQLLLLNGS	LAEK.EIIIR	SENITNNIKT	IIVHLNEPVE
98BWM018_d	VQCTHGIKPV	VSTQLLLLNGS	LAEE.EIIIR	SKNITNNANT	IIVQLKDPVD
98BWM036_a	IQCTHGIKPV	VSTQLLLLNGS	IAEE.EIIIR	SENLTDNVKT	IIVHLKDPID
98BWM037_d	VQCTHGIKPV	VSTQLLLLNGS	IAEE.EIIIR	SENLTNHFRT	IIVQLNQSIE
99BW3932_1	VQCTHGIKPV	VSTQLLLLNGS	LAEE.EIVIR	SENLTNNVKT	IIVHLNESIE
99BW4642_4	VQCTHGIKPV	VSTQLLLLNGS	LAEG.EIIVR	SENLTDNVKT	IIVHLDKPVG
99BW4745_8	VQCTHGIKPV	VSTQLLLLNGS	LAEK.EIIVR	SENLTNNAKI	IIVQLKQSVG
99BW4754_7	VQCTHGIKPV	VSTQLLLLNGS	RAEK.EVVIR	AESLTDNAKV	IIVHLKDSVQ
99BWMC16_8	VQCTHGIKPV	VSTQLLLLNGS	LAEE.DIIIR	SKNLTDNAKT	IIVHLNESVN
A2_CD_97CD	VQCAHGIRPV	ASTQLLLLNGS	LAEG.KVMIR	SENITDNAKN	IIVQFNKPVP
A2_CY_94CY	VQCTHGIKPV	ASTQLLLLNGS	LAEGGKIMIR	SENITNNAKN	IIVQFTKPVV
A2D_97KR	VQCTHGIRPV	ASTQLLLLNGS	LAEGNKTIIR	SANITDNTKN	IIVQFTKPVQ
A2G_CD_97C	VQCTHGIRPV	VSTQLLLLNGS	LAEE.EVMIR	SENITDNAKN	IIVQFDPKVE
A_BY_97BL0	VQCTHXIKPV	VSTQLLLLNGS	LAEKX.VMIR	SENITDNVKI	IIVQLTEPVN
A_KE_Q23_A	VQCTHGIKPV	VSTQLLLLNGS	LAEKN.ITIR	SENITNNAKI	IIVQLVQPVV
A_SE_SE659	VQCTHGIKPV	VSTQLLLLNGS	LAKGG.IRIR	SENITNNVKT	ILVQLDKPVN
A_SE_SE725	VQCTHGIKPV	VSTQLLLLNGS	LAEEK.IMIR	SENISDNAKT	IIVQLTEPVV

A_SE_SE753	VQCTHGIKP	VSTQLLN	LATK..IMIR	SENITNNAKT	IIVQLVEPVE
A_SE_SE853	VQCTHGIKP	VSTQLLN	LAREK.VMIR	SENITNNVKN	IIVQLKEPVE
A_SE_SE889	VQCTHGIRPV	VSTQLLN	LAETE.VMIR	AENITNNIKN	IIVQFNKSVE
A_SE_UGSE8	VQCTHGIRPV	VSTQLLN	LAKEE.VRIR	SENISDNAKT	IIVQFTKPVE
A_UG_92UG0	VQCTHGIRPV	VSTQLLN	LAEGK.VMIR	SENITNNVKN	IIVQLNESVT
A_UG_U455_	VQCTHGIKP	VSTQLLN	LAERE.IRIR	SENFTNNAKT	IIVQLVNPVK
AC_IN_2130	VQCTHGIKP	VSTQLLN	LAEKE.VIIR	SENITNNVKN	IIVQLAEPVR
AC_RW_92RW	VQCTHGIKP	VSTQLLN	LAEEE.IIIR	SENITNNAKT	IIVQLNETVQ
AC_SE_SE94	VQCTHGIKP	ISTQLLN	LSETG.VKIR	SENITNNAKT	IIVQLDEAVE
ACD_SE_SE8	VQCTHGIKP	VSTQLLN	LAEEE.IIVR	SENLTNNAKI	IIIQLNETVK
ACG_BE_VI1	VQCTHGIKP	VSTQLLN	LAEK..VVIR	SENITNNAKT	IIVQFDSPVK
AD_SE_SE69	VQCTHGIKP	VSTQLLN	LA.EGKVRIR	SENITDNTKN	IIVQFTEPVT
AD_SE_SE71	VQCTHGIKP	VSTQLLN	LAKEE.VIIR	SENITNNAKN	IIVQFVKPVT
ADHK_NO_97	VQCTHGIKP	VSTQLLN	LA..EKVIIR	SKNITDNTKN	IIVHFNESVQ
ADK_CD_MAL	VQCTHGIKP	VSTQLLN	LA.EEEIMIR	SENLTNTNKN	IIVQLNETVT
AG_BE_VI11	VQCTHGIKP	VSTQLLN	LA.EEEIIVR	SENFTNNAKV	IIVQLKEPIE
AG_NG_92NG	VQCTHGIKP	VSTQLLN	LA.EGEIVIR	SENLTDNAKV	IIVQLNKTIG
AGHU_GA_VI	VQCTHGIRPV	VTTQLLN	LA.EGEIIR	SENITENTKN	IIVQLNETVE
AGU_CD_Z32	VQCTHGIKP	VSTQLLN	LAEKE.VRIR	SENFSDNAKI	IIVQLAKPVN
AJ_BW_BW21	VQCTHGIKP	VSTQLLN	IA.EEEIIR	SENITNNAKT	IIVQLNNTVE
B_AU_VH_AF	VQCTHGIRPV	VSTQLLN	LA.EKEIVIR	SDNFTDNAKS	IIVQLNESVE
B_CN_RL42_	VQCTHGIRPV	VSTQLLN	LA.EEEVVIK	FSNFTDNARV	IIVQLNESVE
B_DE_D31_U	VQCTHGIRPV	VSTQLLN	LA.EEEVVIR	SDNFTDNAKT	IIVQLKESVE
B_DE_HAN_U	VQCTHGIRPV	VSTQLLN	LA.EKEVVIR	SDNFTDNTKT	IIVHLNESVE
B_FR_HXB2_	VQCTHGIRPV	VSTQLLN	LA.EEEVVIR	SVNFTDNAKT	IIVQLNTSVE
B_GA_OYI_	VQCTHGIKP	VSTQLLN	LA.EEEVIIR	SSNFTNNAKI	IIVQLNKSVE
B_GB_CAM1_	VQCTHGIRPV	VSTQLLN	LA.EKEVVIR	SENFTNNAKT	IIVQLKEPVE
B_GB_GB8_C	VQCTHGIRPV	VSTQLLN	LA.EEKVVIR	SDNFTDNVKT	IIVQLKEAVE
B_GB_MANC_	IQCTHGIRPV	VSTQLLN	LA.EEEVVLR	SDNFTDNAKT	IIVHLNESVE
B_KR_WK_AF	VQCTHGIRPV	VSTQLLN	LA.EEEIVLR	SENFTNNAKT	IIVQLNASVE
B_NL_3202A	VQCTHGIRPV	VSTQLLN	LA.EEEVVIR	SANFSNNAKT	IIVQLNESVA
B_TW_TWCYS	VQCTHGIRPV	VSTQLLN	IA.EEEILIK	SENITNNAKT	IIIQLNKSVK
B_US_BC_L0	VQCTHGIKP	VSTQLLN	LA.EEEVVIR	SANFSDNAKT	IIVQLKEAVE
B_US_DH123	VQCTHGIRPV	VSTQLLN	LA.EEEVVIR	SSNFTDNAKI	IIVQLNETVE
B_US_JRCSF	VQCTHGIRPV	VSTQLLN	LA.EEKVVIR	SDNFTDNAKT	IIVQLNESVK
B_US_MNCG_	VQCTHGIRPV	VSTQLLN	LA.EEEVVIR	SENFTDNAKT	IIVHLNESVQ
B_US_P896_	VQCTHGIRPV	VSTQLLN	LA.EEDIVIR	SENFTDNAKT	IIVQLNESVV
B_US_RF_M1	VQCTHGIRPV	VSTQLLN	LA.EEEVVIR	SENFTDNVKT	IIVQLNASVQ
B_US_SF2_K	VQCTHGIRPI	VSTQLLN	LA.EEEVVIR	SDNFTNNAKT	IIVQLNESVA
B_US_WEAU1	VQCTHGIRPV	VSTQLLN	LA.EEDIVIR	SENFTDNAKN	IIVQLNVSIE
B_US_WR27_	VQCTHGIRPV	VSTQLLN	LA.EEEVVIR	SANFTNNAKT	IIVQLKESVE
B_US_YU2_M	VQCTHGIRPV	VSTQLLN	LA.EEEIVIR	SENFTNNAKT	IIVQLNESVV
BF1_BR_93B	VQCTHGIKP	VSTQLLN	LA.EKDIIIR	SQNISDNAKT	IIVQLNVSPV
C_BR_92BR0	IQCTHGTKPV	VSTQLLN	LAE.EIIR	SKNLTDNVKT	IIVHLNESVE
C_BW_96BW0	VQCTHGIKP	VSTQLLSGS	LAE.EIVIR	SENLTNNAKI	IIVHLNKTVR
C_BW_96BW1	VQCTHGIKP	VSTPLLLN	LAEK.EIIR	FKIITNNAKT	IIVHLNESVE
C_BW_96BW1	VQCTHGIKP	VSTQLLN	LAE.EIIR	SENITDNVKT	IIVHLNKSVE
C_BW_96BW1	VQCTHGIKP	VSTQLLN	LAEGGEIIR	SKNLSNNAYT	IIVHLNDSVE
C_ET_ETH22	VQCTHGIKP	VSTQLLN	IAEG.ETIIR	FENLTNNAKI	IIVQLNESVE
C_IN_93IN1	VQCTHGIKP	VSTQLLN	LAEG.EIIR	SENLTNNVKT	IIVHLNQSVQ
C_IN_93IN9	VQCTHGIKP	VSTQLLN	LAEG.EIIR	SENLTNNAKT	IIVHLNQSVQ
C_IN_93IN9	VQCTHGIKP	VSTQLLN	LAEG.EIIR	SENLTDNVKT	IIVHLNQSVQ
C_IN_94IN1	VQCTHGIKP	VSTQLLN	LSEG.EIIR	SENLTNNVKT	IIVHLNKSVE
C_IN_95IN2	VQCTHGIKP	VSTQLLN	LAEG.GIIR	SENLTNNVKT	IIVHLNQPVE
CRF01_AE_C	VQCTHGIKP	VSTQLLN	LAE.EIIR	SENLTNNAKT	IIVHLNKSVE
CRF01_AE_C	VQCTHGIKP	VSTQLLN	LAE.EIIR	SEDLTDNAKT	IIVHLNKSIE
CRF01_AE_C	VQCTHGIKP	VSTQLLN	LAE.EIIR	SENLTNNAKT	IIVHLNKSVE
CRF01_AE_T	VQCTHGIKP	VSTQLLN	LAE.EIIR	SENLTNNAKT	IIVHLNKSVE
CRF01_AE_T	VQCTHGIKP	VSTQLLN	LAE.EIIR	FENLTNNAKT	IIVHLNKSVE
CRF01_AE_T	VQCTHGIKP	VSTQLLN	LAE.KIIR	SENLTNNAKT	IIVHLHESVE

CRF01_AE_T	VQCTHGIKP	VSTQLLLNGS	LAEE.EIIIR	SENLTNNAKT	IIVHLNKSVE
CRF01_AE_T	VQCTHGIKP	VSTQLLLNGS	LAEE.EIIIR	SEDLTNNAKT	IIVHLNKSVE
CRF01_AE_T	VQCTHGIKP	VSTQLLLNGS	LAKE.EIIIR	SENLTNNAKT	IIVHLNKSVE
CRF02_AG_F	VQCTHGIKP	VSTQLLLNGS	LAEEE.VVIR	SENITNNAKN	IIVQLVAPVR
CRF02_AG_F	VQCTHGIKP	VSTQLLLNGS	LAEEE.VVIR	SENITNNAKN	IIVQLVTPVR
CRF02_AG_G	VQCTHGIKP	VSTQLLLNGS	LAEEE.IVIR	SENITNNVKN	IIVQLAKPVR
CRF02_AG_N	VQCTHGIKP	VSTQLLLNGS	LAEGE.VVIR	SENITNNAKT	IIVQLANPVK
CRF02_AG_S	VQCTHGIKP	VSTQLLLNGS	LAEEE.IVIR	SENFTNNAKI	IIVQLHESVK
CRF02_AG_S	VQCTHGIKP	VSTQLLLNGS	LAEGD.IVIR	SENISNNAKT	IIVQLNKPVW
CRF03_AB_R	VQCTHGIKP	VSTQLLLNGS	LA.EEEVVIR	SVNFTDNTKT	IIVQLKEPVE
CRF03_AB_R	VQCTHGIKP	VSTQLLLNGS	LA.EEEVVIR	SVNFTDNTKT	IIVQLKEPVE
CRF04_cpx_	VRCTHGIKP	VSTQLLLNGS	LA.TEEVVIR	SKNITDNTKN	IIVQLAKAVK
CRF04_cpx_	VQCTHGIKP	VSTQLLLNGS	LA.TGGVVIR	SKNFTDNPKN	IIVQLDKAVK
CRF04_cpx_	VQCTHGIKP	VSTQLLLNGS	LS.TEGVVLR	SKNFTDNTKN	IIVQLAEAVK
CRF05_DF_B	VQCTHGIKP	VSTQLLLNGS	LA.KEGIIIR	SONISDNAKN	IIVHLNESVH
CRF05_DF_B	VQCTHGIKP	VSTQLLLNGS	LA.EESIIIR	SONILDNTKT	IIVHLNESVQ
CRF06_cpx_	VQCTHGIKP	VSTQLLLNGS	LA.EGNITIK	TENITDNTKN	IIVQLNQPVE
CRF06_cpx_	VQCTHGIKP	VSTQLLLNGS	LA.EEEIIIK	SKNLTDNTKI	IIVQLNKSVE
CRF06_cpx_	VQCTHGIKP	VSTQLLLNGS	LA.EDEIIIK	SENHTNNAKI	IIVQLNKTVO
CRF06_cpx_	VQCTHGIKP	VSTQLLLNGS	LA.EEEIIIK	TENLTDNSKN	IIVQLNKSIE
CRF11_cpx_	VQCTHGIKP	VSTQLLLNGS	LA.EEKVKIR	SENFTNNAKT	IIVQFNNTVR
CRF11_cpx_	VQCTHGIKP	VSTQLLLNGS	LA.EGEVRIR	SENLTNNAKT	IIVQLNSTVR
D_CD_84ZR0	VQCTHGIRPV	VSTQLLLNGS	LA.EEEIVIR	SENLTNNAKI	IIVHLNQSVE
D_CD_ELI_K	VQCTHGIRPV	VSTQLLLNGS	LA.EEEVIIR	SENLTNNAKN	IIAHLNESVK
D_CD_NDK_M	VQCTHGIRPV	VSTQLLLNGS	LA.EEEIIIR	SENLTNNVKT	IIVQLNASIV
D_UG_94UG1	VQCTHGIKP	VSTQLLLNGS	LA.EEEIIIR	SENLTNNAKI	IIVQLNESVP
F1_BE_VI85	VQCTHGIKP	VSTQLLLNGS	LA.EEGIVIR	SONISNNAKT	IIVHLNESVQ
F1_BR_93BR	VQCTHGIKP	VSTQLLLNGS	LA.EGEIVIR	SONISDNAKT	IIVHLNESVQ
F1_FI_FIN9	VQCTHGIRPV	VSTQLLLNGS	LS.EGGIIIR	SONLSDNAKT	IIVHLNESVQ
F1_FR_MP41	VQCTHGIRPV	VSTQLLLNGS	LA.EEDIIIR	SONISDNAKT	IIVHLNESVQ
F2_CM_MP25	VQCTHGIKP	VSTQLLLNGS	LA.EEKMIIR	SENISDNNTKT	IIVQFKNPVK
F2KU_BE_VI	VQCTHGIRPV	ISTQLLLNGS	LA.EKEIIIR	SGNISDNNTKN	IIVQLNETVE
G_BE_DRCBL	VQCTHGIKP	VSTQLLLNGS	LA.EKDIIIS	SENISDNAKV	IIVHLNRSVE
G_NG_92NG0	VQCTHGIKP	VSTQLLLNGS	LA.EEDIRIR	SENFTDNTKV	IIVQLNNSIE
G_SE_SE616	VQCTHGIKP	VSTQLLLNGS	LA.EGKIKVR	SENFTDNTKV	IIVQLNKTVE
H_BE_VI991	VQCTHGIRPV	VSTQLLLNGS	LA.EVEEVIIR	SKNITDNTKN	IIVQLNEPVQ
H_BE_VI997	VQCTHGIKP	VSTQLLLNGS	LA.EGQVIIR	SKNISDNNTKN	IIVQLDSPIE
H_CF_90CF0	VQCTHGIRPV	VSTQLLLNGS	LA.EEQIIIR	TKNISDNNTKN	IIVQLKTPVN
J_SE_SE702	VQCTHGIKP	VSTQLLLNGS	VA.EGDIIIR	SENISDNAKN	IIVQLNDTVE
J_SE_SE788	VQCTHGIKP	VSTQLLLNGS	IA.EGDIIIR	SENISDNAKN	IIVQLNKTVE
K_CD_EQTB1	VQCTHGIKP	VSTQLLLNGS	LA.EEEIIIR	SEDITKNNTKN	IIVQLNEAVE
K_CM_MP535	VQCTHGIKP	VSTQLLLNGS	LA.EEEIIIR	SENITDNTKN	IIVQLNETVQ
N_CM_YBF30	VQCTHGIKP	ISTQLILNGS	LNTDGIVIR.	....NDSHSN	LLVQWNETVP
O_CM_ANT70	VTCTHGIRPT	VSTQLILNGT	LS.KGKIRMM	AKDILEGGKN	IIVTLNSTLN
O_CM_MVP51	VTCTHGIRPT	VSTQLILNGT	LS.REKIRIM	GKNITESAKN	IIVTLNTPIN
O_SN_99SE_	VTCTHGIRPT	VSTQLILNGT	LS.EGNIRIM	GKNISDNMKN	IIVTLNSTIN
O_SN_99SE_	VTCTHGIRPT	VSTQLILNGT	IS.EGKIRIM	GKNISDTGKN	IIVTINNSTIN
U_CD___83C	VQCTHGIRPV	VSTQLLLNGS	LSEE.EVIIR	SENITNNAKT	IIVQLNETVK

00BW0762_1	IVCTRPNNN.	.TRRSVRIG.	.PGQTFYATG	.....DIIGN	IRQAHCNISK
00BW0768_2	IECTRPNNN.	.TRKSIRIG.	.PGQTFYATG	.....DIIGD	IREAHCNINK
00BW0874_2	IVCTRPNNN.	.TRKSIRIG.	.PGQTFYATG	.....DVIGD	IRQAHCNTSE
00BW1471_2	IVCTRPNNN.	.TRKSVRIG.	.PGQTFYATG	.....DIIGD	IRQAHCNISN
00BW1616_2	IVCTRPNNN.	.TRKSMRIG.	.PGQTFYATG	.....DIIGN	IREAHCNISK
00BW1686_8	INCTRPNNN.	.TRKSIRIG.	.PGQTFYATG	.....AIIGD	IRQAYCTVNA
00BW1759_3	IVCTRPNNN.	.TRRSVRIG.	.PGQTFYARG	.....DIIGN	IRQAHCNISR
00BW1773_2	ITCTRPNNN.	.TRKSIRIG.	.PGQTFYATG	.....DIIGD	IRQAHCNISA
00BW1783_5	INCTRPNNN.	.TRKSVRIG.	.PGQTFYATG	.....DIIGD	IRQAHCNISE
00BW1795_6	IVCTRPNNN.	.TRKSVRLG.	.PGQAFYATG	.....DIIGD	IRKAYCTINE
00BW1811_3	IVCTRPNNN.	.TRKSIRIG.	.PGQAFFATG	.....EIIGD	IRQAHCNISA
00BW1859_5	IVCIRPNNN.	.TRKSIRIG.	.PGQTFYATG	.....DIIGN	IREAHCNITR
00BW1880_2	IVCTRPNNN.	.TKKSMRIG.	.PGQTFYATG	.....DIIGD	IRQAHCNISE
00BW1921_1	IECTRPNNN.	.TRKSIRIG.	.PGQTFYATG	.....DIIGN	TRQAHCNVSA
00BW2036_1	IECIRPNNN.	.TRKSIRIG.	.PGQVIFYATG	.....DIIGD	IREAHCNITE
00BW2063_6	IVCTRPNNN.	.TRKSVRIG.	.PGQTFYATG	.....EVIGD	IREAHCNISE
00BW2087_2	IVCTRPNNN.	.TRKSIRIG.	.PGQAFYATD	.....AIIGD	IRQAHCNISR
00BW2127_2	IVCTRPNNN.	.TRTSIRIG.	.PGHSFFATN	.....GIIGD	IRQAHCSISK
00BW2128_3	INCTRPNNN.	.TRKSIRIG.	.PGQAFYATG	.....DIIGD	IRQAHCNISK
00BW2276_7	IVCVRPNNN.	.TRKSVRIG.	.PGQTFYATG	.....NIIGD	IREAHCNISE
00BW3819_3	IKCTRPNNN.	.TRRSVRIG.	.PGQAFYTN.	.....DIIGD	IRLAHCNISK
00BW3842_8	IVCTRPNNN.	.TRKSIRIG.	.PGQTFYAAG	.....DIIGN	IRQAHCNISE
00BW3871_3	ITCTRPNNN.	.TRESIRIG.	.PGQTFYATG	.....DIIGD	IRKAYCNISI
00BW3876_9	IVCTRPNNN.	.IRKSVRIG.	.PGQAFYATG	.....DIIGD	IREAYCNING
00BW3886_8	IVCVRPNNN.	.TRKSIRIG.	.PGQTFYATG	.....EIIGN	IRQAYCSISG
00BW3891_6	IECTRPNNN.	.TRRSIRIG.	.PGQTFYATG	.....EIIGD	IRQAYCTINE
00BW3970_2	IECIRPNNN.	.TRKSIRIG.	.PGQTFYATN	.....GMIGD	IRQAHCNISG
00BW5031_1	IECRPNNN.	.TGKSVRIG.	.PGQTFYATG	.....GIIGE	IRRAHCDING
96BW01B21	INCTRPNNN.	.TRKSIRIG.	.PGQTFYAAG	.....EIIGK	IRLAYCNISE
96BW0407	IECTGPNNN.	.TRKSMRIG.	.PGQTFYATG	.....EIVGD	IRQAHCNISE
96BW0502	IVCVRPNNN.	.TRKSVRIG.	.PGQTFYATG	.....EIIGD	IRQAYCIINK
96BW06_J4	IVCTRPNNN.	.TRKSIRIG.	.PGQTFYAT.	.....DIIGD	IRQAYCNVSK
96BW11_06	IVCIRPNNN.	.TRKSVRIG.	.PGQTFYATE	.....AIIGN	IREAHCNISE
96BW1210	IVCTRPNNN.	.TRKSIRIG.	.PGQTFYATG	.....DIIGD	IRQAHCNISK
96BW15B03	IVCTRPNNN.	.TRKGIRIG.	.PGQTFYATE	.....NIIGD	IRQAHCNISA
96BW16_26	IVCIRPNNN.	.TRKSIRIG.	.PGQTFYATG	.....DIIGD	IRQAHCIING
96BW17A09	IVCTRPNNN.	.TRKSTRIG.	.RGQTFYAMG	.....RIIGD	IRQAHCNISG
96BWM01_5	IECTRPNNN.	.TRRSVRIG.	.PGQAFYATG	.....DIIGD	IRAAHCNISE
96BWM03_2	INCTRPNNN.	.TRKSVRIG.	.PGQAFYATG	.....DIIGD	IRKAYCNISK
98BWMC12_2	IVCTRPNNN.	.TRKSMRIG.	.PGQIFYATG	.....DIIGD	IREAHCNISK
98BWMC13_4	IECTRPNNN.	.TRKSMRIG.	.PGQAFYATG	.....EIIGN	IRQAYCNINE
98BWMC14_a	IVCTRPNNN.	.TRKSIRIG.	.PGQTFYATG	.....DIIGD	IRQAHCNISE
98BWM014_1	IVCTRPNNN.	.TRTSIRIG.	.PGQTFYATG	.....DIIGD	IRQAHCNISE
98BWM018_d	ILCVRPSNN.	.TRKSVRIG.	.PGQTFYATG	.....DIIGD	IRQAHCNISA
98BWM036_a	IVCTRPNNN.	.TRKSVRIG.	.PGQTFYATG	.....DIIGD	IRQAHCNISK
98BWM037_d	INCTRPNNN.	.TRKSIRIG.	.PGQAFYATN	.....DIIGD	IRQAHCNISE
99BW3932_1	IVCIRPNNN.	.TRKSIRIG.	.PGQTFYATG	.....AIIGN	IREAYCNISG
99BW4642_4	IVCIRPNNN.	.TRKSIRIG.	.PGQTFYATG	.....DIIGN	IKEAYCNIKE
99BW4745_8	IECIRPNNN.	.TRKSIRIG.	.PGQTFYATG	.....EIIGD	IRKAHTINK
99BW4754_7	INCTRPNNN.	.TRKSMRIG.	.PGQTFYATG	.....EIIGD	IRQAHCNISR
99BWMC16_8	ITCTRPNNN.	.TRKSIRIG.	.PGQTFYATG	.....DIIGD	IRQAHCSINK
A2_CD_97CD	INCTRPNNN.	.TRKSIRFG.	.PGQAFYTNN	.....NIIGD	IRQAHCNISI
A2_CY_94CY	ITCIRPNNN.	.TRKSIRFG.	.PGQAFYTN.	.....EIIGD	IRQAHCNINK
A2D_97KR	INCTRPNNN.	.QRRSVRIG.	.PGRAFYTRQ	TYTR.QAKGD	IRQAQCNISS
A2G_CD_97C	ITCIRPNNN.	.TRKSIRFG.	.PGQAFYTN.	.....SIIGD	IRQAYCNISK
A_BY_97BL0	ITCIRPNNN.	.TRTSIRIG.	.PGQTFYATG	.....DVIXD	IRKAYCNVSR
A_KE_Q23_A	IKCIRPNNN.	.TRKSIRIG.	.PGQAFYATG	.....DIIGD	IRQAHCNVTR
A_SE_SE659	ITCIRPYHN.	.TRTRIHIH.	.PG.RSFYTG	.....DIKGS	IRQAHCTVNR
A_SE_SE725	INCTRPNNN.	.TRTSIRIG.	.PGQAFYATG	.....DITGD	IRQAHCNVSR

A_SE_SE753	INCTRPNNN.	.TRTSVPIG.	.PGKVFYATG	.....EIIGD	IRQAHCNVSK
A_SE_SE853	INCTRPNNN.	.TRKSIRIG.	.PGQAFYATG	.....EVIGD	IRQAHCNVSR
A_SE_SE889	IICIRPNNN.	.TRKSIRIG.	.PGQAFYATG	.....DIIGD	IRQAYCDVNR
A_SE_UGSE8	IICTRPNNN.	.TRKSIRIG.	.PGQAFYGMG	.....DIIGD	IRKAHCNVSR
A_UG_92UG0	INCTRPNNN.	.TRRSVRIG.	.PGQTFYATG	.....DIIGD	IRQAHCNVSG
A_UG_U455_	INCSRPNYTR	KNIRRSYIG.	.SGQAFYVTG	.....KIIGD	IRQAHCNVSR
AC_IN_2130	INCTRPNNN.	.TRTSIRIG.	.PGQTFYTS.	.....NIIGD	IRQAHCNVSR
AC_RW_92RW	INCSRPNNN.	.TRKSVHIG.	.PGQAFYATG	.....DVIGD	IRQAYCTVNG
AC_SE_SE94	INCTRPNNN.	.TRRSVHIG.	.PGQAFYATG	.....DITGD	IRKAHCIVNG
ACD_SE_SE8	INCTRPNNN.	.TRNSIRIG.	.PGQAFYATG	.....AITGD	IRQAHCNVSR
ACG_BE_VI1	INCTRPNNN.	.TRKSVRIG.	.PGQTFYATG	.....DIIGD	IRQAHCNISG
AD_SE_SE69	INCTRPNNNT	.RK.SVRIG.	.PGQALYVTG	GII..G...D	IRQAFCEVNR
AD_SE_SE71	INCTRPNNN.	.TRKSVHMG.	.PGKVFYATG	.....DIIGD	IRQAHCNVSK
ADHK_NO_97	INCTRIANNT	RKS..IHIG.	.PGQAFYAAE	PVI..G...D	IRQAHCNISE
ADK_CD_MAL	INCTRPNNNT	.RR.GIHFG.	.PGQALYTTG	IVG.....D	IRRAYCTINE
AG_BE_VI11	INCTRPNNNT	RKSIGLGP.	...QAFYATG	DII..GD...D	IRQAHCNVSG
AG_NG_92NG	INCTRPNNNT	RKSIRIGP.	...QAFYATG	EII..G....	.....
AGHU_GA_VI	INCTRPNNNT	RKG..IRIG.	.PGRVIYATS	AIT..G...D	IRQAHCNISK
AGU_CD_Z32	ITCMRPNNY.	.TRKSIHIG.	.PGRALYPEG	.....DIIGD	IRQAHCNVSR
AJ_BW_BW21	IKCVRPANNT	RKGIHTGPG.	...QVLYATG	AVV..GD...D	IRQAHCNVSR
B_AU_VH_AF	IHCMRPNNNT	.RK.GIYVG.	.PGRHIYATE	KIV..G...D	IRQAHCNISR
B_CN_RL42_	IKCIRPNNNT	.RK.SIHLG.	.PGKAWYTTG	QII..G...D	IRQAHCNLSS
B_DE_D31_U	INCTRPNNYT	.SK.RIRIG.	.ARRAFYTKG	KII..G...D	IRQAHCNISG
B_DE_HAN_U	INCTRPNNNT	.RK.GIHIG.	.PGRAVYTTG	RIV..G...D	IRLAHCNISR
B_FR_HXB2_	INCTRPNNNT	.RK.RIRIQ.	GPGRAFTIG	KIG.....N	MRQAHCNISR
B_GA_OYI_	INCTRPNNNT	.RN.RISIG.	.PGRAFHTTK	QII..G...D	IRQAHCNLSS
B_GB_CAM1_	INCTRLNNNT	.RK.SIAIG.	.PGRTVYATD	RII..G...D	IRQAHCNLSS
B_GB_GB8_C	INCTRPNNNT	.RK.GIYMG.	.PGRRFYTTG	RII..G...D	IRQAHCNISK
B_GB_MANC_	INCTRPNNNS	.RK.SIYIG.	.PGRRFHVTR	AVT..G...D	IRQAHCNISK
B_KR_WK_AF	INCTRLNNNT	.RK.SIRIG.	.PGSTFYATG	AII..G...D	IRQAHCNISR
B_NL_3202A	INCTRPNNNT	.RK.GIHIG.	.PGKAFYATG	QII..G...D	IRQAHCNLSS
B_TW_TWCYS	INCTRPNNIS	KRR.SMHIG.	.TGRVFTYT	..I..G...N	IRQAHCNLSS
B_US_BC_L0	INCTRPNNKT	.RK.RITTG.	.PGRVYTTG	EIV..G...D	IRQAHCNLSS
B_US_DH123	INCTRPNNNT	.RK.GITLG.	.PGRVFTYT	EIV..G...D	IRKAHCNISK
B_US_JRCSE	INCTRPNNNT	.RK.SIHIG.	.PGRAFYTTG	EII..G...D	IRQAHCNISR
B_US_MNCG_	INCTRPNNYK	.RK.RIHIG.	.PGRAFYTTK	NII..G...T	IRQAHCNISR
B_US_P896_	INCTRPNNNT	.RR.RLSIG.	.PGRAFYARR	NII..G...D	IRQAHCNISR
B_US_RF_M1	INCTRPNNNT	.RK.SITKG.	.PGRVIYATG	QII..G...D	IRKAHCNLSS
B_US_SF2_K	INCTRPNNNT	.RK.SIYIG.	.PGRAFHTTG	RII..G...D	IRKAHCNISR
B_US_WEAU1	INCTRPNNNT	.RK.KITLG.	.PGRVLYTTG	EII..G...D	IRRAHCNLSS
B_US_WR27_	INCTRPNNKI	.RR.RIHIG.	.PGRAFYTDR	..V..G...D	IRQAYCNISG
B_US_YU2_M	INCTRPNNNT	.RK.SINIG.	.PGRALYTTG	EII..G...D	IRQAHCNLSS
BF1_BR_93B	INCTRPNNNT	RKS..IPIG.	.PGRAFYTTG	EII..G...D	IRKAHCNVSG
C_BR_92BR0	INCTRPNNN.	.TRKSIRIG.	.PGQAFYATG	.....EIIGD	IRQAHCNISR
C_BW_96BW0	IVCTRPNNN.	.TRRSVRIG.	.PGQTFYATG	.....EIIGD	IR.AHCNISE
C_BW_96BW1	IVCIRPNNN.	.TRKSVRIG.	.PGQTFYATE	.....AIIGN	ISEAHCNISE
C_BW_96BW1	IVCTRPNNN.	.TRKSIRIG.	.PGQTFYATG	.....DIIGD	IRQAHCNISK
C_BW_96BW1	IVCTRPNNN.	.TRKGIRIG.	.PGQTFYATE	.....NIIGD	IRQAHCNISA
C_ET_ETH22	ITCTRPNNN.	.TRESIRIG.	.PGQTFYATG	.....DIIGD	IRQAHCNISE
C_IN_93IN1	IVCTRPNNN.	.TRKSIRIG.	.PGQTFYATG	.....DIIGD	IRQAHCNISR
C_IN_93IN9	IVCTRPNNN.	.TRKSIRIG.	.PGQTFYATG	.....EIIGD	IRQAHCNISR
C_IN_93IN9	IECVRPNNN.	.TRESIRIG.	.PGQTFYATG	.....EIIGD	IRQAHCNISA
C_IN_94IN1	IVCTRPNNN.	.TRKSIRIG.	.PGQTFYATG	.....EIVGN	IRQAHCNISK
C_IN_95IN2	IMCTRPDNN.	.TRKSIRIG.	.PGQTFYATG	.....DIIGD	IRQAHCNISE
CRF01_AE_C	INCTRPFFKN.	.MRTSARIG.	.PGQVFYKTG	.....SITGD	IRKAYCEING
CRF01_AE_C	INCTRPFFKK.	.VRISARIG.	.PGRVFHTTG	.....NINGD	IRKAYCEINK
CRF01_AE_C	INCTRPFFKK.	.MRTSVRIG.	.PGRVFYKTG	.....SITGD	IRKAYCEING
CRF01_AE_T	INCTRPNNN.	.MRTSMRIG.	.PGQVFYRTG	.....SITGD	IRKAYCEING
CRF01_AE_T	INCTRPNNN.	.TRTSITMG.	.PGQVFYRTG	.....DIIGD	IRKAYCEING
CRF01_AE_T	INCTRPFFYN.	.KRTRTSIG.	.QGRVLYRTG	.....DITGN	IGKPYCEING



CRF01_AE_T	INCTRPSGK.	.EEKRMTIG.	.PGKVFYSTG	.....KITGD	IRKAYCVING
CRF01_AE_T	INCTRPSNN.	.TRTSITIG.	.PGRVfyRTG	.....DIIGN	IRKAYCEING
CRF01_AE_T	INCTRP.TI.	.YKKKTTMG.	.PARVYHRTG	.....DVIGD	IRKAYCQING
CRF02_AG_F	INCPRPNNN.	.TRKSVRIG.	.PGQTFYATG	.....DIIGD	IRQAHCNVSR
CRF02_AG_F	INCTRPNNN.	.TRKSVRIG.	.PGQTFYATG	.....DIIGD	IRQAHCNVSR
CRF02_AG_G	INCTRPNNN.	.TRKSVRIG.	.PGQTFYATG	.....GIIGD	IRQAHCNVSR
CRF02_AG_N	INCTRPNNN.	.TRKGVHIG.	.PGQAFYATG	.....DIIGD	IRQAHCNVSK
CRF02_AG_S	INCTRPGNN.	.TRKSVRIG.	.PGQTFYATG	.....DIIGD	IRQAHCNVSW
CRF02_AG_S	INCTRPSNN.	.TRKSVRIG.	.PGQTFYTTG	.....AVIGD	IRQAHCNVSR
CRF03_AB_R	INCTRPNNNT	.RK.GIHIG.	.PGRAFYATG	DIT..G...D	IRQAHCNISI
CRF03_AB_R	INCTRPNNNT	.RK.GIHIG.	.PGRAFYATG	DII..G...D	IRQAYCNISR
CRF04_cpx_	INCTRPGNNT	RKS..VHIG.	.PGLTWYATG	EII..G...D	IRQAHCNISG
CRF04_cpx_	INCTGLNNNT	GGSERIGIG.	.PGHTWYATG	NIV..G...D	IRQAHCNISG
CRF04_cpx_	INCTRPNNNT	RKG..VHIG.	.PGKTWFATG	EVI..G...D	IRKAHCNISE
CRF05_DF_B	INCTRPNNNT	RKS..IHLG.	.PGQAFYATG	DII..G...D	IRKAHCNVSR
CRF05_DF_B	INCTRPNNNT	RKS..IPLG.	.PGQAFYTTG	DII..G...D	IRKAHCNVSG
CRF06_cpx_	IRCTRPGNNT	RKSISFGPG.	...QAFIATG	DII..GD...D	IRQAHCNVSR
CRF06_cpx_	ISCSRPNNT	RKSIHIGPG.	...QAFYATG	EII..GN...D	IRKAHCNVSR
CRF06_cpx_	IRCTRPSNNT	RKSIPLGPG.	...QAFYATG	DII..GD...D	IRQAHCNVSR
CRF06_cpx_	IKCTRPNNNT	RKSISFAPG.	...QAFYATG	DII..GD...D	IRQAHCNVSR
CRF11_cpx_	INCTRPGNNT	RKSIHLGPG.	...HAFYATG	AII..GD...D	IRQAHCNVSK
CRF11_cpx_	INCTRPNNNT	RKGIHIGPG.	...QAFYATG	DII..GD...D	IKQAHCNVSR
D_CD_84ZR0	INCTRPYKKE	.RQ.RTPIG.	.QGQALYTTR	YT.....TRI	IGQAYCNISG
D_CD_ELI_K	ITCARPYQNT	.RQ.RTPIG.	.LGQSLYTTR	SR.....SI	IGQAHCNISR
D_CD_NDK_M	INCTRPYKYT	.RQ.RTSIG.	.LRQSLYTIT	GKK..KKTGY	IGQAHCNISR
D_UG_94UG1	INCIRPYNNT	.RQ.STRIG.	.PGQALFTTK	VIG.....D	IRQAHCNISG
F1_BE_VI85	INCTRPNNNT	RKG..IHLG.	.PGQTFYATG	AII..G...D	IRKAHCNISG
F1_BR_93BR	INCTRPNNNT	RKR..ISLG.	.PGRVfyTTG	EII..G...D	IRKAHCNVSG
F1_FI_FIN9	INCTRPNNNT	RKS..IRIG.	.PGQSfyATG	EII..G...D	IRKAHCNISG
F1_FR_MP41	INCTRPNNNT	RKS..IHLG.	.PGQAFYATG	DII..G...D	IKKAYCEING
F2_CM_MP25	INCTRPNNNT	RRS..IHIG.	.PGRAFYATG	EII..G...D	TRKAHCNISE
F2KU_BE_VI	IVCIRPGNNT	RKS..IRIG.	.PGQTFYATG	DII..G...D	IRQAHCNITG
G_BE_DRCBL	INCTRPNNNT	RRSVAIGPG.	...QAFYTTG	EVI..GD...D	IRKAHCNVSW
G_NG_92NG0	INCIRPNNT	RKSIPIGPG.	...QAFYATG	DII..GD...D	IRQAHCNVSR
G_SE_SE616	INCTRPNNNT	MKRIRMGIGP	..GQTFYATG	AII..GD...D	IRQAHCNVTK
H_BE_VI991	INCTRTGNNT	RKS..IRIG.	.PGQAFYATG	DII..G...D	IRRAYCNISG
H_BE_VI997	ITCTRPNNNT	RKG..IHFG.	.PGQAFYATG	DII..G...N	IRQAHCNVSE
H_CF_90CF0	ITCTRPNNNT	RTS..IHLG.	.PGRAFYATG	DII..G...D	IRQAHCNISR
J_SE_SE702	IVCTRPNNNT	RKGIHMGPG.	...QVLYATG	EII..GD...D	IRKAYCNISR
J_SE_SE788	IVCYRPNNNT	RKGIHMGPG.	...QVLYATG	EII..GN...D	IRETHCNISE
K_CD_EQTB1	INCTRPSNNT	RKS..IHIG.	.PGRAFYATG	DII..G...D	IRQAHCNISG
K_CM_MP535	INCTRPNNNT	RKS..IHMG.	.PGKAFYTTG	DII..G...D	IRQAHCNISG
N_CM_YBF30	INCTRPGNN.	.TGGQVQIG.	.PAMTFYNIE	K.....IVGD	IRQAYCNVSK
O_CM_ANT70	MTCERP.QI.	.DIQEMRIG.	..PMAWYSMG	IGG..TAGNS	SRAAYCKYNA
O_CM_MVP51	MTCIREGIA.	.EVQDIYTG.	..PMRWRSMT	LKRSNNTSPR	SRVAYCTYNK
O_SN_99SE_	MTCVROGNQ.	.SVQEIQIG.	..PMAWYSMS	LAQE.GKPNN	SRIAYCKYNI
O_SN_99SE_	MTCERPGNQ.	.TVQKILTG.	..PVAWYSMG	LKN...NLTN	SRAASCKYNS
U_CD___83C	INCTRPGSDK	KIRQSIRIG.	.PGKVFYAKG	.....GI	TGQAHCNITD

	401				450
00BW0762_1	TKWNKTLRSRI	GEKLKEHFPN	...KTIRFN.	.SSAGGDLEI	TTHSFNCRGE
00BW0768_2	EKWNSTLQGV	REKLEKHFPN	...KNITFE.	.PSSGGDLEI	TTHSFNCRGE
00BW0874_2	QKWNKTLQV	GKKLAEHFPN	...KTIIFN.	.SSSGGDLEI	TTHSFNCGGE
00BW1471_2	SNWNSTLQV	ARKLEKYFPN	...KTIKFO.	.PSSGGDLEI	TTHSFNCRGE
00BW1616_2	TKWENTLHMV	SEKLKENFPN	...KTIVFN.	.SSAGGDLEI	TTHSFNCRGE
00BW1686_8	SKWNETLQKV	KKKLGEHFPD	...KNITFE.	.SPSGGDLEI	TTHTFNCRGE
00BW1759_3	GEWNETLMEV	SKELRKYFPN	...KNITFA.	.PSSGGDLEI	TTHSFNCRGE
00BW1773_2	AQWNKTLQEV	GAKLEEHPN	...KTIKFN.	.QSSGGDLEI	TTHSFICRGE
00BW1783_5	KAWNKTLLHRV	SEXLKEHFPN	...KTIKFT.	.SPSGGDLEI	IQHTFNCGGE
00BW1795_6	SKWITTLHRV	SEKLKEHFPN	...KAINFT.	.QPKGGDLEI	TTHSFNCRGE
00BW1811_3	TNWNKTLQMV	SEKLOQHFPN	...KTIKFD.	.KHSGGDLEI	TTHSFNCRGE
00BW1859_5	EEWNKTLQGV	EEKLKEHFPN	...KKITFK.	.PSSGGDLEV	TTHSFNCGGE
00BW1880_2	DVWRKTLFNV	SNKLKEYFPK	...RNITFN.	.SSTGGDLEI	TTHSFNCRGE
00BW1921_1	GAWNKTLLQV	GEELRKHFPN	...KTIQFN.	.SSSGGDLEI	TTHTFNCRGE
00BW2036_1	SAWNRTLLHRV	SKKLREHFPN	...TTIKFO.	.PASGGDLEI	TTHSFNCRGE
00BW2063_6	EKWNKTLRV	SEKLKEYFPN	...KTIKFD.	.QPTGGDLEI	TKHSFNCRGE
00BW2087_2	DKWNKTLQV	GEKLAEHFPN	...KTIKFA.	.PSSGGDLGI	TTHSFNCRGE
00BW2127_2	DAWNKTLQV	GKKLEEFYFPN	...KTIKFA.	.NSSGGDLEI	TTHSFNCGGE
00BW2128_3	EEWNKTLREV	KGKLGHFPN.	...KTIKFA.	.PSSGGDLEI	TAHSFNCRGE
00BW2276_7	NQWNKTLQV	GKKLKEHFPN.	...KTIKFE.	.QSSGGDLEI	TMHSFNCRGE
00BW3819_3	KAWNKTLQLV	VKKLKEHFPN	...RTIKFT.	.PPPGGNLEI	TTHSFNCRGE
00BW3842_8	GNWTKTLQV	SRKLRQIFNK	...SNIEFK.	.PHSGGDPEI	TTHSFNCRGE
00BW3871_3	HEWNKTLQV	KKKLGEHFPN	...KTIKFO.	.PSSGGDLEI	ATHTFNCRGE
00BW3876_9	SDWNRTLLQV	KNKLGEHFPN	...TVIKFE.	.PSSGGDLEI	TTHSFNCRGE
00BW3886_8	GNWTETLLRV	KNKLGEHFPN	...KTITFG.	.PSSGGDLEI	TTHSFNCRGE
00BW3891_6	STWNRTLLQV	SRKLVERFPN	...KTIRFO.	.PPSGGDLEI	TTHSFNCRGE
00BW3970_2	ADWNRTLLQV	GRKLAGEYFPN	...KTISFO.	.PSSGGDLEI	TTHSFNCGGE
00BW5031_1	TKWTETLLQKI	SEKLRGYFK.	...KTIIFA.	.PSSGGDPEI	TTHSFNCRGE
96BW01B21	EVWKKTLQV	GRKLKEHFPN	...KTIQFO.	.PPSGGDLEV	TTHSFNCRGE
96BW0407	KDWNKTLHRV	RKKLAEHFS.	...KNITFK.	.PSSGGDLEI	TTHSFNCGGE
96BW0502	TEWNSTLQGV	SKKLEEHFSK	...KAICKE.	.PSSGGDLEI	TTHSFNCRGE
96BW06_J4	TNWNKTLKGV	KGELRKHFPN.	...KNITFO.	.PASGGDLEI	TTHTFNCRGE
96BW11_06	SQWNKTLHRV	IEKLKEHFPN	...KTIGFS.	.QAAGGDLEI	TTHSFNCGGE
96BW1210	GAWNKTLQV	GKKLKEHFPN	...KTIRFK.	.ESSGGDLEI	TTHSFNCGGE
96BW15B03	GEWNKAVQV	SAKLREHFPN	...KTIEFO.	.PSSGGDLEI	TTHSFNCRGE
96BW16_26	SEWKRTLLQV	SEKLGHFPN	...KTIKFA.	.PHSGGDLEI	TTHVLNCRGE
96BW17A09	..WNNTLQV	VKKLRKHFPN	...KTITFA.	.PPSGGDLEI	TTHSFNCGGE
96BWM01_5	SKWNKILRV	SEKLKEHFPN	...KTIQFG.	.QPIGGDLEI	TTHSFNCRGE
96BWM03_2	GEWAKVMQV	TGKLKEHFP.	...KNITFO.	.PPSGGDLEI	TTHSFNCRGE
98BWMC12_2	QKWNKTLQV	GKKLAEFYFPN	...RTIAFN.	.SSARGDLEI	ATHSFNCRGE
98BWMC13_4	SLWNKTLKYV	SEKLKEYFPN.	...TTIEFO.	.QPAGGDLEI	TTHSFNCRGE
98BWMC14_a	EEWNNSLQV	AKKLREHFPN	...KTIAFN.	.SSSGGDLEI	TTHTFNCRGE
98BWM014_1	GNWTKTLHRV	GEKLKEHFPN	...KTIKFA.	.PPSGGDLEI	IMHSFNCGGE
98BWM018_d	DDWKSTLLQV	SEKLRRHFPN	...KTIVFN.	.SPSGGDLEI	ITHSFNCEGE
98BWM036_a	ERWNKTLQEV	GEKLERHFPN	...KTIEFK.	.PSSGGDLEI	TTHSFNCRGE
98BWM037_d	KKWYKALHGV	REKLKVLFPN	...KNISFO.	.PAAGGDLEV	TTHSFNCKGE
99BW3932_1	DAWNKTLQV	GRKLKEYFPG	...STIRFA.	.PHSGGDLEI	TTHSFNCRGE
99BW4642_4	SEWNRTLLQV	GEKLGYFPS	...KTIKFN.	.SSSGGDLEI	TTHSFNCRGE
99BW4745_8	KAWNNTLLQEV	GRKLAEHFPN	...KTIKFO.	.PHSGGDPEI	TMHSFTCGGE
99BW4754_7	SQWNKTLYEY	SEKLREKFPN	...KTIQFN.	.SSTGGDLEI	TTHSFNCGGE
99BWMC16_8	EAWNKTLLRV	SKKLREHFPN	...KTIIFD.	.KSSGGDLEI	TTHSFNCGGE
A2_CD_97CD	TEWNATLLKV	VEQLREHFPN	...KTIIFN.	.SSSGGDLEI	TTHSFNCGGE
A2_CY_94CY	TLWNTLLQV	AEQLREKFPK	...KTIIFT.	.NSSGGDPEI	TTLNCFNAGE
A2D_97KR	RQWNTLLQV	AEQLRKYFSN	...KTIIFT.	.NSSGGDLEI	TTHSVNCGGE
A2G_CD_97C	AGWNTLLQV	AEQLGKHFSG	...KNITFA.	.NSSGGDLEI	TTHSFNCGGE
A_BY_97BL0	AAXNSTLQKI	STQLRKYFNN	...KTIIFK.	.SSTGXDLEV	TTHSFNCGGE
A_KE_Q23_A	SRWNKTLQEV	AEKLRTYFGN	...KTIIFA.	.NSSGGDLEI	TTHSFNCGGE
A_SE_SE659	SEWNNTLQV	AKQLRTYFGN	...KTIIFT.	.NSSGGDLEI	TTHSFNCKGE
A_SE_SE725	SSWNKTLQDI	VTQLRVYWN.	...RTIIFN.	.SSSGGDLEI	TTHSFNCGGE

A_SE_SE753	SKWNATLQKV	AIKLREYFDD	...KTIIFT.	.KPSGGDLEI	TTHSFNCGGE
A_SE_SE853	AKWNKTLHEV	AKQLRITYFNN	...KTIIFT.	.NSSGGDLEI	TTHTVNCGGE
A_SE_SE889	TEWNEALQKV	VNQLKTHFKN	...KTIIFN.	.SSSGGDLEI	TTHSFNCGGE
A_SE_UGSE8	SKWNETLKKV	AIQLRKYWN.	...TTIIFT.	.NSSGGDLEI	TTHSFNCGGE
A_UG_92UG0	SQWNKTLHQV	VEQLRKYWNN	...NTIIFN.	.SSSGGDLEI	TTHSFNCAGE
A_UG_U455_	RDWNRTIQQV	AEQLKKKFNN	...KTIIFA.	.SSSGGDIEI	TTHSFNCGGE
AC_IN_2130	AEWNKALNKI	GKQLRKYFVN	...KTIKFA.	.NSSGGDLEI	TTHSFNCEGE
AC_RW_92RW	TKWNRTLQKV	AEKLSHYFEN	..ITTIIFK.	.NSSGGDLEI	TTHSFNCGGE
AC_SE_SE94	TKWNKTLHKV	VTQLRKYFVN	...KPIIFT.	.PSSGGDVEV	TTHSFNCRGE
ACD_SE_SE8	SEWNKTLQQV	AKKLGDP LNK	...TEIIFK.	.PPSGGDLEI	TTHSFNCGGE
ACG_BE_VI1	KEWNKTLQAV	GKKLAEYYPN	...KTINFT.	.QASGGDLEI	VTHSFNCGGE
AD_SE_SE69	TKWDKTLREV	AIQLKHYYG.	..NKTIVIFAN	.SS.GGDIEI	TTHSFNCRGE
AD_SE_SE71	SAWNNTLQQV	VIQLRRYFNN	...KTIIFT.	.NSSGGDLEI	TTHSFNCGGE
ADHK_NO_97	GSWMKTLHKV	ATQLXQHFS.	..NKTIIFNA	.SA.GGDIEI	TTHSFNCGGE
ADK_CD_MAL	TEWDKTLQQV	AVKLGSLLN.	..KTKIIFNS	.SS.GGDPEI	TTHSFNCRGE
AG_BE_VI11	KDWGKMLQEV	SRQLKKFFNN	...KTIFFNS	.SA.GGDLEI	TTHSFNCRGE
AG_NG_92NG	QEWQEMLQKV	QAQLEQVFN.	...KSITFNS	.SA.GGDLEI	TTHSFNCRGE
AGHU_GA_VI	EQWNRTLERV	KEKLGRHFK.	..NKTITFKP	.AS.GGDPEV	TMHIFNCRGE
AGU_CD_Z32	KEWSETLSKV	AAQLRKHFVN	T.RTDIIFA.	.NSSGGDVEI	TTHSFNCGGE
AJ_BW_BW21	KNWTDTLHKV	TAKLKEYFN.	...TTIEFQP	.AS.AGDLEI	MTHTFNCGGE
B_AU_VH_AF	TNWTSVLRQI	AVKLRRERFK.	..NKTIVFNH	.SS.GGDPEI	VRHSFNCGGE
B_CN_RL42_	TKWNNTLKQI	TKKLREQFG.	..NKTIVFNQ	.SS.GGDPEI	VMHSFNCGGE
B_DE_D31_U	AKWDSTLRQI	VKKLRERFG.	..NKTIVFNQ	.SS.GGDPEI	VTHSFNCGGE
B_DE_HAN_U	ARWNKTLNQI	FRKLREIRQF	.ENKTIVFNR	.SS.GGDPEI	VMHSFNCGGE
B_FR_HXB2_	AKWNNTLKQI	ASKLREQFG.	.NNKTIIFKQ	.SS.GGDPEI	VTHSFNCGGE
B_GA_OYI_	ATWEKTLEQI	ATKLRLKQFR.	.N.KTIAFDR	.SS.GGDPEI	VMHSFNCGGE
B_GB_CAM1_	TKWNNTLKQI	VTKLKEQFG.	..NKTIIFNQ	.SS.GGDPEI	VMHSFNCGGE
B_GB_GB8_C	EKWNNTLHQI	VIELRKQFR.	..NKTIVFNQ	.SS.GGDPEI	VMHSFNCGGE
B_GB_MANC_	AKWEKTLKQI	VEKLREKFG.	..NKTIIFNQ	.SS.GGDPEI	VTHSFNCGGE
B_KR_WK_AF	EKWNNTLKQI	VIKLGEQFG.	.NSNIIVFKQ	.SS.GGDPEI	VMHSFICGGE
B_NL_3202A	AKWNNTLKQI	VSKLRKQFG.	..NKTIVFSQ	.PL.GGDPEI	VMHSFNCGGE
B_TW_TWCYS	AEWNNTLPQI	VKKFREQFG.	..NKTIVFNQ	.SS.GGDLEI	VMHSFNCGGE
B_US_BC_L0	AKWNNTLRQI	VIKLRL..EQF	.ENKTIVFNQ	.SS.GGDPEI	VMHSFNCGGE
B_US_DH123	VKWHNTLKRV	VEKLREKFE.	..NKTIVFNK	.SS.GGDPEI	VMHSFNCGGE
B_US_JRCSF	AQWNNTLKQI	VEKLRL..EQF	.NNKTIVFTH	.SS.GGDPEI	VMHSFNCGGE
B_US_MNCG_	AKWNNTLRQI	VSKLKEQFK.	..NKTIVFNQ	.SS.GGDPEI	VMHSFNCGGE
B_US_P896_	AKWNNTLQOI	VIKLRL..EKF	.RNKTIAFNQ	.SS.GGDPEI	VMHSFNCGGE
B_US_RF_M1	AQWNNTLKQV	VTKLRL..EQF	.DNKTIVFTH	.SS.GGDPEI	VLHSFNCGGE
B_US_SF2_K	AQWNNTLEQI	VKKLREQFG.	.NNKTIVFNQ	.SS.GGDPEI	VMHSFNCRGE
B_US_WEAU1	TSWNNTLKQI	VEKLREIKQF	.KNKTIVFKQ	.SS.GGDPEI	VMHSFNCGGE
B_US_WR27_	TKWKNTLEKI	VAKIREIKQF	.KNKTIVFNH	.SS.GGDPEI	VMHSFNCGGE
B_US_YU2_M	TQWENTLEQI	AIKLKEQFG.	.NNKTIIFNP	.SS.GGDPEI	VTHSFNCGGE
BF1_BR_93B	TKWNNTLEKV	RAKLKPHFPN	...ATIKFNS	.SS.GGDLEI	TMHSFNCRGE
C_BR_92BR0	TAWNNTLQEV	GKKLAEHFPN	...KAIFKA.	.KHSGGDLEI	TTHSFNCRGE
C_BW_96BW0	RDWNNTLNRV	SKKLAHFPN	...KTIEFK.	.PSSGGDLEI	TTHSFNCRGE
C_BW_96BW1	SQWNNTLQRV	SEKLKEHFPN	...KTIKFN.	.QPAGGDLEI	TTHSFNCGGE
C_BW_96BW1	GAWNNTLQV	GKKLKEHFPN	...KTIRFK.	.ESSGGDLEI	TTHSFNCGGE
C_BW_96BW1	GEWNKAVQRV	SAKLREHFPN	...KTIEFQ.	.PSSGGDLEI	TTHSFNCRGE
C_ET_ETH22	EKWNNTLQKV	KEKLQKHFPN	...KTIEFK.	.PSSGGDLEI	TTHSFNCGGE
C_IN_93IN1	DKWNNTLQRV	GKKLAEHFHN	...KTIKFA.	.SSSGGDLEI	TTHSFNCRGE
C_IN_93IN9	ENWTDTLQRV	SKKLAHFPN	...KTIKFD.	.SPSGGDLEI	TTHSFNCRGE
C_IN_93IN9	DRWNNTLQV	GEKLAEHFPN	...KTIKFA.	.PSSGGDLEI	TTHSFNCRGE
C_IN_94IN1	RDWNNTLQRV	SEKLAKHFPN	...KTIKFA.	.PSSGGDLEI	TTHSFNCRGE
C_IN_95IN2	DKWNNTLQNV	SKKLAHFPN	...KTIIFN.	.SSSGGDLEI	TTHSFNCRGE
CRF01_AE_C	TKWNNTLKQV	TKKLREHFKN	...KTIIFQ.	.PSSGGDPEI	TMHHFNCRGE
CRF01_AE_C	TKWKETLKQV	TRKLREHLNG	...TMTISFR	.PSSGGDPEI	TMHHFNCRGE
CRF01_AE_C	TKWNNTLQOI	IRKLEEHFNN	...KTIQFKP	.PYSGGDLEI	TMHHFNCRGE
CRF01_AE_T	TKWNKVLKQV	TEKLKEHFNN	...KTIIFQ.	.PPSGGDLEI	TMHHFNCRGE
CRF01_AE_T	TKWNEVLKQV	AGKLKEHFNN	...KTIIFK.	.PPSGGDLEI	TMHHFNCRGE
CRF01_AE_T	TKWNKVLNQV	TEKLKEHFNN	...RNISFQ.	.PPSGGDLEI	TMHHFICRGE

CRF01_AE_T	TKWNETLKQV	AGKLREHFNN	...KTIIFQ.	.PPSGGDLEI	TMHHFNCRGE
CRF01_AE_T	TKWNKVLRQV	TEKLKEHFN.	...KTIIFQ.	.PPSGGDLEI	TMHHFNCRGE
CRF01_AE_T	TKWNKVLRQV	TEKLKEHFN.	...KTIIFQ.	.PPSGGDLEI	TMHHFNCRGG
CRF02_AG_F	SEWNRTLQQV	ATQLRKHFN.	...KTIIFA.	.NSSGGDIEI	TTHSFNCGGE
CRF02_AG_F	SKWNNTLQQV	AIQLRKHFN.	...TTIIFA.	.NPSGGDIEI	TTHSFNCGGE
CRF02_AG_G	TDWNNTLQQV	ATQLGKYFRD	T..TRIKFD.	.NPSGGDLEI	MTHSFNCGGE
CRF02_AG_N	TEWNKTLHQV	VTQLKTYFKN	...TTIIFA.	.NPLGGDVEI	TTHSFNCGGE
CRF02_AG_S	QQWNKTLHDV	ATKLREYFNN	...TTIIFD.	.EPSGGDLEI	TTHSFNCGGE
CRF02_AG_S	EKWNSTLQKV	VTKLKGKFNS	...SKIIFT.	.NSSGGDLEI	TTHSFNCGGE
CRF03_AB_R	TKWNNTLKQI	VIKLRKQFG.	..NKTIVFNQ	.SS.GGDPEI	VMHSFNCGGE
CRF03_AB_R	TKWNNTLEQI	VSKLRKQFR.	..NKTIVFNQ	.SS.GGDPEI	VMHSFNCGGE
CRF04_cpx_	NDWNNTLQVI	SEELKRLFP.	..NKTIFKAP	.PV.GGDLEI	TTHSFNCKGE
CRF04_cpx_	SDWNEALQKV	VVKLREHFP.	..NKTIIFNQ	.SS.GGDLEI	TTHSFNCGGE
CRF04_cpx_	KDWNNTLQKI	VDELKSHFP.	..NKNITFAP	.SA.GGDVEI	TTHSFRLGGE
CRF05_DF_B	EQWNKTLIQV	AKELQSHFP.	..NKTIFKNS	.SS.GGDLEI	TMHSFNCRGE
CRF05_DF_B	AQWNKTLQV	KEELRAHIKD	IGNKTIVFNS	.SA.GGDLEI	TSHIFNCRGE
CRF06_cpx_	ANWTDILGEV	KVKLEEVFNN	...THITFKS	.SA.GGDLEI	TTHSFNCGGE
CRF06_cpx_	KAWNSMLQNV	TAKLKELFNN	...KNITFNS	.SA.GGDLEV	TTHSFNCGGE
CRF06_cpx_	TAWKETLQNV	TEKLKQLLN.	...TNITFNP	.SA.GGDLEI	TTHSFNCRGE
CRF06_cpx_	TDWNNMLKNV	TTKLIEVFK.	...KNITFNS	.SA.GGDLEI	TTHSFNCGGE
CRF11_cpx_	AEWLNTLQQV	ATQLRGKFN.	...KTIIFDN	.PSPGGDIEI	TSHSFNCRGE
CRF11_cpx_	ADWNNTLQQV	AEQLHNNFN.	...KTIVFNE	.HS.GGDLEV	TTHSFNCGGE
D_CD_84ZR0	VKWNNTLRQV	ARKLGNLLN.	..QTKIIFKP	.SS.GGDPEI	TTHSFNCGGE
D_CD_ELI_K	AQWSKTLQQV	ARKLGTLLN.	..KTIIFKP	.SS.GGDPEI	TTHSFNCGGE
D_CD_NDK_M	AEWNKALQQV	ATKLGNLLN.	..KTTITFKP	.SS.GGDPEI	TSHMLNCGGD
D_UG_94UG1	AGWNKTLQQV	AEKLGNLLN.	..QTTIIFKP	.SS.GGDPEI	TTHSFNCGGE
F1_BE_VI85	TQWNNTLEYV	KAELKSHFPN	N..TAIKFNQ	.SS.GGDLEI	TMHSFNCRGE
F1_BR_93BR	TQWRNTLAKV	KAKLGSYFPN	...ATIKFNS	.SS.GGDLEI	TRHNFNCMGE
F1_FI_FIN9	EQWNKTLDRV	KAELKLHFNK	...TIQFNS	.SS.GGDLEI	TMHSFNCRGE
F1_FR_MP41	TQWSKTKTQV	QEKLRALFNK	...TIKFNQ	.SS.GGDLEI	TMHSFNCRGE
F2_CM_MP25	KQWYDTLIKI	ATEFKDQYN.	...KTVGFQP	.SA.GGDLEI	TTHSFNCRGE
F2KU_BE_VI	ENWNKTLEGV	KAKLHGFFTN	...KTIIFKP	.HS.GGDPEV	VMHTFNCGGE
G_BE_DRCBL	TKWNETLRDV	QAKLQEYFIN	...KSIEFNS	.SS.GGDLEI	TTHSFNCGGE
G_NG_92NG0	IKWREMLKNV	TAQLRKIYN.	..NKNITFNS	.SA.GGDLEI	TTHSFNCRGE
G_SE_SE616	RKWKEALQNV	AAELGKIFNK	S.SENITFNS	.SA.GGDLEI	TTHSFICRGE
H_BE_VI991	KQWNETLHKV	ITKLGSYFD.	..NKTIIILQP	.PA.GGDIEI	ITHSFNCGGE
H_BE_VI997	EKWNKTLQQI	ATQLSKYFV.	..NRTLIFKP	.HS.GGDLEV	TTHSFNCRGE
H_CF_90CF0	TDWNKTLHQV	VTQLGIHLN.	..NRTISFKP	.NS.GGDMEV	RTHSFNCRGE
J_SE_SE702	KDWNNTLRRV	AKKLREHFN.	...KTIDFTS	.PS.GGDIEI	TTHSFNCGGE
J_SE_SE788	RDWSNTLRRV	ATKLREHFN.	...KTINFTS	.PS.GGDIEI	VTHSFNCGGE
K_CD_EQTB1	GQWNKTVNQV	KKELGKHFN.	...KTIIFQP	.SS.GGDPQV	TRHIFNCRGE
K_CM_MP535	EKWNMTLSRV	KEKLKEHFKN	...GTITFKP	.PNPGGDPEI	LTHMFNCAGE
N_CM_YBF30	ELWPEMWNRT	REEIKKILGK	...NNITFRA	RERNEGDLEV	THLMFNCRGE
O_CM_ANT70	TDWGKILKQT	AERYLELVNN	TGSINMTFN.	.HSSGGDLEV	THLHFNCHGE
O_CM_MVP51	TVWENALQQT	AIRYLNLVNQ	TENVTIIFS.	.RTSGGDAEV	SHLHFNCHGE
O_SN_99SE_	SDWEKALKQT	AERYLDRNN	TNTVNITFE.	.RSIGGDSEV	THLHFNCHGE
O_SN_99SE_	SVWEEALKQT	AERYLELMNN	TNTVNITFN.	.HSTGGDPEV	THLHFNCHGE
U_CD___83C	GEWRNTLQQV	AIALRRQFNN	...KSIIFN.	.SSSGGDIEI	TTHTFNCGGE

	451			500
00BW0762_1	FFYCNTTRLF	NGTYN.....	.....STGD	TNS.....TN STITLQCRIK
00BW0768_2	FFYCDTSNLF	NKTRR.....	.....DN..	.....AN ETITLPCRIK
00BW0874_2	FFYCNTSRLF	NSTYN.....	.....PNST	YIEGR...SN ATITLQCRIK
00BW1471_2	FFYCYTTKLF	NSTYN.....	.....STYT	GSESN..... ITITPCRIK
00BW1616_2	FFYCNTSKLF	NGTYN.....	.....SNNN	TA..... DITLQCRIK
00BW1686_8	FFYCNTSNLS	NETYL.....	.....ANLT	SNVTK....N ATITLPCRIK
00BW1759_3	FFYCNTSNLF	NNTYR.....	.....ADNN	ITNDNSN... ITLQCRIK
00BW1773_2	FFYCNTSALF	NSTYN.....	.....STNT	SGHN....DT RIITLPCRIK
00BW1783_5	FFYCNTSKLF	NGTYN.....	.....GTS..	...ISS...N SSITLQCRIK
00BW1795_6	FFYCNTSELF	NGTYN.....	.....STG..	...DSN...S NLITLQCRIK
00BW1811_3	FFYCNTSQLF	NGTYM.....	.....PNTY	MS....SSDN RNITIPCR
00BW1859_5	FFYCNTTHLF	NGNG.....	.....	.....ESD INITLPCRIK
00BW1880_2	FFYCDTTKLF	NGTYN.....	.....STEQ	TN..... STITLQCRIK
00BW1921_1	FFYCNTSQLF	NGTYN.....	.....DT.Y	ESNSG....N STITLPCRIK
00BW2036_1	FFYCDTSKLF	NSSYN.....	.....DTEL	YSYNS....T ANITLPCRLK
00BW2063_6	FFYCNTSQLF	NSSYS.....	.....RHN..	...NTS...N STITLPCNIK
00BW2087_2	FFYCNTSGLF	N.....	.....GTF	NGT...HSTN TNITLPCRIK
00BW2127_2	FFYCNTTILF	NSTYY.....	.....P...	NTK...SDTT ETITLPCRIK
00BW2128_3	FFYCNTSLLF	DETQL.....	.....SKE..	.....N NTINIQCRIK
00BW2276_7	FFYCNTSKLF	NGTYM.....	.....PNYN	TSN...SSNN SNITLPCRIK
00BW3819_3	FFYCNTSGLF	NGTYN.....	.....G...	TND...NDTD SDITLPCRIK
00BW3842_8	FFYCNTSLLF	NSSYN.....	.....GNSS	YNDTGS...N STITLQCRIK
00BW3871_3	FFYCNTSILF	NDTYW.....	.....FNGT	ANDTG....S NNITIPCR
00BW3876_9	FFYCNTSGLF	NNNLI.....	.....NNG..	.....AE DTIRLPCRIK
00BW3886_8	FFYCNTSKLF	NSTNN.....	.....NTE..	..SES....N ATITLPCRIK
00BW3891_6	FFYCNISRLF	NRPNM.....	.....TKNM	TSDIKNN... STITLPCRIK
00BW3970_2	FFYCNTSSLF	NNTYR.....	.....PTYW	PGTE....SN STITLQCRIK
00BW5031_1	FFYCNTSQLF	NSTYR.....	.....ANTS	NS..... NITLPCRIK
96BW01B21	FFYCDTSELF	NSTYM.....	.....SNGG	NISS.....S TIIMLPCRIE
96BW0407	FFYCNTSRLF	NESYN.....	.....FDES	YWN.N...TN KTIMLPCRIK
96BW0502	FFYCDTSQLF	NSTYS.....	.....PSNG	TENK....LN GTITITCR
96BW06_J4	FFYCNTSRLF	DETYL.....	.....S...	GTDED....N GTITLPCRIK
96BW11_06	FFYCNTSKLF	NSTYI.....	.....QLN..	.STETP...N STITLPCRIK
96BW1210	FFYCNTSQLF	NSTYN.....	.....Y	MPS...NNTG TNITLQCRIK
96BW15B03	FFYCNSKLL	NSSYN.....	.....GTSY	RGTESN...S SIITLPCRIK
96BW16_26	FFYCNTSKLF	NSTYN.....	.....STDR	SNN.....T DNITIQCRIK
96BW17A09	FFYCNTSILF	NSTYN.....	.....STYT	GSDSNS....TITIPCR
96BWM01_5	FIYCNTSKLF	NGTYN.....	.....STG..	...TS...N STITLSCR
96BWM03_2	FFYCNTSELF	NGTYN.....	.....GTD..	..NNS....N KTITLLCR
98BWMC12_2	FFYCNTSGLF	NSTYN.....	.....PNST	YTESK...AN SNITLHCR
98BWMC13_4	FFYCNTTKLF	NGTYS.....	.....QPN..	.STGTP...H SNITLPCRIK
98BWMC14_a	FFYCNTSQLF	NSTYN.....	.....G...	RNSTT....N ATITLPCRIK
98BWM014_1	FFYCNTSKLF	NSTYN.....	.....ATY	NST...DTSN STITIPCR
98BWM018_d	FFYCNTSGLF	NS.....	.....	AFNDN...SG GTITLQCRIE
98BWM036_a	FFYCNTSGLF	NSTYY.....	.....SNKT	SSN...MTTN EIITIPCK
98BWM037_d	FFYCNTSKLF	NTSWL.....	.....DSYI	SNTG...NN SIITLPCRIK
99BW3932_1	FFYCNTSRLF	NSTYN.....	.....P...	NTK...SNTG SWIILPCRIK
99BW4642_4	FFYCNTSKLF	TYQSN.....	.....TY..	.....VAN STITLPCRIK
99BW4745_8	FFYCNTSELF	NSTYN.....	.....ANTY	NTATGNNS.. TTILPCRIK
99BW4754_7	FFYCNTSKLF	NSTFN.....	.....SNGH	DST.....GN DPLTIPCR
99BWMC16_8	FFYCNTSNLF	NNTYY.....	.....PNMT	NTDTK...SN LTITLPCRIK
A2_CD_97CD	FFYCNTTGLF	NSTWEN....	.....GTNK	QNYTE...SN DTITLQCRIK
A2_CY_94CY	FFYCNTTGLF	NGTWNN....	.....GTWN	GPYTPNN.TN GSIILPCRIK
A2D_97KR	FFYCDTSGLF	NSTWPAN...	.....ASRE	NEEKD...R. .NVTLP
A2G_CD_97C	FFYCNTTNLF	NSTFNTT...	.....SLFN	STGRNGTNDN TTITIPCR
A_BY_97BL0	FFYCNTTDLF	NSTX.....	.....DGTVT	NSTKAN.... GTITLPCRIK
A_KE_Q23_A	FFYCNTSGLF	NSTWY.....	.....VNSTW	NDTDSTQESN DTITLPCRIK
A_SE_SE659	FFYCNTSSLF	NSTWS.....	.....NDNNT	QGSNSTET.K GTITLPCRIK
A_SE_SE725	FFYCNTSGLF	NSTWS.....	.....Q.NDT	GVSNSTES.N DTIILPCRIK

A_SE_SE753	FFYCNTSGLF	NSTIL.....	.....NSTKM	NDNASRESYD	DTITLQCRIK
A_SE_SE853	FFYCNTSGLF	NSTWS.....	.....SNASE	PMSNSTES.N	DTITLQCRIR
A_SE_SE889	FFYCNTSGLF	NSTWN.....	.....GTDSM	QKLNST....	GNITLPCRIK
A_SE_UGSE8	FFYCNTSGLF	NSSWN.....	.....END.T	KVNYNTES.N	DTITLQCRIK
A_UG_92UG0	FFYCNTSGLF	NSTWV.....	.....NGTTS	STSN.....	GTITLPCRIK
A_UG_U455_	FFYCNTSGLF	NSIWN.....	.....GSMNS	DMGP.....N	GTITLQCRIK
AC_IN_2130	FFYCNTSGLF	NGTWNASMQ.	.....ES	NSTESN....	ETIILPCRIK
AC_RW_92RW	FFYCNTSGLF	NSTWS.....	.....KR	NGTWQSNNGTE	LNITLPCRIK
AC_SE_SE94	FFYCDTSGLF	NSTWPFNS..	.....T	NSTGPN....	GTITLQCRIK
ACD_SE_SE8	FFYCNTSGLF	NSTWV.....	.....NGSRE	SNSTDN....	DTITLPCRIK
ACG_BE_VI1	FFYCNTSGLF	NSTYN.....	.....PSYN	STESVN...E	TTIILPCKIK
AD_SE_SE69	FFYCNTTGLF	NSTWNDTAT.	.....EQKP	.....N..	DTIRLQCRIK
AD_SE_SE71	FFYCNTSGLF	NSTWN.....	.....NTDSM	QESHSTET.N	DTITLPCRIK
ADHK_NO_97	FFYCNTSGLF	NSTWNHTST.	.....YNST	EN.....	GTITLPCRIK
ADK_CD_MAL	FFYCNTSKLF	NSTWQNGA.	.....RLSN	S..TE.ST..	GSITLPCRIK
AG_BE_VI11	FFYCNTSALF	NFSSETNST.	.....FP.N.....	.....	TTLTLPCRIK
AG_NG_92NG	FFYCNTSGLF	NESGGNDT..	.....	.....	.TITLPCRIK
AGHU_GA_VI	FFYCNTTKLF	NDTENKN...	.....	..NDAEN...	KTITLPCRIR
AGU_CD_Z32	FFYCNTSGLF	NSTWK.....	.....NSTSI	NDTVSN....	GTITLPCRIK
AJ_BW_BW21	FFYCNTSGLF	NKSLLNETS.	.....NETT	DGAN.....	NTITLTCRIK
B_AU_VH_AF	FFYCNTSQLF	NSTWFNSTG.	.....NDTE	RATNN..T..	ENITLPCRIK
B_CN_RL42_	FFYCNTSQLF	NSTWNDTG..	.....T	WNDTTGNS..	.TITLPCRIK
B_DE_D31_U	FFYCNSAQLF	NSTWNDTK..	.....ES	NNTNG.....	.TITLPCRIK
B_DE_HAN_U	FFYCNTKKLF	NSTWNNTST.	.....WN..	DNGND.....	.TITLPCRIK
B_FR_HXB2_	FFYCNTSQLF	NSTWFNSTW.	.....STEG	SNNTEGSD..	.TITLPCRIK
B_GA_OYI_	FFYCNTSQLF	NSTWNDTTR.	.....AN..	.STEV.....	.TITLPCRIK
B_GB_CAM1_	FFYCNTTQLF	NTTWLFNGT.	.....WNDT	EGLNNTER..	.NITLPCRIK
B_GB_GB8_C	FFYCKTAQLF	NSTWNSTGN.	.....GTIK	SNTTE.....	.IITLPCRIK
B_GB_MANC_	FFYCNTSQLF	NSTWNTGND.	.....TRES	NDTNN..T..	GNITLPCRIK
B_KR_WK_AF	FFYCNTTQLS	NSTWQSRDG.	.....TWNR	TGGLNETK..	ENITLPCRIK
B_NL_3202A	FFYCNTSQLF	NSTWNDTGN.	.....VTER	SNNNE.....	.NITLPCRIK
B_TW_TWCYS	FFYCNPATPLF	NSTWNATST.	.....LNAT	NEENE.....	.NITLLCRIK
B_US_BC_L0	FFYCKSTQLF	NSTWAGNNT.	.....WNSS	AERSDDTG..	GNITLPCRIK
B_US_DH123	FFYCNTKKLF	NSTWNGTEG.	.....SYNI	EGND.....	.TITLPCRIK
B_US_JRCSF	FFYCNTSQLF	NSTWNDTEK.	.....SSG.	TEGND.....	.TITLPCRIK
B_US_MNCG_	FFYCNTSPLF	NSTWNGNNT.	.....WNNT	TGSNN.....	.NITLQCKIK
B_US_P896_	FFYCNTAQLF	NSTWNVTGG.	.....TNG.	TEGND.....	.IITLQCRIK
B_US_RF_M1	FFYCNTTQLF	NSTWNSTEG.	.....SNNT	GGND.....	.TITLPCRIK
B_US_SF2_K	FFYCNTTQLF	NNTWRLNHT.	.....EG..	TKGND.....	.TITLPCRIK
B_US_WEAU1	FFYCNTSQLF	NSTWHANGT.	.....WKNT	EGADN.....	.NITLPCRIK
B_US_WR27_	FFYCNTSQLF	NSTWNSTEG.	.....NS..	TWSDK.....	.IIRLPCRIK
B_US_YU2_M	FFYCNTSQLF	..TWNDTRK.	.....LN..	.NTGR.....	.NITLPCRIK
BF1_BR_93B	FFYCNTSGLF	NDTVDN....	.....	.....	GTITLPCRIK
C_BR_92BR0	FFYCNTSSLF	NSTYT.....	.....PNST	ENITGT..EN	SIITIPCRIK
C_BW_96BW0	FFYCNTSRLF	NESYS.....	.....FNES	HWSND...TN	ATITLPCRIK
C_BW_96BW1	FFYCNTSKLF	NGTYI.....	.....QPNS	.TEDTP...N	STITLPCRIK
C_BW_96BW1	FFYCNTSQLF	NSTYN.....	.....S.TY	MPS...NNTG	TNITLQCRIK
C_BW_96BW1	FFYCNTSSKLL	NSSYN.....	.....GTSY	RGTESN...S	SIITLPCRIK
C_ET_ETH22	FFYCNTSNLF	NSTKL.....	.....E...	LFNSS...TN	LNITLQCRIK
C_IN_93IN1	FFYCNTSGLF	NGTYM.....	.....PTYM	PNGTESN.SN	STITIPCRIK
C_IN_93IN9	FFYCNTSGLF	NGTYN.....	.....TSSD	GNS.....S	STITIPCRIK
C_IN_93IN9	FFYCNTSSLF	DSLFN.....	.....PNGT	RNDT....N	LTITLPCRIK
C_IN_94IN1	FFYCNTSGLF	NSTYM.....	.....SGTY	MNSSADM.NS	SYITIPCRIK
C_IN_95IN2	FFYCNTSGLF	NRTYM.....	.....PNDT	KSNSSSN.PN	ANITIPCRIK
CRF01_AE_C	FFYCNTTKLF	NSTWT.....	.....TNE	IMEEFKGTNS	STITLPCRIK
CRF01_AE_C	FFYCNTTALF	NSTWI.....	.....N.G	TMQEVNGTNS	GNITLPCRIK
CRF01_AE_C	FFYCNTTRLF	N.....	.....	..ISTNGTTN	GTITLPCRIK
CRF01_AE_T	FFYCNTTQLF	NNTCI.....	.....GNE	TMK...GCNG	.TITLPCRIK
CRF01_AE_T	FFYCNTTQLF	NSTWT.....	.....GNE	TME...GSNG	.TITLPCRIK
CRF01_AE_T	FFYCNTTRLF	NNTCI.....	.....GNK	TMK...ECND	.TITLPCRIK

CRF01_AE_T	FFYCNTTKLF	NSTWI.....	.....GNE	TIG....SSG	.NIILPCRIK
CRF01_AE_T	FFYCNTTKLF	NNTCL.....	.....GNE	TMA...GCND	.TITLPCCKIK
CRF01_AE_T	FFYCNTTKLF	NSTWR.....	.....GNE	TIESREGYNK	.TIILPCCKIK
CRF02_AG_F	FFYCNTSELF	NSTW.....	..NSTWDNSS	NHIESNHT.E	GNITLQCRIK
CRF02_AG_F	FFYCNTSELF	N.....	...STWDNSL	NHTESNHT.E	DNITLQCRIK
CRF02_AG_G	FFYCNTSGLF	NSTWYKN...	..STWYSNST	ASSNHTEL.N	STITLQCKIK
CRF02_AG_N	FFYCNTSKLF	N.....	...STWDNSN	STANHTGS.N	DTITLQCRIK
CRF02_AG_S	FFYCNTSNLF	NRTWNHNGTW	NAPGPFNDTE	DKTINGTE.D	KTITLQCRIK
CRF02_AG_S	FFYCNTAELF	NSTWASN...	.TNGIWASNI	NASNNKDA.N	DTITLKCKIK
CRF03_AB_R	FFYCNTTKLF	NSTWNGTEE.	.....LN..	.NTEG.....	DIVTLPCRIK
CRF03_AB_R	FFYCNTTKLF	NSTWNNTTEE.	.....SN..	.NTKG.....	DIVTLPCRIK
CRF04_cpx_	FFYCNTTPLF	NSTHMQNGT.	.....NIT.	S.TDSTN...	STITLQCRLK
CRF04_cpx_	FFYCNTSGLF	NSTYMFNST.	.....NRTN	T.TNGTN...	STITLPCRIK
CRF04_cpx_	FFYCNTSDLF	NRTYMVNKN.	.....ETNS	T.NTTDE...	KIIRLPCRIK
CRF05_DF_B	FFYCDTSKLF	NATVFNDTV.	.....FNAT	MFNND...SD	KNIIILPCCKIK
CRF05_DF_B	FFYCNTSGLF	NVTVP.....	.....	..NNE.....	.TITLPCRIK
CRF06_cpx_	FFYCNTSNLF	NTSDLFNTS.	.....R..G	NDTN.....	TTITLPCCKIK
CRF06_cpx_	FFYCNTSQLF	NNNITDSNE.	.....	...T.....	TNFTLPCCKIK
CRF06_cpx_	FFYCNTSQLF	NSSIPESENE.	.....	...T.....	DIITLPCCKIK
CRF06_cpx_	FFYCNTSQLF	NSSNLNNNS.	.....	SDNN.....	GTITLPCRIN
CRF11_cpx_	FFYCNTSGLF	NNTWLFNST.	.....WNSS	QELNGT...E	PNITLPCRIK
CRF11_cpx_	FFYCNTSGLF	NSTWYANDN.	.....TSTQ	NDMQSN...D	.TITLPCRIK
D_CD_84ZR0	FFYCNTSGLF	NSAWNISGH.	.....STGL	N.....D..	TIITIPCKIK
D_CD_ELI_K	FFYCNTSGLF	NSTWNISAW.	.....NNIT	ESNNS.TN..	TNITLQCRIK
D_CD_NDK_M	FFYCNTSRLF	NSTWNQTNNS.	.....TGFN	.....N..	GTVTLPCRIK
D_UG_94UG1	FFYCNTTRLF	NSTWKRNNNS.	.....EWRS	D..NT.PD..	ETITLQCRIK
F1_BE_VI85	FFYCDTSGLF	NDTGSN....	.....	.....N	GTITLPCRIK
F1_BR_93BR	FFYCNTDELF	NDTKFND...	.....	...TG...FN	GTITLPCRIK
F1_FI_FIN9	FFYCNTSLLF	NNTVPN....	.....	.....N	GTITLPCRIK
F1_FR_MP41	FFYCDTSGLF	NESEKY....	.....	.....N	GTIILPCCKIK
F2_CM_MP25	FFYCNTTILF	NHTRVNDIL.	.....SNNH	TR.....EN	DTITLPCRIK
F2KU_BE_VI	FFYCNTTRLF	NDTLNHT...	.....	.....ID	QNITLPCCKIK
G_BE_DRCBL	FFYCNTSGLF	NNSILKSNI.	.....	SENN.....	DTITLNCKIK
G_NG_92NG0	FFYCNTSGLF	NNNISNIN..	.....	...N.....	ETITLPCCKIK
G_SE_SE616	FFYCNTSGLF	NSSLLRSNS.	.....	SE.N.....	GTITLPCCKIK
H_BE_VI991	FFYCNTTKLF	NSTWTNSSY.	.....TNDT	YNSNSTEDIT	GNITLQCKIK
H_BE_VI997	FFYCNTSGLF	NSSWTGDNI.	.....NMPN	DTG.....	KNITLPCRIK
H_CF_90CF0	FFYCNTSGLF	NSSWEMHTN.	.....YTSN	DTKG...N..	ENITLPCRIK
J_SE_SE702	FFYCNTSTLF	NSSWDENNI.	.....KDTN	STNDN.....	TTITIPCKIK
J_SE_SE788	FLYCNTSKLF	NSSWDKNSI.	.....EATN	DTSX.....	ATITIPCKIK
K_CD_EQTB1	FSYCDTTDTV	DDTEEE....	.....	.....ED	TTITIPCKIK
K_CM_MP535	FFYCNTTKLF	NETGE.....	.....	.....N	GTITLPCRIK
N_CM_YBF30	FFYCNTSKLF	NEELLN....	.....ETG.	.....	EPITLPCRIR
O_CM_ANT70	FFYCNTAKMF	NYTFS.....	....CNGTTC	SVSNVSQ.G.	NNGTLPCCKLR
O_CM_MVP51	FFYCNTSGMF	NYTFIN....	....CTKSGC	QEIKGSNETN	KNGTIPCKLR
O_SN_99SE_	FFYCNTSKMF	NYTFS.....	....CIGTNC	TSNQNSSNS.	NDTRIYCRIK
O_SN_99SE_	FFYCNTSQMF	NYTFS.....	....CTRNC	IRQSNSS...	INGTISCRIK
U_CD___83C	FFYCNTSELF	TGIWNG....	.....TWDK	NCTSTESNCT	GNITLPCRIK

	501				550
00BW0762_1	QIINMWQGVG	KAMYAPPIAG	NIICKSNITG	LLLTRDGGEE	N.....TTE
00BW0768_2	QIINMWQEVG	RAMYAPPIEG	NITCKSNITG	LLLVRDGGKT	ED....NKSE
00BW0874_2	QIINLWQEVG	RAIYAPPIAG	NITCKSNITG	LLLTRD.GG.	NNS....TTE
00BW1471_2	QIINMWQGVG	QAMYAPPIAG	NITCRSNITG	LLLTRDGGIN	...EDDNTE
00BW1616_2	QIINLWQGVG	RAMYAPPIAG	NITCKSNITG	LLLTRDGGGE	N.....NSTE
00BW1686_8	QIINMWQEVG	RAIYAPPIAG	KITCISNITG	TLLTRDGGVS	NTTE...GNE
00BW1759_3	QIINMWQEVG	RAMYAPPIEG	NITCNSSITG	LLLTRDGGKN	S...TNNGTE
00BW1773_2	QIINMWQKVG	RAMYAPPIAG	NITCKSNITG	LLLTRDGGNT	S.....STEE
00BW1783_5	QIINMWQGVG	QAIYAPPIAG	NITCKSNITG	LLLTRDGG..	NN...TENTE
00BW1795_6	QIINMWQKVG	RAMYAPPIEG	NITCISNITG	LLLTRDGG..	YE...ANHTE
00BW1811_3	QIINLWQEVG	RAMYAPPIAG	NITCKSNITG	LLLTRDGGGS	NTTN...ATE
00BW1859_5	QIINMWQEVG	RAMYAPPIAG	NITCKSKITG	LLLTRDGGKQ	.....NESK
00BW1880_2	QIINMWQGVG	RAMYAPPIEG	NITCNNSITG	LLLTRNRGRE	NGD...NTTE
00BW1921_1	QIINMWQGVG	RAIYAPPIEG	NITCKSNITG	LLLTRDGGKG	NDT....AE
00BW2036_1	QIINMWQKVG	RGIYAPPIEG	SITCNSNITG	LLLVRDGG..	IN...TSTVE
00BW2063_6	QIINMWQGVG	RAMYAPPIAG	NITCTSNTG	LILTRDGGG.	NE...TNETE
00BW2087_2	QIINMWQEVG	RAMYAPPIAG	NITCKSNITG	ILLTRDGGED	TKN....KTE
00BW2127_2	QIVNMWQGVG	RAIYAPPIAG	NITCNSSITG	LLLLRDGGTE	TENN...RTE
00BW2128_3	QIINLWQEVG	RAMYAPPIEG	NITCKSNITG	LLLTRDGGTN	..N...NTE
00BW2276_7	QIINMWQGVG	RAIYASPIEG	SITCKSNITG	LLLVHDGG..	NSNT...STE
00BW3819_3	QIINMWQEVG	RAIYAPPIAG	NITCTSNTG	LLLTRDGEPS	TE.....
00BW3842_8	QVINMWQVRG	QAIYAPPIEG	IITCNSSITG	LLLVRDGD..	NQ...TSDTE
00BW3871_3	QIINMWQEVG	RAIYAPPIRG	IITCTSNTG	LLLTRDGGNT	GGN....TTE
00BW3876_9	QIINMWQEVG	RAMYAPPIAG	NITCTSNTG	LLLTRDGG.N	GG....NTE
00BW3886_8	QFIRMWQVRG	QAMYAPPIAG	NITCRSNITG	LLLTRDG...	.....KNDTE
00BW3891_6	QIINMWQGVG	RAMYAPPIAG	RIICKSNITG	LLLVRDGGQD	N...VMNATE
00BW3970_2	QIINMWQKVG	RAIYAPPIAG	KITCKSNITG	LLLVRDGGGG	NN....TATE
00BW5031_1	QIINMWQGVG	RAMYAPPIAG	NIICKSNITG	VLLTYDGGEE	N.....E
96BW01B21	QIINMWQGVG	RAMYAPPIKG	SITCRSNITG	LLLTRDGGLN	RS...TEEPE
96BW0407	QIINMWQGVG	RAIYAPPIAG	NITCVSNITG	LLLTWDGGHQ	SN.....E
96BW0502	QIINMWQKVG	RAMYAPPIAG	NLTCESDITG	LLLTRDGGKT	G....PNLTE
96BW06_J4	QIINMWQEVG	RAIYAPPIAG	NITCKSNITG	LLLTRDGGLN	NDS.....E
96BW11_06	QFINLWQEVG	RAMYAPPIAG	NIICKSNITG	LLLTRDG...	.D....KNDSE
96BW1210	QIINRWQEVG	RAMFAPPIAG	NITCKSNITG	ILLVRDGGNT	SEN.....IE
96BW15B03	QIINMWQKVG	RAIYAPPIEG	NITCSSSITG	LLLARDGG..	LD...NVTTE
96BW16_26	QIINMWQGVG	RAMYAPPIEG	NITCKSNITG	LLLVRDGGTE	ENN...TGTE
96BW17A09	QIINMWQGXG	QAMYVPPIAG	NITCRSNITG	LLLTRDGGK.	...VTGNTTE
96BWM01_5	QIINMWQGVG	RAMYASPIAG	NITCKSNITG	LLLTRDGG..	NE...TSGIE
96BWM03_2	QIINTWQEVG	RAIYAPPIAG	NIICISNITG	LLLTRDGGKT	ND...TNDTE
98BWMC12_2	QIINMWQEVG	RAMYAPPIAG	NITCRSNITG	LLLTRD.GGN	TTE....TKE
98BWMC13_4	QIINMWQGVG	RAMYAPPIAG	NITCISNITG	LILTRDGG..	VN...RSDTE
98BWMC14_a	QIINMWQEVG	RAIYAPPIKG	NITCESNITG	LLLTRDGGSN	DTT.....E
98BWM014_1	QIINMWQGVG	QAMYAPPIAG	NITCKSNITG	ILLTRDGGIN	NTN...GTE
98BWM018_d	QIINMWQKVG	RAIYAPPIAG	NITCSSRITG	LLLTRDGGKN	.....DTHE
98BWM036_a	QIINMWQEVG	RAMYAPPIAG	NITCKSNITG	LLLVRDGGNN	NTT.....E
98BWM037_d	QIINMWQKVG	RAMYANPIEG	NITCRSNITG	LLLENDG...	N.....M
99BW3932_1	QIINMWQKVG	RAMYAPPIAG	NITCKSNITG	LLLVRDGGTA	TD.....E
99BW4642_4	QIINMWQEVG	RAMYAPPIAG	NITCQSNITG	LLLTRDGGTE	TD...NKTE
99BW4745_8	QIINMWQEVG	RAMYAPPIEG	NITCKSNITG	LLLVRDGGGK	N...ATNDTE
99BW4754_7	QIINMWQEVG	RAMYAPPIAG	RIICNSTITG	LILTRDGGNT	N.....NTE
99BWMC16_8	QIINRWQEVG	RAMYAPPIAG	NITCTSNTG	LLLVRDGGRT	SD....STKE
A2_CD_97CD	QIINMWQVRG	RAMYAPPIAG	VIKCTSNITG	MILTRDG..G	KNS....INE
A2_CY_94CY	QIINMWQVRG	RAMYAPPIAG	IICKTSNTG	IILTRDG..G	NNG....TNE
A2D_97KR	QIVNMWQVRG	RAMYAPPING	TIKCTSNITG	MILTRDGNSG	GNA....TNE
A2G_CD_97C	QIINMWQVRG	RAMYAPPIAG	IINCTSNITG	IILTRDGEKG	GDN....TIE
A_BY_97BL0	QIINMWQVRG	QAMYAXPIKX	SIRCESNITG	LLLTRDGXGX	TNX....SNE
A_KE_Q23_A	QIINMWQRAG	QAMYAPPIPG	VIKCESNITG	LLLTRDGGKD	NN.....VNE
A_SE_SE659	QIINMWQRAG	KAMYAPPIQG	VIRCESNITG	LILTRDG.GD	AG....ENE
A_SE_SE725	QIINMWQRAG	QAIYAPPIPG	IIRCESNITG	LLLTRDG.GV	VNS....TNE



A_SE_SE753	QIINMWQRVG	QAMYAPPIRG	AIRCKSNITG	LLLTRDGGNS	NSS....TNE
A_SE_SE853	QIINMWQRAG	KAIYAPPIPG	IIKCVSNITG	LILTRDG.GS	NNS....TNE
A_SE_SE889	QIINMWQRAG	QAIYAPPIQG	VIRCESNITG	LILTRDG.GN	DNN....ESE
A_SE_UGSE8	QIINMWQRTG	QATYAPPIPG	VIQCRSNITG	LLLTRDGGVT	NNT....NNE
A_UG_92UG0	QIINMWQRVG	QAMYAPPIQG	VIKCESNITG	LILTRDG.GV	NSS....DSE
A_UG_U455_	QIINMWQRVG	QAMYAPPIQG	VIRCESNITG	LLLTRDG.GT	NNT....KNE
AC_IN_2130	QIINMWQRVG	QAMYAPPIQG	IIKCVSNITG	LILTRDGK.S	SNS....TDE
AC_RW_92RW	QIINMWQRTG	QAMYAPPIQG	VISCVSNITG	LLLTRDG.GN	NNT....TTE
AC_SE_SE94	QIIRMWQRTG	QAIYAPPIPG	EINCVSNITG	LLLTRDG..G	NNI....TNE
ACD_SE_SE8	QIINMWQRVG	QAMYALPIRG	VIRCESNITG	LILTRDG.GN	NTS....TNE
ACG_BE_VI1	QIINMWQEVG	RAMYANPIAG	NITCNSNITG	LLLTRDGGVN	ET....TETE
AD_SE_SE69	QIINMWQRAG	RAIYAPPIQG	VINCVSDITG	LILTRDGGVN	.NT.N....E
AD_SE_SE71	QIINMWQRVG	QAMYAPPIQG	VIKCTSNITG	LILTRDG.GG	NNS....INA
ADHK_NO_97	QIVNMWQRVG	QAMYAPPIKG	NITCVSNITG	LILTIDXG..	..N.MSAENF
ADK_CD_MAL	QIINMWQKTG	KAMYAPPIAG	VINCLSNITG	LILTRDGGNS	.SD.NS.DNE
AG_BE_VI11	QIVRMWQRVG	QAMYAPPIAG	KITCRSNITG	LILTRDGGNP	N....NTNNE
AG_NG_92NG	QIVRMWQRVG	QAMYAPPIAG	DITCRSNITG	LLLTRDGGVN	N....TGNE
AGHU_GA_VI	QIVNMWQRVG	RAMYAPPIAG	NITCRSNITG	IILTRDGG..	.SN.NESTNE
AGU_CD_Z32	QIVNMWQRVG	QAMYAPPIKG	VIKCESNITG	ILLTRDGVG.	NNT....ANE
AJ_BW_BW21	QIVRMWQRVG	QAIYAPPIAG	NITCTSNITG	LLLTRDGGYT	..N.NTNGTE
B_AU_VH_AF	QIINMWQKVG	KAMYAPPING	QIRCSSNITG	LILTRDGGNQ	....ENKTE
B_CN_RL42	QIVNMWQEVG	KAMYAPPIEG	QIRCSSNITG	LLLTRDGGNN	.E..S.KPTE
B_DE_D31_U	QIINMWQEVG	KAMYAPPISG	QIRCSSNITG	LLLTRDGGKN	.K..D.NETE
B_DE_HAN_U	QIINMWQEVG	KAMYAPPIGG	LIRCSSNITG	LILTRDGGND	.N..S.STTE
B_FR_HXB2_	QIINMWQKVG	KAMYAPPISG	QIRCSSNITG	LLLTRDGGNS	.N..N..ESE
B_GA_OYI_	QIVNMWQEVG	KAMYAPPISG	QIRCSSKITG	LLLTRDGGKN	....TTNGIE
B_GB_CAM1_	QIINRWQEVG	KAMYAPPITG	TISCSSNITG	LLLTRDGGRG	.E..N..ETE
B_GB_GB8_C	QIVNMWQEVG	KAMYAPPITG	QIRCASHITG	LLLTRDGGRE	.N..NTNETE
B_GB_MANC_	QILNLWQEVG	KAMYAPPISG	QISCSSNITG	LLLTRDGGNT	.NT.TGNTTE
B_KR_WK_AF	QIINRWQEVG	KAMYAPPISG	LIRCSSNITG	LLLTRDGGNE	.NN.GTNGTE
B_NL_3202A	QIINMWQGVG	KAMYAPPISG	QIRCSSNITG	LLLTRDGGKD	.E..NKTGTE
B_TW_TWCYS	QIINMWQRVG	KAMYAPPIEG	LIKCSSNITG	LMLTRDGGTN	.D....SEVE
B_US_BC_L0	QIINMWQEVG	KAMYAPPIEG	QIRCTSNITG	LLLTRDGGTS	.D..T.NTTE
B_US_DH123	QIINMWQEVG	KAMYAPPISG	QIWCSSNITG	LLLTRDGGKN	....SSTE
B_US_JRCSF	QIINMWQEVG	KAMYAPPIKG	QIRCSSNITG	LLLTRDGGK.	....NESEIE
B_US_MNCG_	QIINMWQEVG	KAMYAPPIEG	QIRCSSNITG	LLLTRDGGKD	.T..DTNDTE
B_US_P896_	QIINMWQKVG	KAMYAPPITG	QIRCSSNITG	LLLTRDGGNS	....TETETE
B_US_RF_M1	QIVNMWQEVG	KAMYAPPISG	QIKCISNITG	LLLTRDGGED	.T..T.NTTE
B_US_SF2_K	QIINMWQEVG	KAMYAPPIGG	QISCSSNITG	LLLTRDGGTN	.V..T.NDTE
B_US_WEAU1	QIINRWQEVG	KAMYAPPIEG	QIRCLSNITG	LLLTRDGGSS	.E..E.NQTE
B_US_WR27_	QIINMWQEVG	KAMYAPPIDG	QIRCSSNITG	LLLTRDGGN.	....SNETTE
B_US_YU2_M	QIINMWQEVG	KAMYAPPIAG	QIRCSSNITG	LLLTRDGGK.	....DTNGTE
BF1_BR_93B	QIVNMWQEVG	RAMYAAPPIAG	NITCNSNITG	LLLTRDGG..	Q....NNQTEE
C_BR_92BR0	QIINMWQGVG	RAMYAPPIEG	ILTCRSNITG	LLLTRDGGTG	....MHDTE
C_BW_96BW0	QIINMWQGVG	RAIYAPPIAG	NITCISNITG	LLLTRDGGTT	RNN....ESE
C_BW_96BW1	QFINLWQEVG	RAMYAPPIAG	NIICKSNITG	LLLTRDG...	.D...KNDSE
C_BW_96BW1	QIINRWQEVG	RAMFAPPIAG	NITCKSNITG	ILLVRDGGNT	SEN....IE
C_BW_96BW1	QIINMWQKVG	RAIYAPPIEG	NITCSSSITG	LLLARDGG..	LD...NVTTE
C_ET_ETH22	QIINMWQGVG	RAMYAPPIEG	IIMCRSNITG	LLLTRDGAKE	PH....STKE
C_IN_93IN1	QIINMWQEVG	RAMYAPPIAG	NITCTSNITG	LLLVDHGGIK	EN.DTENKTE
C_IN_93IN9	QIINMWQEVG	RAMYAPPIEG	NITCKSNITG	LLLVRDGGAE	AK...TNNTE
C_IN_93IN9	QIINMWQEVG	RAMYAPPIAG	NITCKSNITG	LLLVRDGGRG	ND...TENNTE
C_IN_94IN1	QIINMWQEVG	RAMYAPPIAG	NITCKSNITG	ILLERDG..G	SG...SNGTE
C_IN_95IN2	QIINMWQEVG	RAMYAPPIEG	KITCRSNITG	LLLVRDGGED	KNNTETNKTE
CRF01_AE_C	QVVNMWQEVG	KAMYAPPISE	AVNCVSNITG	IILTRDGGNA	TNET.....
CRF01_AE_C	QIVNMWQEVG	RAMYAPPISE	VINCVSNITG	ILLTRDGGIN	QNQTNK..NE
CRF01_AE_C	QVIKMWQEVG	QAMYAPPIDE	AINCVSNITG	ILLVRDGGKI	ENET....IE
CRF01_AE_T	QIINMWQGTG	QAMYAPPIDG	KINCVSNITG	ILLTRDGG..	ANNTS...NE
CRF01_AE_T	QIIRMWQGAG	QAMYAPPISG	IINCVSNITG	ILLTRDGGG.	ANNTN...NE
CRF01_AE_T	QIINMWQGVG	QAMYNPPISG	NINCVSNITG	ILLTRDGGGG	NGTNN...EE

CRF01_AE_T	QIINMWQEVG	QAMYAPPITG	KINCVSNITG	ILLTRDGG..	ANNKS...SE
CRF01_AE_T	QIINMWQGAG	QAMYAPPISG	RINCVSNITG	ILLTRDGG..	VNNTD...NE
CRF01_AE_T	QIINMWQGAG	QAMYAPPING	TINCISNITG	ILLTRDGGD.	NNNTI...NE
CRF02_AG_F	QIVNMWQKVG	LAMYAPPISG	EIRCKSNITG	LLLTRDG.GS	NNS....TNE
CRF02_AG_F	QIVNMWQKVG	RAMYAPPIPG	EIRCESNITG	LLLTRDG.GS	NNS....TNE
CRF02_AG_G	QIINMWQKVG	QAMYAPPIQG	VIRCDSNITG	LLLTRDG.GS	NNN....TPE
CRF02_AG_N	QIVNMWQKVG	QAMYAPPIQG	IIRCDSNITG	LLLTRDG.G.	NNS....TNE
CRF02_AG_S	QIVRMWQKVG	QAMYAPPIPG	EIRCESNITG	LLLTRDG.GN	DNN....NTE
CRF02_AG_S	QIINMWQKVG	QAIYAPPIEG	VIRCDSNITG	ILLTRDG.GD	NTN....GDE
CRF03_AB_R	QIINMWQEVG	KARYAPPIAG	QIRCSSNITG	LLLTRDGGNQ	.S....NVTE
CRF03_AB_R	QIINMWQEVG	KAMYAPPIAG	QIRCSSNITG	LLLTRDGGNQ	.N....NVTE
CRF04_cpx_	QFVRMWQEVG	QAMYASPIAG	SINCSSDITG	IILTRDG...	....GTNNT
CRF04_cpx_	QIVRMWQGVG	QAMYAPPIAG	SINCSSDITG	IILTRDGGIS	NNN.ETNDNE
CRF04_cpx_	QIVNRWQEVG	QAIYAPPIQG	SLTATQVITG	IILTRDGG..	.NR.SDTGNE
CRF05_DF_B	QIVRMWQGVG	QAMYAAPPIAG	NIACNSTITG	ILLARDGGNG	.ND.SSNDTE
CRF05_DF_B	QIINMWQGVG	QAMYAAPPIAG	NITCNSNITG	ILLTRDG..G	.VN.ITNDTE
CRF06_cpx_	QIVRMWQRVG	QAMYAPPIAG	NITCVSNITG	IILTRDGN.N	EN....VSE
CRF06_cpx_	QIVRMWQRVG	QAMYAPPIAG	NIICTSNITG	LLLTRDGGRN	DS....NSE
CRF06_cpx_	QIVRMWQRVG	QAIYAPPIAG	NITCISNITG	LLLTRDGN.T	NT....TSE
CRF06_cpx_	QIIRMWQRVG	QAMYAPPIAG	NITCTSNTG	LLLTRDGH.N	D.....TE
CRF11_cpx_	QIVRMWQRVG	QAMYAPPIQG	EIRCDSNITG	LLLTRDGG..	....LNSTNE
CRF11_cpx_	QIINMWQRVG	QAVYAPPIQG	ELRCDNITG	LLLTRDGGEG	..N.DTIGKE
D_CD_84ZR0	QIINMWQEVG	KAMYAPPIEG	QINCSSNITG	LLLTRDGGAN	.NT.Q...ND
D_CD_ELI_K	QIIKMWQAG.	.AIYAPPIER	NILCSSNITG	LLLTRDGGIN	.NS.T...NE
D_CD_NDK_M	QIVNLWQRVG	KAMYAPPIEG	LIKCSSNITG	LLLTRDGGAN	.NS.S...HE
D_UG_94UG1	QIINMWQEVG	KAMYAPPIEG	FINCSSNITG	LLLTRDGGAI	.NS.SQ..NE
F1_BE_VI85	QIVNMWQGVG	RAMYTSPIAG	NITCNSNITG	LLLTRDGG..	....NESNIE
F1_BR_93BR	QIVNMWQEVG	RAMYANPIAG	NITCNSNITG	LLLTRDGG..	....LNSTNE
F1_FI_FIN9	QFVNMWQEVG	RAMYAAPPIAG	NITCNSNITG	LLLTRDGG..	QS..NNSDSE
F1_FR_MP41	QIINMWQGVG	QAMYSAPIAG	RINCNSTITG	LLLTRDGG..	QSN.DTNRTE
F2_CM_MP25	QIVNMWQRVG	QAMYAPPIAG	KIQCNSNITG	LLLTIDGG..	....EGNESE
F2KU_BE_VI	QIINRWQGVG	QAMYAPPIAG	NITCRSNITG	MILTRDGGNS	N...DTIDNE
G_BE_DRCBL	QIVRMWQRVG	QAMYAPPIAG	NITCRSNITG	LILTRDGGDN	N....STSE
G_NG_92NG0	QIVRMWQKVG	QAMYALPIAG	NLVCKSNITG	LILTRDGGNN	N....DSTEE
G_SE_SE616	QIVRMWQRVG	QAMYAPPIAG	NIECNSSITG	LILTRDGGNN	NNT.NTSESE
H_BE_VI991	QIVNMWQRVG	QAMYAPPIRG	NITCISNITG	LILTFD....	..R.NNTNNV
H_BE_VI997	QIVNMWQRVG	QAMYAPPIKG	SITCVSNITG	LILTYDED..	..K.GNNDNV
H_CF_90CF0	QIVNMWQRVG	RAMYAPPIQG	NIMCVSNITG	LILTIDEG..	..N.ASAENY
J_SE_SE702	QIVRMWQRTG	QAIYAPPIAG	NITCKSNITG	LLLTRDGGNR	.NG.SENGTE
J_SE_SE788	QIVRMWQRTG	QAIYAPPIAG	NITCTSNTG	LLLTRDGGNR	GNG.SENGTE
K_CD_EQTB1	QIINMWQKVG	QAIYAPPTAG	NITCRSNITG	MILTRDGGND	N...NTRTEE
K_CM_MP535	QIINMWQKVG	KAIYAPPIAG	SINCSSNITG	MILTRDGGNN	.....THNE
N_CM_YBF30	QIVNLWTRVG	KGIYAPPIRG	VLNCTSNITG	LVLEYSGGPD	.....TKET
O_CM_ANT70	QVVRWIRGQ	SGLYAPPIKG	NLTCMSNITG	MILQMDNTWN	SSNN....NV
O_CM_MVP51	QLVRSWMKGE	SRIYAPPIPG	NLTCHSNITG	MILQLDQPWN	STGE....N
O_SN_99SE_	QVVRWIIQGG	SGLYAPPRKG	NLTCSNLITG	MILQLDMPWN	STNNS...NA
O_SN_99SE_	QVVRWIIQGG	SGLYAPPRPG	YLTCSNITG	MILQLDKTWN	RTNNS...ES
U_CD___83C	QVVRTWQGVG	QAMYAPPIEG	TIRCSSNITG	LLLTRDGGNG	N....ATQNE

00BW0762_1	TFRPAGGDMR	DNWRSELYKY	KVVEIKPLGI	APTSAKRRVV	EREKR.....
00BW0768_2	IFRPGGGDMR	DNWRSELYKY	KVVEIKPLGV	APTEAKRRVV	EREK.R....
00BW0874_2	IFRPQGGNMK	DNWRSELYKY	KVVEVKPLGV	APTKAKRRVV	EREK.R....
00BW1471_2	IFRPGGGNMR	DNWRSELYKY	KVVEIKPLGV	APNKAKRRVV	EREK.R....
00BW1616_2	TFRPAGGEMR	DNWRSELYKY	KVVEVKPLGI	APTEAKRRVV	QREKR.....
00BW1686_8	TFRPGGGDMR	NNWRSELYKY	KVVEIRPLGV	APTEARRRVV	EREK.R....
00BW1759_3	IFRPGGGDMR	DNWRSELYKY	KVVKIKPLGI	APTKAQRRVV	KREKR.....
00BW1773_2	IFRPEGGDMR	DNWRSELYKY	KVVEIKPLGV	APTKAKRRVV	EREK.R....
00BW1783_5	TFRPGGGDMR	DNWRSELYKY	KVVEIKPLGI	APTSAKRRVV	EREK.R....
00BW1795_6	IFRPIGGDMR	DNWRSELYKY	KVVEIKPLGL	APTESKRRVV	EREK.R....
00BW1811_3	TFRPGGGDMR	DNWRSELYKY	KVVEVKPLGL	APTEAKRRVV	EREK.R....
00BW1859_5	IFRPGGGDMR	NNWRSELYKY	KVVEIKPLGL	APTGAARRVV	EREK.R....
00BW1880_2	TFRPAGGDMR	DNWRSELYKY	KVVEIKPLGI	APTKAKRRVV	EREK.R....
00BW1921_1	IFRPEGGDMK	NNWRSELYKY	KVVEIRPLGV	APTKAKRRVV	EREK.R....
00BW2036_1	TFRPEGGNMR	DNWRSELYKY	KVVEIKPLGV	APTEAARRVV	EKQK.R....
00BW2063_6	TFRPAGGDMR	DNWRSELYKY	KVVEIKPLGL	APTKAKRRVV	EREK.R....
00BW2087_2	TFRPGGGDMR	DNWRSELYKY	KVVEIKPLGV	APTKAKRRVV	EREK.R....
00BW2127_2	TFRPGGGDMR	DNWRSELYKY	KVVEIKPLGV	APTKAKRRVV	EREK.R....
00BW2128_3	TFRPVGGDMR	DNWRSELYKY	KVVEIKPLGV	APTEAKRRVV	KREK.R....
00BW2276_7	IFRPGGGDMR	DNWRSELYKY	KVVEVKPLGI	APTEAKRRVV	EREK.R....
00BW3819_3	TFRPGGGDMR	DNWRSELYKY	KVVEVKPLGI	APTGAARRVV	EREK.R....
00BW3842_8	TFRPQGGEMR	DNWRSELYKY	KVVEIKPLGV	APTTAKRRVV	EREK.R....
00BW3871_3	IFRPEGGDMR	NNWRSELYKY	KVVEIKPLGI	APTGAARRVV	EREK.R....
00BW3876_9	TFRPGGGNMK	DNWRSELYKY	KVVEIKPLGV	APTEAKRRVV	EREK.R....
00BW3886_8	TFRPGGGNMR	DNWRSELYKY	KVVEIKPLGI	APTEAKRRVV	EREK.R....
00BW3891_6	TFRPGGGDMR	DNWRSELYKY	KVVEIKPLGV	APTSAKRRVV	EREK.R....
00BW3970_2	IFRPGGGNMK	DNWRSELYKY	KVVEIKPLGI	APTGAARRVV	GREK.R....
00BW5031_1	TFRPAGGNMK	DNWRSELYKY	KVVEIKPLGI	APTKAKRRVV	EREK.R....
96BW01B21	IFRPGGGDMR	NNWRSELYKY	KVVEIKPLGV	APTGAARRVV	EREK.R....
96BW0407	TFRPGGGDMR	DNWRSELYKY	KVVEIKPLGI	APTEARRRVV	EREKR.....
96BW0502	IFRPGGGDMR	DNWRSELYKY	KVVEIKPLGV	APTEAKRRVV	EREK.R....
96BW06_J4	TFRPIGGEMR	NNWRSELYKY	KVVEIKPLGI	APTKAKRRVV	EREK.R....
96BW11_06	TFRPAGGDMR	DNWRSELYKY	KVVEIKPLGL	APTKAKRRVV	EREK.R....
96BW1210	TFRPGGGNMK	DNWRSELYKY	KVVEVKPLGI	APTRAKRRVV	EREK.R....
96BW15B03	IFRPQGGDMK	DNWRSELYKY	KVVEIKPLGV	APTEAKRRVV	EREK.R....
96BW16_26	IFRPEGGDMR	DNWRSELYKY	KVVEIKPLGI	APTKAKRRVV	EREK.R....
96BW17A09	TFRPGGGNMR	DNWRSELYKY	KVVEVKPLGV	APTAARRRVV	EREK.R....
96BWM01_5	IFRPAGGDMR	DNWRSELYKY	KVVEIKPLGL	APTKSKRRVV	GREK.R....
96BWM03_2	IFRPGGGNMK	DNWRSELYKY	KVVEIKPLGV	APTKAKRRVV	EREK.R....
98BWMC12_2	TFRPGGGDMR	DNWRSELYKY	KVVEIKPLGV	APTEAKRRVV	ERGKR.....
98BWMC13_4	IFRPAGGDMR	DNWRSELYKY	KVVEIKPLGL	APTKAKRRVV	EREK.R....
98BWMC14_a	TFRPEGGDMR	NNWRSELYKY	KVVEIRPLGI	APTGAARRVV	NREK.R....
98BWM014_1	TFRPGGGDMR	DNWRSELYKY	KVVEVKPLGI	APTKAQRRVV	EREK.R....
98BWM018_d	TFRPAGGDMR	DNWRSELYKY	KVVEIKPLGV	APSEAKRRVV	EREK.R....
98BWM036_a	TFRPGGGNMK	DNWRSELYKY	RVVEIKPLGI	APTGAARRVV	EREK.R....
98BWM037_d	TFRPGGGDMK	DNWRSELYKY	KVVEIKPLGI	APTEAKRRVV	EREK.R....
99BW3932_1	IFRPGGGDMR	DNWRSELYKY	KVVEIKPLGI	APTEAKRRVV	EREK.R....
99BW4642_4	TFRPGGGDMR	DSWRSELYKY	KVVEIKPLGV	APTKAKRRVV	EREK.R....
99BW4745_8	IFRPEGGDMR	NNWRSELYKY	KVVEIKPLGV	APTKAKRRVV	DKEK.....
99BW4754_7	IFRPIGGNMR	DNWRSELYKY	KVVEIKPLGI	APTKAKRRVV	EREKR.....
99BWMC16_8	IFRPGGGDMR	DNWRSELYKY	KVVEIKPLGI	APTEAKRRVV	EREK.R....
A2_CD_97CD	TFRPGGGDMR	DNWRSELYKY	KVVKIEPLGI	APTEARRRVV	QREK.R....
A2_CY_94CY	TFRPGGGDMR	DNWRSELYKY	KVVKLEPLGV	APTRAKRRVV	EREK.R....
A2D_97KR	TFRPGGGDMR	DNWRSELYKY	KVVKLEPLGV	APTRARRRVV	EREK.R....
A2G_CD_97C	VFRPVGGDMR	DNWRSELYKY	KVVKIKPLGI	APTRARRRVV	EKEK.R....
A_BY_97BL0	TFRPIXGDXR	NNWRSELYKY	KVVKIEPIXV	APTRAKRRXX	EREK.R....
A_KE_Q23_A	TFRPGGGDMR	DNWRSELYKY	KVVEIEPLGV	APTRAKRRVV	EREK.R....
A_SE_SE659	TFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTQARRRVV	KREK.R....
A_SE_SE725	TFRPGGGNMK	DNWRSELYKY	KVVKIEPLGV	APTRARRRVV	QREK.R....

A_SE_SE753	TFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTKAKRRVV	EREK.R....
A_SE_SE853	TFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTKAKRRVV	EREK.R....
A_SE_SE889	IFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTKAKRRVV	EREK.R....
A_SE_UGSE8	TFRPGGGDMR	DNWRSELYKY	KVVKLEPLGV	APTKAQRVV	KREK.R....
A_UG_92UG0	TFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTKARRVV	EREK.R....
A_UG_U455_	TFRPGGGDMR	DNWKSELYKY	KVVKIEPLGV	APTRAKRRVV	EREK.R....
AC_IN_2130	IFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTRARRAV	GREK.R....
AC_RW_92RW	TFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTRAKRRVV	EREK.R....
AC_SE_SE94	TFRPGGGDMQ	DNWRSELYKY	KVVQIEPLGV	APTKARRVV	EREK.R....
ACD_SE_SE8	TIRPAGGDMR	DNWRSELYKY	KVVKIEPLGV	APTKARRVV	EREK.R....
ACG_BE_VI1	IFRPGGGNMK	DNWRSELYKY	KVVEIKPLGV	APTKAKRRVV	EREK.R....
AD_SE_SE69	TFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTRAKRRVV	EREK.R...V
AD_SE_SE71	TFRPGGGDMR	DNWRSELYKY	KVVKIEPVG	APNRAKRRVV	EREK.R....
ADHK_NO_97	TFRPGGGDMR	DNWRSELYKY	KVVXXXPLGV	APTXARRVV	QREK.R....
ADK_CD_MAL	TLRPGGGDMR	DNWISELYKY	KVVRIEPLGV	APTKAKRRVV	EREK.R...A
AG_BE_VI11	TFRPGGGDMR	DNWRSELYQY	KVVKIKSLGV	APTKARRVV	EREK.R...A
AG_NG_92NG	TFRPGGGDMR	DNWRSELYKY	KIVKIKPLGI	APTKARRVV	ERKG.R...A
AGHU_GA_VI	TFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTRARRVV	EREK.R...A
AGU_CD_Z32	TFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTKAKRRVV	AREK.R....
AJ_BW_BW21	IFPTGRNMR	DNWRSELYKY	KVVKIEPIGV	APTRAKRRVV	GREK.R...A
B_AU_VH_AF	IFRPGGGDMR	DNWRSELYKY	KVVRIEPLGV	APTKAKRRVV	QREK.R...A
B_CN_RL42	TFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTKARRVV	QREK.R...A
B_DE_D31_U	TFRPGGGNMR	DNWRSELYKY	KVVKIEPLGV	APTKAKRRVV	QREK.R...A
B_DE_HAN_U	IFRPGGGNMR	DNWRNELYKY	KVVKIEPLGV	APTKAKRRVV	QREK.R...A
B_FR_HXB2_	IFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTKAKRRVV	QREK.R...A
B_GA_OYI_	IFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTKARRVV	QREK.R...A
B_GB_CAM1_	TFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTKAKRRVV	QREK.R...A
B_GB_GB8_C	TFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTKAKRRVV	QREK.R...A
B_GB_MANC_	TFRPGGGNMR	DNWRSELYKY	KVVKVEPLGI	APTKAKRRVV	QREK.R...A
B_KR_WK_AF	TFRPEGGNMK	DNWRSELYKY	KVVRIEPLGI	APTRARRVV	QREK.R...A
B_NL_3202A	IFRPGGGDMK	DNWRSELYKY	KVVKIEPLGV	APTRAKRRVV	QREK.R...A
B_TW_TWCYS	VFRPGGGDMK	DIWRNELYKY	KVVKVEPLGL	APTRARRVV	QREK.R...A
B_US_BC_L0	TFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTTAKRRVV	QREK.R...A
B_US_DH123	IFRPGGGDMR	DNWRSELYKY	KVVRVEPLGI	APTKAKRRVV	QREK.R...A
B_US_JRCSF	IFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTKAKRRVV	QREK.R....
B_US_MNCG_	IFRPGGGDMR	DNWRSELYKY	KVVTIEPLGV	APTKAKRRVV	QREK.....
B_US_P896_	IFRPGGGDMR	DNWRSELYKY	KVVRIEPIGV	APTRAKRRTV	QREK.R....
B_US_RF_M1	IFRLGGGNMR	DNWRSELYKY	KVVRIEPLGV	APTRAKRRVV	QREK.R...A
B_US_SF2_K	VFRPGGGDMR	DNWRSELYKY	KVIKIEPLGI	APTKAKRRVV	QREK.R...A
B_US_WEAU1	IFRPGGGNMK	DNWRSELYKY	KVVKIEPLGV	APTKAKRRVV	QREK.R...A
B_US_WR27_	IFRPGGGDMR	DNWRSELYKY	KVXXIEPLGV	APTKXKRRVV	XREK.R...X
B_US_YU2_M	IFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTKAKRRVV	QREK.R...A
BF1_BR_93B	TFRPGGGNMK	DNWRSELYKY	KVVEIEPLGV	APTKAKRQVV	KREK.R...A
C_BR_92BR0	IFRPEGGDMR	DNWRSELYKY	KVVEIKPLGI	APTKAKRRVV	EREK.R....
C_BW_96BW0	IFGPGGGDMR	DNWRSELYKY	KVVEIKPLGI	APTEARRVV	EREKR....
C_BW_96BW1	TFRPAGGDMR	DNWRSELYKY	KVVEIKPLGL	APTKAKRRVV	EREK.R....
C_BW_96BW1	TFRPGGGNMK	DNWRSELYKY	KVVEVKPLGI	APTRAKRRVV	EREK.R....
C_BW_96BW1	IFRPQGGDMK	DNWRNELYKY	KVVEIKPLGV	APTEAKRRVV	EREK.R....
C_ET_ETH22	IFRPEGGDMR	DNWRSELYKY	KVVEIKPLGV	APTKPKRRVV	EREK.....
C_IN_93IN1	IFRPGGGDMR	DNWRSELYKY	KVVEIKPLGV	APTAAKRRVV	EREK.R....
C_IN_93IN9	TFRPGGGDMR	DNWRSELYKY	KVVEIKPLGV	APTTAKRRVV	EREK.R....
C_IN_93IN9	IFRPGGGDMR	NNWRSELYKY	KVVEIKPLGV	APTKAKRRVV	EREKRA....
C_IN_94IN1	TFRPGGGDMR	NNWRSELYKY	KVVEIQPLGV	APTEAKRRVV	ERKG.R....
C_IN_95IN2	TFRPGGGDMR	DNWRSELYKY	KVVEVKPLGV	APTTAKRRVV	EREK.R....
CRF01_AE_C	.FRPGGGNMK	DNWRSELYKY	KVVQIEPLGI	APTRARRVV	EREK.R....
CRF01_AE_C	TFRPGGGNIK	DNWRSELYKY	KVVQIEPLGI	APTKARRVV	EREK.R....
CRF01_AE_C	TFRPGGGNMK	DNWRSELYKY	KVVQIEPLGV	APTGAKRRVV	EREK.R....
CRF01_AE_T	TFRPGGGNIK	DNWRSELYKY	KVVQIEPLGI	APTRAKRRVV	EREK.R....
CRF01_AE_T	TFRPEGGNIK	DNWRSELYKY	KVVQIEPLGI	APTRAKRRVV	EREK.R....
CRF01_AE_T	TFRPGGGNMK	DNWRNELYKY	KVVEIEPLGI	APTKAKRRVV	EREK.R....

CRF01_AE_T	TFRPGGGNIK	DNWRSELYKY	KVVEIEPLGI	APTRAKRRVV	EREK.R....
CRF01_AE_T	TFRPGGGNIK	DNWRSELYKY	KVVQIEPLGI	APTRAKRRVV	EREK.R....
CRF01_AE_T	TFRPGGGNIK	DNWRSELYKY	KVVQIEPLGI	APSKAKRRVV	EREK.R....
CRF02_AG_F	TFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTRPKRRVV	EREK.R....
CRF02_AG_F	TFRPGGGDMR	DNWRSELYKY	KVVKIEPLGI	APTHAKRRVV	EREK.R....
CRF02_AG_G	IFRPGGGNMR	DNWRSELYKY	KVVKIEPLGV	APTRAKRRVV	EREK.R....
CRF02_AG_N	TFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTRAKRRVV	EREK.R....
CRF02_AG_S	TFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APSHAKRRVV	EREKRA....
CRF02_AG_S	TFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APSHAKRRVV	EREK.R....
CRF03_AB_R	IFRTGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTRAKRRVV	QREK.R...A
CRF03_AB_R	IFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTKAKRRVV	QREK.R...A
CRF04_cpx_	IFRPGGGDMR	DNWRSELYKY	KVVKIEPIGV	APNKARRRVV	QREK.....
CRF04_cpx_	TLRPGGGDMR	DNWRSELYKY	KVVKIEPVG	APTGARRRVV	QKEK.R....
CRF04_cpx_	TFRPGGGDMR	DNWRSELYKY	KVVQIEPVG	APTRARRRVV	QREK.R....
CRF05_DF_B	IFRPGGGDMR	DNWRSELYKY	KVVEIQPLGI	APTRAKRQVV	KREK.R...A
CRF05_DF_B	TFRPGGGDMR	DNWRSELYKY	KVVEIEPLGV	APTRAKRQVV	QREK.R...A
CRF06_cpx_	TFRPGGGDMR	DNWRSELYKY	KVVKIKPLGI	APTWARRRVV	GREK.R...A
CRF06_cpx_	TFRPGGGDMR	DNWRSELYKY	KVVKIKPLGI	APTRARRRVV	GKEKRA...V
CRF06_cpx_	IIRPGGGDMR	DNWRSELYKY	KVVKIKPLGI	APTEARRRVV	GREK.R...A
CRF06_cpx_	IFRPGGGNMK	DNWRSELYKY	KVVKIKPLGI	APTKARRRVV	GREKRA...V
CRF11_cpx_	TFRPTGGDMR	DNWRSELYKY	KVVEIKPLGV	APTRAKRRVV	EREK.R...A
CRF11_cpx_	TFRPTGGDMR	DNWRSELYKY	KVVEIKPLGV	APTKAKRRVV	EREK.R...A
D_CD_84ZR0	TFRPGGGDMR	DNWRSELYKY	KVVQIEPLGV	APTKAKRRVV	EREK.R...A
D_CD_ELI_K	TFRPGGGDMR	DNWRSELYKY	KVVQIEPLGV	APTRAKRRVV	EREK.R...A
D_CD_NDK_M	TIRPGGGDMR	DNWRSELYKY	KVVKIEPIGV	APTKARRRVV	EREK.R...A
D_UG_94UG1	TFRPGGGDMR	DNWRSELYKY	KVVKLEPIGL	APTAARRRVV	EREK.R...A
F1_BE_VI85	TFRPEGGMK	DNWRSELYKY	KVVEIEPLGV	APTKAKRQVV	QREK.R...A
F1_BR_93BR	TFRPGGGNMK	DNWRSELYKY	KVVEIEPLGV	APTKAKRQVV	KREK.R...A
F1_FI_FIN9	TFRPGGGDMK	DNWRSELYKY	KVVEIEPLGV	APTRPKRPVV	RRER.R...A
F1_FR_MP41	TFRPEGGMK	DNWRSELYKY	KVVEIEPLGV	APTKARRRVV	QREK.R...A
F2_CM_MP25	TLRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTKAKRQVV	QREK.R...A
F2KU_BE_VI	TFRPGGGNMK	DNWRSELYKY	KVVKIEPLGI	APTKARRRVV	QREK.R...G
G_BE_DRCBL	IFRPGGGDMK	DNWRSELYKY	KTVKIKSLGI	APTRARRRVV	EREK.R...A
G_NG_92NG0	TFRPGGGDMR	DNWRSELYKY	KTVKIKSLGV	APTRARRRVV	EREK.R...A
G_SE_SE616	IFRPGGGDMR	DNWRSELYKY	KTVKIKSLGV	APTRARRRVV	EREK.R...A
H_BE_VI991	TFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTEARRRVV	EREK.R....
H_BE_VI997	TFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTEARRRVV	EREK.R....
H_CF_90CF0	TFRPGGGDMR	DNWRSELYKY	KVVKIEPLGI	APTKTRRRVV	EREK.R....
J_SE_SE702	TFRPTGGNMK	DNWRSELYKY	KVVEIEPLGV	APTKAKRRVV	EREK.R...A
J_SE_SE788	TFRPTGGNMK	DNWRSELYKY	KVVEIEPLGV	APTKAKRRVV	EREK.R...A
K_CD_EQTB1	TFRPGGGDMR	DNWRSELYKY	KVVQIEPLGI	APTRARRRVV	QREK.R...A
K_CM_MP535	TFRPGGGDMR	DNWRSELYKY	KVVQIEPLGI	APTRARRRVV	QREK.R...A
N_CM_YBF30	IVYPSGGMV	NLWRQELYKY	KVVSIEPIGV	APGKAKRRTV	SREK.R...A
O_CM_ANT70	TFRPIGGDMK	DIWRTELFNY	KVVRVKPFSV	APTARIAPVI	STRTHR.EKR
O_CM_MVP51	TLRPVGGDMK	DIWRTKLNY	KVVQIKPFSV	APTKMSRPII	NIHTPHREKR
O_SN_99SE_	TFRPTGGDMK	DIWRTELFKY	KVVVKPFSV	APTKIAPVI	GTGTQR.EKR
O_SN_99SE_	TFRPIGGDMK	DIWRTELFKY	KVVKIKPFSV	APTKIAPVI	GTGTTR.EKR
U_CD___83C	TFRPGGGDMK	DNWRSELYKY	KVVKIEPLGV	APTRAKRRVV	EREK.R....

	601			650
00BW0762_1	AVGIGAVFLG	.FLGAAGSTM	GAASITLMVQ	ARQLLSGIVQ QQNNLLRAIE
00BW0768_2	AVGIGAVLLG	.FLGAAGSTM	GAASITLTVQ	ARQVLSGIVQ QQSNLLRAIE
00BW0874_2	AVGIGAVFLG	.FLGAAGSTM	GAASMTLTVQ	ARQLLSGIVQ QQSNLLRAIE
00BW1471_2	AVGLGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ QQNNLMRAIE
00BW1616_2	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ QQNNLLRAIE
00BW1686_8	AVGIGAVLLG	.FLGAAGSTM	GAASMTLTVQ	ARQLLSGIVQ QQSNLLRAIE
00BW1759_3	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ QQSNLLRAIE
00BW1773_2	AVGIGAMFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ QQSNLLRAIE
00BW1783_5	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	VRQLLSGIVQ QQNNLLRAIE
00BW1795_6	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ QQSNLLRAIE
00BW1811_3	AVGIGAVFLG	.FLGAAGSTM	GAASMTLTVQ	ARQLLSGIVQ QQSNLLKAIE
00BW1859_5	AVGIGAVFLG	.FLGAAGSTM	GAASTTLTAQ	ARQVLSGIVQ QQSNLLRAIE
00BW1880_2	AVGIGAVFLG	.FLGAAGSTM	GAASMTLTVQ	ARQLLSGIVQ QQSNLLRAIE
00BW1921_1	RAALGAVLLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ QQSNLLKAIE
00BW2036_1	AVGIMGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ QQSNLLRAIE
00BW2063_6	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ QQSNLLRAIE
00BW2087_2	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	TKQLLSGIVQ QQSNLLKAIE
00BW2127_2	AVGIMGAVILG	.FLGAAGSTM	GAASITLTVQ	ARQLLFGIVQ QQNNLLRAIK
00BW2128_3	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ QQSNLLRAIE
00BW2276_7	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLFGIVQ QQSNLLRAIE
00BW3819_3	AVGIGAVFLG	.FLGAAGSTM	GAASITLTIQ	ARQLLSGIVQ QQSNLLRAIE
00BW3842_8	AVGIMGAMILG	.FLSAAGSTM	GAASITLTVQ	ARQLLSGIVQ QQSNLLRAIE
00BW3871_3	AVGIGAVFLG	.FLGAAGSTM	GAASITLTAQ	ARQLLSGIVQ QQSNLLRAIE
00BW3876_9	AVEIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ QQSNLLRAIE
00BW3886_8	AVGIGAVILG	.FLGAAGSTM	GAASITLTAQ	ARQLLSGIVQ QQSNLLRAIE
00BW3891_6	RAAIGAMFLG	.FLGAAGSTM	GAASITLTVQ	ARKLLSGIVQ QQSNLLRAIE
00BW3970_2	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ QQSNLLKAIE
00BW5031_1	RAALGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ QQSNLLRAIE
96BW01B21	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ QQSNLLRAIE
96BW0407	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ QQSNLLRAIE
96BW0502	AVGIGAVCLG	.FLGAAGSTM	GAASITLTVQ	ARLLLSGIVQ QQNNLLRAIE
96BW06_J4	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	AKQLLSGIVQ QQSNLLKAIE
96BW11_06	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ QQSNLLRAIE
96BW1210	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ QQSNLLRAIE
96BW15B03	AVGIGAVIFG	.FLGAAGSTM	GAASITLTAQ	ARQLLSGIVQ QQSNLLRAIE
96BW16_26	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ QQSNLLQAIE
96BW17A09	AVGLGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ QQSNLLRAIE
96BWM01_5	AVTFGAMFLG	.FLGAAGSTM	GAASMTLTVQ	ARQLLSGIVQ QQSNLLRAIE
96BWM03_2	AVGIGAVLLG	.FLGTAGSTM	GAASITLTVQ	ARQVLSGIVQ QQSNLLRAIE
98BWMC12_2	AAGLGAVLFG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ QQSNLLRAIE
98BWMC13_4	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	VRQLLSGIVQ QQSNLLRAIE
98BWMC14_a	AVGVAAVFLG	.FLSAAGSTM	GAASITLTVQ	ARQSLSGIVQ QQSNLLRAIE
98BWM014_1	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ QQSNLLRAIE
98BWM018_d	RAALGAVFLG	.FLGAAGSTM	GAASITLTVQ	TRKLLSGIVQ QQSNLLKAIE
98BWM036_a	AVTLGAMFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ QQSNLLRAIE
98BWM037_d	AVGIGAVFLG	.FLGAAGSTM	GAASITLMVQ	ARQLLSGIVQ QQSNLLRAIE
99BW3932_1	AVGLGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ QQNNLLRAIE
99BW4642_4	AVGIGAVLLG	.FLGAAGSTM	GAASIALTAQ	ARQVLSGIVQ QQSNLLRAIE
99BW4745_8	RAIAGAVFLG	.FLGVAGSTM	GAASVALTVQ	ARQLLSGIVQ QQSNLLRAIE
99BW4754_7	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ QQSNLLRAIE
99BWMC16_8	AVTIGAMFLG	.FLSAAGSTM	GAASITLTVQ	ARQLLSGIVQ QQSNLLRAIE
A2_CD_97CD	AVGLGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLTGIVQ QQSNLLKAIE
A2_CY_94CY	AVGLGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ QQSNLLQAIE
A2D_97KR	RAAVGLFFLG	.FLGAAGSTM	GAASVTLTVQ	ARQLLSGIVQ QQSNLLKAIE
A2G_CD_97C	AVGLGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ QQNNLLKAIE
A_BY_97BL0	AIGLXAAFLX	.FLGAAXSTX	GAASMTLTVQ	ARQLLSGIVQ QQSNLLXAIX
A_KE_Q23_A	AVGIGAVFLG	.FLGAAGSTM	GATSITLTVQ	ARQLLSGIVQ QQNNLLRAIE
A_SE_SE659	AVGLGAVFIG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVR QQSNLLKAIE
A_SE_SE725	AVGLGALFIG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ QQSNLLRAIE

A_SE_SE753	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
A_SE_SE853	AIGIGAVFIG	.FLGAAGSTM	GAASITLTVQ	ARQLLSXIVQ	QQSNLLRAIE
A_SE_SE889	AIGIGAVFIG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLMAIE
A_SE_UGSE8	AVGLAAVFFG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQNNLLRAIE
A_UG_92UG0	AVTLGAVFIG	.FLGTAGSTM	GAASITLTVQ	ARKLLSGIVQ	QQSNLLRAIE
A_UG_U455_	AVGLGAIFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
AC_IN_2130	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
AC_RW_92RW	AVGLGAVFIG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
AC_SE_SE94	AVGMGAVFIG	.FLGAAGSTM	GAASVTLTVQ	ARQLLSGIVR	QQSNLLRAIE
ACD_SE_SE8	AVGIGAVFLG	.FLGAAGSAM	GAASATLTVQ	ARQLLSGIVQ	QQSNLLKAIE
ACG_BE_VI1	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
AD_SE_SE69	AG.LGAVFIG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQNNLLKAIE
AD_SE_SE71	AVGIGVVFFG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
ADHK_NO_97	AVGMGAFFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLKAIQ
ADK_CD_MAL	IG.LGAMFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQNNLLRAIE
AG_BE_VI11	VGLG.AVFLG	.FLGAAGSTM	GAASITLTVQ	VRQLLSGIVQ	QQSNLLRAIE
AG_NG_92NG	VGLG.AVFLG	.FLGAAGSTM	GAGSITLTVQ	VRQLLSGIVQ	QQSNLLRAIE
AGHU_GA_VI	IVGVGAVFLG	.FLGVAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLKAIE
AGU_CD_Z32	AIGMGAVFLG	.FLGAAGSTM	GAASITLTVH	VRQLLSGIVQ	QQSNLLRAIE
AJ_BW_BW21	VGIMGAMFLG	.FLGTAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLKAIE
B_AU_VH_AF	VGMIGAMILG	.FLGAAGSTM	GAASLALTVQ	TRQLLSGIVQ	QQNNLLRAIE
B_CN_RL42	VGTIGAMFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQRNLLRAIE
B_DE_D31_U	VGLLGAVFLG	.FLGAAGSTM	GARSMALTVQ	ARQLLSGIVQ	QQNNLLRAIE
B_DE_HAN_U	VGMLGAMFLG	.FLGAAGSTM	GARSITLTVQ	ARQLLSGIVQ	QQNNLLRAIE
B_FR_HXB2_	VG.IGALFLG	.FLGAAGSTM	GAASMTLTVQ	ARQLLSGIVQ	QQNNLLRAIE
B_GA_OYI_	VGMLGAMFLG	.FLGAAGSTM	GARSMTLTVQ	ARQLLSGIVQ	QQNNLLRAIE
B_GB_CAM1_	VGAIGALFLG	.FLGAAGSTM	GAVALTLTVQ	TRQLLSGIVQ	QQNNLLRAIE
B_GB_GB8_C	VGMIGAMFLG	.FLGAAGSTM	GAASLTLTVQ	ARLLLSGIVQ	QQNNLLRAIE
B_GB_MANC_	VGMLGAMFLG	.FLGAAGSTM	GARSITLTVQ	ARQLLSGIVQ	QQNNLLRAIE
B_KR_WK_AF	VT.FGALFLG	.FLGAAGSTM	GCTSMTLTVQ	ARLLLSGIVQ	QQNNLLRAIE
B_NL_3202A	VG.IGALFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQNNLLRAIE
B_TW_TWCYS	VG.IGALFLG	.FLGAAGSTM	GAASLTLTVQ	ARQLLSGIVQ	QQNNLLRAIE
B_US_BC_L0	VG.IGALFLG	.FLGAAGSTM	GAASMTLTVQ	ARQLLSGIVQ	QQNNLLRAIE
B_US_DH123	VG.IGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQNNLLRAIE
B_US_JRCSE	AVGIGALFLG	.FLGAAGSTM	GARSMTLTVQ	ARQLLSGIVQ	QQNNLLRAIE
B_US_MNCG_	RAAIGALFLG	.FLGAAGSTM	GAASVTLTVQ	ARLLLSGIVQ	QQNNLLRAIE
B_US_P896_	AVGIGAVFLG	.FLGAAGSTM	GAASVTLTVQ	ARLLLSGIVQ	QQNNLLRAIE
B_US_RF_M1	VGTIGAMFLG	.FLGAAGSTM	GAGSITLTVQ	ARHLLSGIVQ	QQNNLLRAIE
B_US_SF2_K	VGIVGAMFLG	.FLGAAGSTM	GAVSLTLTVQ	ARQLLSGIVQ	QQNNLLRAIE
B_US_WEAU1	VGMLGAMFLG	.FLGAAGSTM	GAASMTLTVQ	ARLLLSGIVQ	QQNNLLRAIE
B_US_WR27_	VGVIGVMFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQNNLLRAIE
B_US_YU2_M	VG.LGALFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQNNLLRAIE
BF1_BR_93B	VG.MGALFLG	.FLGAAGSTM	GAASITLTAQ	ARQLLSGIVQ	QQNNLLRAIE
C_BR_92BR0	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	VRQLLSGIVQ	QQSNLLRAIE
C_BW_96BW0	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
C_BW_96BW1	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARRLLSGIVQ	QQSNLLRAIE
C_BW_96BW1	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
C_BW_96BW1	AVGIGAVIFG	.FLGAAGSTM	GAASITLTAQ	ARQLLSGIVQ	QQSNLLRAIE
C_ET_ETH22	RAALGALFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLKAIE
C_IN_93IN1	AVGIGAVFLG	.FLGAAGSTM	GAASITLTAQ	ARQLLSGIVQ	QQSNLLRAIE
C_IN_93IN9	AVGIGALFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
C_IN_93IN9	VVGLGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
C_IN_94IN1	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
C_IN_95IN2	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
CRF01_AE_C	AVGIGAMIFG	.FLGAAGSTM	GAASLTLTVQ	ARQLLSGIVQ	QQSNLLRAIE
CRF01_AE_C	AVGIGAMIFG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
CRF01_AE_C	AVGIGAMIFG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRTIE
CRF01_AE_T	AVGIGAMIFG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
CRF01_AE_T	AVGIGAMIFG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
CRF01_AE_T	AVGIGAMIFG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE

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CRF01_AE_T	AVGIGAMIFG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
CRF01_AE_T	AVGIGAMIFG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
CRF02_AG_F	AVGLGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
CRF02_AG_F	AVGLGAVFFG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
CRF02_AG_G	AVGLGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
CRF02_AG_N	AVGLGAVFLG	.FLGAAGSTM	GARSITLTVQ	ARQLLSGIVQ	QQSNLLKAIE
CRF02_AG_S	LVGLGAFFFG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLKAIE
CRF02_AG_S	AVGLGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQNNLLKAIE
CRF03_AB_R	VG.IGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQNNLLRAIE
CRF03_AB_R	VG.IGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQNNLLRAIE
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D_CD_84ZR0	IG.LGAMFLG	.FLGAAGSTM	GAASMTLTVQ	ARQVLSGIVQ	QQNNLLRAIE
D_CD_ELI_K	IG.LGAMFLG	.FLGAAGSTM	GARSVTLTVQ	ARQLMSGIVQ	QQNNLLRAIE
D_CD_NDK_M	IG.LGAVFLG	.FLGAAGSTM	GAASVTLTVQ	ARQLMSGIVH	QQNNLLRAIE
D_UG_94UG1	IG.LGALFLG	.FLGTAGSTM	GAVSLTLTVQ	ARQVLSGIVQ	QQNNLLRAIE
F1_BE_VI85	AG.LGALFLG	.FLGDSREHM	GAASITLTVQ	ARQLLSGIVQ	QQNNLLRAIE
F1_BR_93BR	VG.LGALFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
F1_FI_FIN9	VA.IGAVFLG	.FLSAAGSTM	GAASLTLTVQ	ARQLLSGIVQ	QQNNLLQAIE
F1_FR_MP41	VG.IGALFLR	.FLGAAGSNI	GAASITLTVQ	ARQLLSGIVQ	QQNNLLRAIE
F2_CM_MP25	VG.MGAMFLG	.FLGAAGSTM	GAASITLTVQ	ARNLLSGIVQ	QQSNLLKAIE
F2KU_BE_VI	AG.LGALFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSDLLRAIE
G_BE_DRCBL	VGVG.AIFLG	.FLGTAGSTM	GAASITLTVQ	VRQLLSGIVQ	QQSNLLRAIE
G_NG_92NG0	VGLG.AVFLG	.FLGAAGSTM	GAASITLTAQ	VRQLLSGIVQ	QQSNLLRAIE
G_SE_SE616	VGLG.AVFLG	.FLGAAGSTM	GAASITLTVQ	VRQLLSGIVQ	QQGNLLRAIE
H_BE_VI991	AVGMGAFFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIQ
H_BE_VI997	AVGMGAFFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIQ
H_CF_90CF0	AVGMGASFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIQ
J_SE_SE702	VGIG.AVFLG	.FLGTAGSTM	GAASITLTVQ	VRQLLSGIVQ	QQSNLLKAIX
J_SE_SE788	VGIG.AVFLG	.FLGTAGSTM	GAASITLTVQ	VRQLLSGIVQ	QQSNLLKAIE
K_CD_EQTB1	VG.IGALFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQNNLLRAIE
K_CM_MP535	VG.LGAVFFG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
N_CM_YBF30	AFGLGALFLG	.FLGAAGSTM	GAASITLTVQ	ARTLLSGIVQ	QQNILLRAIE
O_CM_ANT70	AVGLGMLFLG	.VLSAAGSTM	GAAATTAVQ	THTLLKGIVQ	QQDNLLRAIQ
O_CM_MVP51	AVGLGMLFLG	.VLSAAGSTM	GAAATALTVR	THSVLKGIVQ	QQDNLLRAIQ
O_SN_99SE_	AVGLGMLFLG	.VLSAAGSTM	GAAATALAVQ	TQSLMKGIVQ	QQDNLLRAIQ
O_SN_99SE_	AVGLGMLFLG	.VLSAAGSTM	GAAATTAVQ	THTLMKGIVQ	QQDNLLRAIQ
U_CD___83C	AVGMGALFLG	.FLGAAGSTM	GAASMALTAQ	ARQLLSGIVQ	QQNNLLRAIE



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00BW3876_9	AQQHLLQLTV	WGIKQLQTRV	LAVERYLKDQ	QLLGIWGCSG	KLICTTNVPW
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96BW06_J4	AQQHMLQLTV	WGIKQLQTKV	LAIERYLKDQ	QLLGFWGCSG	KLVCCTAVPW
96BW11_06	AQQHMLQLTV	WGIKQLQTRV	LAIERYLKDQ	QLLGIWGCSG	KLICTTAVPW
96BW1210	AQQHMLQLTV	WGIKQLQARV	LALERYLRDQ	QLLGIWGCSG	KLICTTNVPW
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96BW16_26	AQQHLLQLTV	WGIKQLQTRV	LAIERYLKDQ	QLLGIWGCSG	KLICTTAVPW
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A2D_97KR	AQQHMLRLTV	WGIKQLQARV	LAVERYLQDQ	QLLGIWGCSG	KLICTTFVPW
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A_KE_Q23_A	AQQHLLKLTV	WGIKQLQARV	LAVERYLRDQ	QLLGIWGCSG	KLICTTNVPW
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A_UG_92UG0	AQQHLLKLTV	WGIKQLQARV	LAVERYLRDQ	QLLGIWGCSG	KLICPTNVPW
A_UG_U455_	AQQHLLKLTV	WGIKQLQARV	LAVERYLQDQ	QLLGIWGCSG	KLICTTTVPW
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AC_RW_92RW	AQQHLLKLTV	WGIKQLQARV	LALERYLRDQ	QLLGIWGCSG	KLICTTNVPW
AC_SE_SE94	AQQHLLKLTV	WGIKQLQARI	LAVERYLKDQ	QLLGIWGCSG	KIICTTNVPW
ACD_SE_SE8	AQQHLLKLTV	WGIKQLQARV	LAVERYLKDQ	QLLGIWGCSG	KLICATNVPW
ACG_BE_VI1	AQQHMLQLTV	WGIKQLQTRV	LAIERYLQVQ	QLLGIWGCSG	KLICTTSPVP
AD_SE_SE69	AQQHLLKLTV	WGIKQLQARV	LAVERYLKDQ	QLLGIWGCSG	KLICTTNVPW
AD_SE_SE71	AQQHLLKLTV	WGIKQLQARV	LALERYLKDQ	QLLGIWGCSG	KLICPTTVPW
ADHK_NO_97	AQQHMLQLTV	WGIKQLQARV	LAVERYLKDQ	QLLGIWGCSG	KLICTTNVPW
ADK_CD_MAL	AQQHLLQLTV	WGIKQLQARV	LAVERYLQDQ	RLLGMWGCSG	KHICTTFVPW
AG_BE_VI11	AQQHMLQLTV	WGIKQLQARV	LAVERFLKDQ	QLLGIWGCSG	KLICTTNVPW
AG_NG_92NG	AQQHLLQLTV	WGIKQLQARV	LAVERYLKDQ	QLLGIWGCSG	KLICTTNVPW
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B_US_YU2_M	AQQHLLQLTV	WGIKQLQARV	LAVERYLRDQ	QLLGIWGCSG	KLICTTTVPW
BF1_BR_93B	AQQHLLQLTV	WGIKQLQARI	LAVERYLKDQ	QLLGLWGCSG	KLICTTDVPW
C_BR_92BR0	AQQHMLQLTV	WGIKQLQTRV	LAIERYLRDQ	QLLGIWGCSG	KLICTTAVPW
C_BW_96BW0	AQQHMLQLTV	WGIKQLQTRV	LAIERYLKDQ	QLLGIWGCSG	KLICTTNVPW
C_BW_96BW1	AQQHMLQLTV	WGIKQLQTRV	LAIERYLKDQ	QLLGIWGCSG	KLICTTAVPW
C_BW_96BW1	AQQHMLQLTV	WGIKQLQARV	LALERYLRDQ	QLLGIWGCSG	KLICTTNVPW
C_BW_96BW1	AQQHMLQLTV	WGIKQLQARV	LAIERYLKDQ	QLLGIWGCSG	KLICTTTVPW
C_ET_ETH22	AQQHMLQLTV	WGIKQLQTRV	LAIERHLRDQ	QLLGIWGCSG	KLICTTAVPW
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CRF06_cpx	NISWSN....	KTYSEIWDN.	.MTWIEWDRE	INNYTQQIYN	LIEESQNQQE
CRF11_cpx	NISWSN....	KSYYDEIWDN.	.MTWIEWERE	IDNYTQTIYT	LLEESQTQQE
CRF11_cpx	NVSWSN....	KTYNEIWEENE	NMTWIKWERE	IDNYTQTIYT	LIEESQNQQE
D_CD_84ZR0	NSSWSN....	RSVEYIWGN.	.MTWMQWERE	IDNYTGIIYN	LIEESQIQQE
D_CD_ELI_K	NSSWSN....	RSLNEIWDN.	.MTWMEWERE	IDNYTGIIYS	LIEESQTQQE
D_CD_NDK_M	NSSWSN....	RSLDEIWDN.	.MTWMEWERE	IDNYTGIIYS	LIEESQIQQE
D_UG_94UG1	NSSWSN....	RSVDEIWNN.	.MTWMEWERE	IDNYTELVS	LLEVSQIQQE
F1_BE_VI85	NSSWSN....	KSQEEIWNN.	.MTWMEWEKE	ISNYSNIIYK	LIEESQNQQE
F1_BR_93BR	NSSWSN....	KSLEEIWGN.	.MTWMEWEKE	VSNYSKEIYR	LIEDSQNQQE
F1_FI_FIN9	NSSWSN....	KSQDEIWNN.	.MTWMQWEKE	ISNYSKTIYM	LIEKSQSQQE
F1_FR_MP41	NTSWSN....	KSHDEIWNN.	.MTWMQWEKE	INNYSNTIYR	LIEESQNQQE
F2_CM_MP25	NLSWSN....	KSQDEIWDN.	.MTWMEWEKE	IGNYTDTIYR	LIESAQNQQE
F2KU_BE_VI	NSSWSN....	RSQDEIWNN.	.MTWMEWENE	INNYTGIIYQ	LIEQSQNQQE
G_BE_DRCBL	NTSWSN....	KSYYNEIWEN.	.MTWIEWERE	IDNYTYHIYS	LIEQSQIQQE
G_NG_92NG0	NTSWSN....	KSYYNEIWDN.	.MTWLEWERE	IHNYTQHIYS	LIEESQNQQE
G_SE_SE616	NVSWSN....	KSYYNEIWDN.	.MTWIEWERE	INNYTYQIYS	LLEESQNQQE
H_BE_VI991	NSSWSN....	KSLDEIWDN.	.MTWMEWDKQ	INNYTDEIYR	LLEVSQNQQE
H_BE_VI997	NSTWSN....	KSLAEIWDN.	.MTWMEWDRQ	IDNYTEVIYR	LLELSQTQQE
H_CF_90CF0	NSSWSN....	KSQSEIWDN.	.MTWMEWDKQ	ISNYTEEIYR	LLEVSQTQQE
J_SE_SE702	NASWSN....	KSYYEDIWEN.	.MTWIQWERE	INNYTGIIYS	LIEEAQNQQE
J_SE_SE788	NASWSN....	KSYYEDIWEN.	.MTWIQWERE	INNYTGIIYS	LIEEAQNQQE
K_CD_EQTB1	NSSWSN....	KSQSEIWEN.	.MTWMQWEKE	ISNHTSTIYR	LIEESQIQQE
K_CM_MP535	NSSWSN....	KSWEIWN.	.MTWMEWEKE	IGNYSDTIYK	LIEESQTQQE
N_CM_YBF30	NETWSNN...	TSYDTIWNN.	.LTWQQWDEK	VRNYSGVIFG	LIEQAQEQQN
O_CM_ANT70	NRTWIG....	NES..IWD.	.LTWQEWDRQ	ISNISSTIYE	BIQKAQVQQE
O_CM_MVP51	NTSWSGRYN.	DDS..IWD.	.LTWQQWDQH	INNVSIIYD	BIQAQDQQE
O_SN_99SE	NTTWTNCTNT	NKLDDIWDK.	.LTWQQWDQQ	ISNVSSIIYE	EIRNAQVQQE
O_SN_99SE	NRTWTN..NN	TDLDTIWGN.	.LTWQEWDDQ	ISNISATIYD	BIQKAQVQQE
U_CD___83C	NSSWSN....	KSLDNIWDN.	.LTWMEWDRE	ISNYTQVIYG	LLEDQKQQE

00BW0762_1	QNEKDLLALD	SWKNLWSWFD	ISNWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
00BW0768_2	RNERDLLALD	SWKNLWSWFD	ISNWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
00BW0874_2	KNEKDLLALD	SWKNLWSWFD	ISN.LWYIRI	FIMIVGGLIG	LRIVFAVLSL
00BW1471_2	KNEQELLALD	SWENLWNWFS	ISRWLWYIKI	FIMIVGGLIG	LRIIFAVLSV
00BW1616_2	KNEKDLLALD	SWNSLWNWFD	ITNWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
00BW1686_8	QNEKDLLALD	SWKNLWNWFD	ISNWLWYIKI	FIIIVGGLIG	LRIIFAVLSI
00BW1759_3	INEKDLLALD	SWKNLWNWFD	ITKWLWYIKI	FIMIVGGIIG	LRIIFAVLSI
00BW1773_2	KNEKDLLALD	SWKNLWNWFG	ITKWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
00BW1783_5	KNEKDLLALD	SWNNLWNWFT	ITNWLWYIKI	FIMIVGGLIG	LRIIFAVLSL
00BW1795_6	KNEKDLLALD	SWKNLWNWFD	ITNWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
00BW1811_3	INEKDLLALD	SWKNLWSWFD	ISNWLWYIRI	FIMIVGGLIG	LRIIFAVLSI
00BW1859_5	KNEKDLLALD	SWKNLWSWFD	ITNWLWYIRI	FIIIVGGLIG	LRIIFAVLSI
00BW1880_2	QNEKNLLALD	SWKNLN.WFS	IT.HLWYIKI	FIMIVGGLIG	LRIVLVVLSV
00BW1921_1	KNEKDLLALD	SWNNLWNWFS	ITKWLWYIKI	FIIIIIGGLIG	LRIIFAVLSI
00BW2036_1	QNEKDLLALD	SWKNLWTWFD	ISNWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
00BW2063_6	KNERDLLALD	SWKNLWNWFD	ISNWLWYIKI	FIMIVGGLIG	LRIIFAVLSM
00BW2087_2	NNEKDLLALD	SWNNLWNWFD	ITKWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
00BW2127_2	QNEKDLLALD	RWDSLWNWFG	ISKWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
00BW2128_3	KNEEDLLALD	SWDSLWNWFS	ITKWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
00BW2276_7	QNEKDLLALD	SWKNLWSWFD	ISNWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
00BW3819_3	QNEKDLLALD	SWKNLWTWFD	ISNWLWYIKI	FIMIVGGLIG	LRIIFTVFSI
00BW3842_8	INEKDLLALD	SWNSLWNWFD	ITKWLWYIKI	FIMVVGGLIG	LRIIFAVLSI
00BW3871_3	KNEKDLLALD	SWKNLWNWFD	ITNWLWYIKI	FIIIIIGGLIG	LRIIFAVLSI
00BW3876_9	QNEKDLLALD	SWNSLWSWFD	ITRWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
00BW3886_8	KNEQELLALD	SWKSLWNWFD	ITNWLWYIKI	FIMVVGGLIG	LRIIFAVLSL
00BW3891_6	RNEKDLLAMD	SWKNLWNWFD	ITNWLWYIKI	FIMIVGGLIG	LRIVFAVLSI
00BW3970_2	QNEQDLLALN	KWQHLWNWFD	ITKWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
00BW5031_1	QNEKDLLALD	SWKNLWSWFD	ISNWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
96BW01B21	KNEKDLLALD	SWQNLWNWFS	ITNWLWYIKI	FIMIVGGLIG	LRIVFAVLSI
96BW0407	KNEKDLLALD	SWNNLWNWFS	ITNWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
96BW0502	KNEKDLLALD	SWQNLWNWFS	ITNWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
96BW06_J4	KNEKDLLALD	SWKNLWNWFG	ITNWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
96BW11_06	KDEKDLLALD	SWQNLWNWFD	IPKWLWYIKI	FIMIVGGLIG	LRIIFAVISM
96BW1210	QNEKDLLALD	SWANLWNWFD	ISNWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
96BW15B03	QNEKDLLALD	SWNNLWSWFD	ISNWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
96BW16_26	KNEKDLLALD	SWNSLWNWFS	IVNWLRYIKI	FIMIVGGLIG	LRIIFAVLSI
96BW17A09	KNEQELLALD	SWANLWNWFA	ISNWLWYIKI	FIMIVGGLIG	LRIVFAVLSV
96BWM01_5	RNEKDLLALD	SWKTLWSWFD	ISNWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
96BWM03_2	KNEQDLLALD	SWANLWNWFD	ISNWLWYIKI	FIMIVGGLIG	LRIVFAVLSI
98BWMC12_2	ENEKDLLALD	SWKNLWNWFD	ITNWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
98BWMC13_4	KNEKDLLALD	SWKNLWNWFD	ITNWLWYIKI	FIMIVGGLIG	LRIIFAVLSM
98BWMC14_a	QNEKDLLALD	KWKDLRNWFD	ISNWLWYIRI	FIMIVGGLIG	LRIIFAVLSI
98BWM014_1	KNEKDLLALD	SWNNLWTWFG	ISSWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
98BWM018_d	RNEKDLLALD	SWNNLWNWFD	ISNWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
98BWM036_a	QNEKDLLALD	SWQSLWNWFS	ITKRLWYIKI	FIMIVGGLIG	LRIIFAVLSI
98BWM037_d	QNEKDLLALD	SWQNLWSWFS	ITNWLWYIKI	FIMIVGGLIG	LRIIFAVLSL
99BW3932_1	KNEKDLLALD	SWQNLWNWFD	ITNWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
99BW4642_4	KNEKDLLALD	SWKNLWTWFD	ISNWLWYIRI	FIMIVGGLIG	LRIIFAVLSI
99BW4745_8	QNEKELLALD	RWDTLWSWFD	ITNWLWYIRL	FIMIVGGLIG	LRIIFAVLSI
99BW4754_7	KSEKDLLALD	SWKNLWNWFD	ITNWLWYIKI	FIMIVGGLIG	LRIIFAVLSV
99BWMC16_8	RNEKDLLALD	SWKNLWNWFD	ISNWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
A2_CD_97CD	KNEQDLLALD	KWANLWNWFD	ITRWLWYIKI	FIMIVGGLIG	LRIVIAIISV
A2_CY_94CY	KNEQDLLALD	KWADLWSWFD	ISHWLWYIRI	FIMIVGGLIG	LRIVFAIITV
A2D_97KR	KNEKDLLALD	KWASLWNWFD	ISNWLWYIKI	FIMIVGGLIG	LRIVMAIISV
A2G_CD_97C	KNKQDLLALD	KWASLWNWFD	ITKWLWYIKI	FIMIVGGLIG	LRIVFAVLSI
A_BY_97BL0	KNXQDLLALD	KAG.LXSXXD	ISNWLXYIXI	FIIIVGGLIX	LRIIFAVLSI
A_KE_Q23_A	KNEKELLELD	KWANLWSWFD	ISNWLWYIKI	FIIIVGGLIG	LRIVFAVLSV
A_SE_SE659	MNEQDLLALD	KWANLWNWFD	ITNWLWYIRI	FIMIVGGLIG	LRIVFAVLSI
A_SE_SE725	KNEQDLLALD	KWANLWNWFE	ITKWLWYIKI	FIMIVGGLIG	LRIVFAVFSV

A_SE_SE753	KNEQDLMALD	KWTNLWTWFS	ISNWLWYIRI	FIMIVGGLIG	LRIVFAVLAI
A_SE_SE853	KNEQDLLALD	KWASLWNWFD	ISRWLWYIRI	FIMIVGGLIG	LRIVFAVL SV
A_SE_SE889	KNEQDLLALD	KWANLWNWFD	ISKWLWYIKI	FIMIVGGLIG	LRIVIAVISI
A_SE_UGSE8	KNEKELLELD	KWANLWNWFD	ISNWLWYIKI	FIMIVGGLIG	LRIVFAVLTV
A_UG_92UG0	RNEKDLELD	KWASLWNWFD	ISKWLWYIKI	FIMIVGGLIG	LRIVFAVL SV
A_UG_U455_	KNELDLLALD	KWANLN . WFN	ISNWLWYIRL	FVIIVGGLIG	LRIVFTVLSI
AC_IN_2130	KNEQDLLALD	KWADLWNWFD	ISNWLWYIKI	FIMIVGGLIG	LRIVFAVL SV
AC_RW_92RW	KNEQDLLALD	KWANLWNWFD	ISNWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
AC_SE_SE94	KNEQDLLALD	KWASLWNWFD	ISKWLWYIRI	FIMIVGGLIG	LRIVFAVL SI
ACD_SE_SE8	KNEQDLLALD	KWGS LWNWFE	ISKWLWYIRI	FIMIVGGLIG	LRIVFAVL SV
ACG_BE_VI1	QNEKDLLALD	KWQNLWSWFN	ISNWLWYIKI	FIMIVGGLIG	LRIIFAIL SI
AD_SE_SE69	KNEQDLLALD	KWANLWSWFD	ISNWLWYIKI	FIMIVGGLIG	LRIVFAVL SL
AD_SE_SE71	MNEQDLLQLD	KWASLWNWFD	ITNWLWYIRI	FIIIVGGLIG	LRIVFAVL SI
ADHK_NO_97	KNEQDLLALD	KWASLWNWFD	ISKWLWYIKI	FIMIVGGVIG	LRIVFAVL SI
ADK_CD_MAL	KNEKELLELD	KWASLWNWFS	ISKWLWYIRI	FIIIVGGLIG	LRIIFAVL SL
AG_BE_VI11	KNEQDLLSLD	KWASLWTWFD	IANWLWYIRI	FIMIVGGLIG	LRVVFVAVL NV
AG_NG_92NG	KNEQDLLALD	KWASLWNWFD	ITKWLWYIKI	FIMIVGGLIG	LRIVFAVL SI
AGHU_GA_VI	KNEQELLALD	KWASLWSWFD	ISKWLWYIRI	FIMIVGGLIG	LRIFFAVL SM
AGU_CD_Z32	INERDLLALD	KWANLWNWFD	ISNWLWYIKI	FIMIVGGLIG	LRIVFAVL SI
AJ_BW_BW21	KNEQDLLSLD	KWASLWNWFS	ISNWLWYIRI	FIMIVGGLIG	LRIIFAVL AI
B_AU_VH_AF	KNEQELLALD	KWASLWNWFS	ITKWLWYIKI	FIMIVGGLVG	LRIVFAVL SL
B_CN_RL42_	KNELELELD	KWASLWNWFD	ITKWLWYIKI	FIMIVGGLVG	LRIVFAVL SI
B_DE_D31_U	KNEQELLELN	KWENLWSWFD	ISNWLWYIKI	FIMIVGGLVG	LRIVFAVL SI
B_DE_HAN_U	KNEQELLELD	KWASLWSWYD	ISNWLWYIKI	FIMIVGGLIG	LRIVFAVL SI
B_FR_HXB2_	KNEQELLELD	KWASLWNWFN	ITNWLWYIKL	FIMIVGGLVG	LRIVFAVL SI
B_GA_OYI_	KNEQELLELD	KWAGLWSWFS	ITNWLWYIRI	FIIIVGGLVG	LRIVFAVL SI
B_GB_CAM1_	KNEKDLELD	TWASLWNWFD	ITNWLWYIKI	FIMIIGGLIG	LRIVFTIL SL
B_GB_GB8_C	KNEQELLELD	KWANLWNWFD	ITNWLWYIKI	FIMIIGGLIG	LRIIFAVI ST
B_GB_MANC_	KNEQELLELD	KWGS LWSWFS	ITNWLWYIKI	FIMIVGGLVG	LRIVFAVL SL
B_KR_WK_AF	KNEQELLELD	KWASLN . WFN	ITKWLWYIKI	FIMIVGGLVG	LRIIFFVL SI
B_NL_3202A	KNEQELLELD	KWASLWNWFD	ITKWLWYIKI	FIMIVGGLVG	LRIIFAVL SI
B_TW_TWCYS	KNEQDLELD	KWASLWNWFD	ITNWLWYIRI	FIMIVGGLIG	LRIVFAVL SI
B_US_BC_L0	KNEQELLELD	KWASLWNWFT	ITNWLWYIKI	FIMIVGGLIG	LRIVFTVLSI
B_US_DH123	KNEQELLALD	KWASLWNWFN	ISNWLWYIKI	FIMIVGGLIG	LRIVFSVL SI
B_US_JRCSF	KNEQELLELD	KWASLWNWFG	ITKWLWYIKI	FIMIVGGLIG	LRIVFSVL SI
B_US_MNCG_	KNEQELLELD	KWASLWNWFD	ITNWLWYIKI	FIMIVGGLVG	LRIVFAVL SI
B_US_P896_	KNEKELLELD	KWASLWNWFD	ITNWLWYIRL	FIMIVGGLIG	LRIVFAVL SI
B_US_RF_M1	KNEQELLELD	KWANLWNWFD	ITQWLWYIRI	FIMIVGGLVG	LKIVFAVL SI
B_US_SF2_K	KNEQELLELD	KWASLWNWFS	ITNWLWYIKI	FIMIVGGLVG	LRIVFAVL SI
B_US_WEAU1	KNEQELLELD	KWASLWTWFD	ISNWLWYIKI	FIMIVGGLIG	LRIVFTVLSI
B_US_WR27_	KNEQELLELD	KWASLWNWFN	ITQWLWYIKI	FXMIVGGLIG	LRIVFAVL SI
B_US_YU2_M	KNEQELLALD	KWASLWNWFD	ITKWLWYIKI	FIMIVGGLIG	LRIVFVVL SI
BF1_BR_93B	KNEQELLALD	KWASLWNWFD	ISKWLWYIKI	FIMIVGGLIG	LRIVFAVL SI
C_BR_92BR0	KNEQDLLALD	KWQNLWTWFG	ITNWLWYIKI	FIKIVGGLIG	LRIIFAVL SI
C_BW_96BW0	KNEKDLLALD	SWNNLWNWFG	ITKWLWYIKI	FIMIVGGLIG	LRIIFAAL SI
C_BW_96BW1	KNEKDLLALD	SWKNLWNWFD	ISKWLWYIKI	FIMIVGGLIG	LRIIFAVI SM
C_BW_96BW1	QNEKDLLALD	SWANLWNWFN	ISNWLWYIKI	FIMIVGGLIG	LRIIFAVL SI
C_BW_96BW1	QNEKDLLALD	SWNNLWSWFN	ISNWLWYIKI	FIMIVGGLIG	LRIIFAVL SI
C_ET_ETH22	KNEKDLLALD	KWENLWNWFN	ITNWLWYIKI	FIMIVGGVIG	LRIIFAVL SI
C_IN_93IN1	KNEKDLLALD	SWKNLWSWFD	ITNWLWYIKI	FIMIVGGLIG	LRIIFAVL SI
C_IN_93IN9	KNEKDLLALD	SWKNLWSWFD	ITNWLWYIKI	FIMIVGGLIG	LRIIFAVL SI
C_IN_93IN9	RNEKDLLALD	SWESLWNWFS	ISKWLWYIKI	FIMIVGGLIG	LRIIFAVL SI
C_IN_94IN1	KNEKDLLALD	SWKNLWSWFD	ITNWLWYIKI	FIMIVGGLIG	LRIIFAVL SI
C_IN_95IN2	ENEKDLLALD	SWKNLWNWFD	ITKWLWYIKI	FIIIVGGLIG	LRIIFAVI SI
CRF01_AE_C	KNEQDLLALD	KWANLWNWFS	ITNWLWYIKI	FIMVVGGLIG	LRIVFAVL SI
CRF01_AE_C	RNEKDLLALD	KWASLWNWFD	ITRWLWYIKI	FIIIVGGLIG	LRIVFAVL SI
CRF01_AE_C	RNEKDLELD	KWTS LWNWFD	ITRWLWYIRI	FIMIVGGLIG	LRIVFAVL SI
CRF01_AE_T	RNEKDLELD	KWASLWNWFD	ITNWLWYIKI	FIMIVGGLIG	LRIIFAVL SI
CRF01_AE_T	RNEKDLELD	KWANLWNWFS	ISNWLWYIKI	FIMIVGGLIG	LRIIFAVL SI
CRF01_AE_T	RNEKDLELD	KWASLWNWFG	ITKWLWYIKI	FIMIVGGLIG	LRIIFAVL SI



CRF01_AE_T	KNEKDLELD	KWASLWNWFD	ITSWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
CRF01_AE_T	RNEKDLELD	KWASLWNWFD	ITNWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
CRF01_AE_T	RNEKDLLKLD	KWASLWNWFD	ISRWLWYIRI	FIMIVGGLIG	LRIVFAVLSI
CRF02_AG_F	KNEQDLLALD	QWANLWNWFG	ITKWLWYIKI	FIMIVGGLIG	LRIVFAVLT
CRF02_AG_F	KNEKDLLALD	KWESLWNWFD	ITKWLWYIKI	FIMIVGGLIG	LRIVFAVLT
CRF02_AG_G	KNEQDLLALD	KWASLWNWFD	ITKWLWYIKI	FIMIVGGLIG	LRIVFAVLT
CRF02_AG_N	KNEQDLLALD	KWASLWNWFD	ITNWLWYIRI	FIMIVGGLIG	LRIVFAVLT
CRF02_AG_S	KNEQDLLALD	KWASLWDWFS	ISSWLWYIRI	FIIIVGGLIG	LRIVFAVLAI
CRF02_AG_S	KNEQDLLALD	KWASLWNWFD	ITNWLWYILI	FLMVVGGLIG	LRIVFAVLAI
CRF03_AB_R	KNEQEILALD	KWASLWNWFD	ISKWLWYIKI	FIMIVGGLVG	LRIIFAVLSI
CRF03_AB_R	KNEQEILALD	KWASLWNWFD	ISKWLWYIKI	FIMIVGGLVG	LRIIFAVLSI
CRF04_cpx_	KNEQDLLALD	KWASLWNWFS	ITKWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
CRF04_cpx_	KNEQDLLAFD	KWANLWNWFD	ISNWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
CRF04_cpx_	KNEQDLLALD	KWANLWSWFD	ISHWLWYIKI	FIMIVGGLIG	LRIVFAVLSI
CRF05_DF_B	KNEQEILSLD	QWASLWNWFD	ITKWLWYIKI	FIMIVGGLIG	LRIVFTVLSI
CRF05_DF_B	KNEKDLLALD	KWASLWNWFS	ISNWLWYIRI	FIMIVGGLIG	LRIVFTVLSV
CRF06_cpx_	KNEQDLLALD	KWANLWSWFD	ITNWLWYIKI	FIMIVGGLIG	LRIVFAVISI
CRF06_cpx_	KNEQDLLALD	KWASLWSWFD	ISNWLWYIRI	FVIIVGGLIG	LRIVFAVFSI
CRF06_cpx_	KNEQDLLALD	KWASLWNWFD	ISNWLWYIKI	FIMIVGGLIG	LRIVFAVLSI
CRF06_cpx_	KNEQEILALD	KWASLWSWFD	ISNWLWYIKI	FIMIVGGLIG	LKIVFAVLSL
CRF11_cpx_	KNEQDLLSLD	KWASLWSWFD	ITNWLWYIKI	FIMIVGGLIG	LRIIFAVLSV
CRF11_cpx_	KNEQDLLALD	KWASLWNWFD	ISNWLWYIRI	FIMIVGGLIG	LRIIFAVLSI
D_CD_84ZR0	KNEKELLELD	KWASLWNWFS	ITQWLWYIKI	FIMIVGGLIG	LRIVFAVLSI
D_CD_ELI_K	KNEKELLELD	KWASLWNWFS	ITQWLWYIKI	FIMIIGGLIG	LRIVFAVLSL
D_CD_NDK_M	KNEKELLELD	KWASLWNWFS	ITKWLWYIKL	FIMIVGGLIG	LRIVFAVLSV
D_UG_94UG1	KNEQEILKLD	TWASLWNWFS	ITQWLWYIKI	FIMIVGGLIG	LRIVFAVLSV
F1_BE_VI85	KNEQEILALD	KWASLWNWFD	ISNWLWYIKI	FIMIVGGLIG	LRIVFAVLSI
F1_BR_93BR	KNEQEILALD	KWASLWNWFD	ITQWLWYIKI	FIMIVGGLIG	LRIVFTVLSI
F1_FI_FIN9	RNEQEILALD	KWDSLWSWFD	ITNWLWYIKI	FIMIVGGLIG	LRIVFAVLSI
F1_FR_MP41	KNEQEILALD	KWASLWSWFD	ISNWLWYIKI	FIMIVGGMIG	LRIVFAVLSI
F2_CM_MP25	KNEQDLLALD	KWDNLWNWFS	ITRWLWYIEI	FIMIIGSLIG	LRIVFTVLSI
F2KU_BE_VI	KNEQDLLALD	QWASLWSWFD	ITQWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
G_BE_DRCBL	KNEQDLLALD	QWASLWSWFS	ISNWLWYIRI	FVMIVGGLIG	LRIVFAVLSI
G_NG_92NG0	KNEQDLLALD	KWASLWNWFD	ISNWLWYIRI	FIMIVGGLIG	LRIVFAVLSI
G_SE_SE616	KNEQDLLALD	QWASLWNWFG	ITRWLWYIKI	FIMIVGGLIG	LRIVFAVLSI
H_BE_VI991	KNEQDLLALD	KWANLWNWFS	ITNWLWYIRI	FIMIVGGIIG	LRIVFAVLSI
H_BE_VI997	QNEQDLLALD	KWDSLWNWFS	ITNWLWYIKI	FIIIVGALIG	LRIIFAVLSI
H_CF_90CF0	KNEQDLLALD	KWASLWTWFD	ISHWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
J_SE_SE702	TNEKDLLALD	KWTNLWNWFD	ISNWLWYIKI	FIMIIGGLIG	LRIIFAVLAI
J_SE_SE788	NNEKDLLALD	KWTNLWNWFD	ISNWLWYIKI	FIMIIGGLIG	LRIIFAVLAI
K_CD_EQTB1	KNEQDLLALD	KWASLWNWFD	ISNWLWYIKI	FIMIVGGLIG	LRIVFTVLSV
K_CM_MP535	KNEQDLLALD	KWASLWNWFD	ITKWLWYIKI	FIMIIGGLIG	LRIAFVLSV
N_CM_YBF30	TNEKSLELD	QWDSLWSWFG	ITKWLWYIKI	AIMIVAGIVG	IRIISIVITI
O_CM_ANT70	QNEKKLELD	EWASIWNWLD	ITKWLWYIKI	AIIIVGALVG	VRVIMIVLNI
O_CM_MVP51	KNVKALLELD	EWASLWNWFD	ITKWLWYIKI	AIIIVGALIG	IRVIMIILNL
O_SN_99SE_	QNEKKLELD	EWASIWNWLD	ITKWLWYIKI	AIIIVGALIG	VRIVMIVLNL
O_SN_99SE_	HNEKKLELD	EWASIWNWLD	ITKWLWYIKI	AIIIVGALIG	VRIVMIVLNL
U_CD_83C	KSEKDLELD	KWASLWNWFD	ITNWLWYIKI	FIMIVGGLIG	LRIVFTVFSI

	801			850
00BW0762_1	VNRVRQGYSP	LSFQTLTP..	NQR.GPDRLG	GIEEEGGEQD RDRSIRLVSG
00BW0768_2	VNRVRQGYSP	LSFQTLIP..	NPR.GPDRLG	RIEEEGGEQD KDRSIRLVSG
00BW0874_2	VNRVRQGYSP	LSFQTLTP..	SPR.EPDRLG	RIEEEGGEQD KDRSIRLVGG
00BW1471_2	VNRVRQGYSP	LSFQTLIP..	NPR.GPDRLE	RIEEEGGEQD RGRSVRLVSG
00BW1616_2	VNRVRQGYSP	LSFQTLTP..	NPR.ELDRLG	RIEEEGGEQD RDRSIRLVSG
00BW1686_8	VNRVRQGYSP	LSLQTLTP..	NPR.GPDRPR	GIEEEGGEQD KDRSIRLVNG
00BW1759_3	VNRVRQGYSP	SSFQTLIP..	NPE.GPDRLR	RIEEEGGEQD RDRSIRLVNG
00BW1773_2	VNRVRQGYSP	LSFQTLTP..	NPR.GPDRLG	RIEEEGGEQD RDRSVRLVSG
00BW1783_5	VNRVRQGYSP	LSFQTLIP..	NPR.GPDRLE	RIEEEGGEQD RDRSIRLVSG
00BW1795_6	VNRVRQGYSP	LSFQTLIP..	NPR.GPDRLG	RIEEEGGEQD RDRSIRLVSG
00BW1811_3	VNRVRQGYSP	LSFQTLIP..	NPG.GPDRLG	RIEEEGGEQD RDRSVRLVNG
00BW1859_5	VNRVRQGYSP	LSFQTLTP..	NPR.GPDRLG	GIEEEGGEQD KDRSIRLVNG
00BW1880_2	VNRVRQGYSP	LSLQTLSP..	NQR.GLDRLG	RIEEEGGEQD RDKSIRLVSG
00BW1921_1	VNRVRQGYSP	LSLQTLTP..	NPR.ELDRLG	RIEEEGGEQD RGRSIRLVNG
00BW2036_1	VNRVRQGYSP	LSFQTLTP..	NPR.GLDRLG	RIEEEGGEQD RGRSIRLVQG
00BW2063_6	VNRVRQGYSP	LSFQTLTP..	NPR.GPDKLE	RIEEEGGEQD RNRSIRLVSG
00BW2087_2	VNRVRQGYSP	LSFQTLTP..	NPR.EPDRLG	RIEEEGGEQD RERSIRLVSG
00BW2127_2	VNRVRQGYSP	LSFQTLTP..	NPR.GPDRLG	RTEEEGGEQD NDRSIRLASG
00BW2128_3	VKRVRQGYSP	LSFQTLTP..	NPG.GPDRLG	RIEEEGGEQD REKSVRLVNG
00BW2276_7	VNRVRQGYSP	LSFQTLTP..	NPR.GPDRLG	GIEEEGKQD RDRSIRLVSG
00BW3819_3	VNRVRQGYSP	LSLQTLTP..	SPR.GPDGLR	GIEEEGGEQD KDRSIRLVNG
00BW3842_8	VNRVRQGYSP	LSLQTLTP..	NPR.ELDRLG	RIEEEGGEQD RDRSIRLVNG
00BW3871_3	VNRVRQGYSP	LSLQTLTP..	NPR.ELDRLG	RIEEEGGEQD KDRSIRLVNG
00BW3876_9	VNRVRQGYSP	LSFQTLTP..	NPR.EPDRPG	RIEKEGGEQD KRSRIRLVSG
00BW3886_8	VNRVRQGYSP	LSFQTLTP..	NTR.ELDRLG	RIEEEGGEQG RDRSIRLLNG
00BW3891_6	VNRVRQGYSP	LSFQTLIP..	NPR.GLDRLG	RIEEEGGEQD RDRSIRLVNG
00BW3970_2	VNRVRQGYSP	LSLQTLTP..	NQR.EPDRLG	RIEEEGGEQD RKRSIRLVSG
00BW5031_1	VNRVRQGYSP	LSFQTLTP..	SQR.ELDRLG	RIEEEGGEQD RDRSIRLANG
96BW01B21	VNRVRQGYSP	LSFQTLTQ..	NPG.GPDGLG	RIEEEGGEQD KDRSIRLVNG
96BW0407	VNRVRQGYSP	LSFQTLIP..	NPR.RSDRLG	RIEEEGGEQD RGRSIRLVSG
96BW0502	VNRVRQGYSP	LPFQTLTP..	NPR.EPDRLG	RIEEEGGEQD RGRSIRLVSG
96BW06_J4	VNRVRQGYSP	LSFQTLPP..	NPR.GIDRLG	RIEEGGGEQD RDRSIRLVNG
96BW11_06	VKRVRQGYSP	LSFQTLTP..	NPR.GPDRLE	RIEEEGGEQD RNRSIRLVSG
96BW1210	VNRVRQGYSP	LSFQTLIP..	SPR.EPDKLE	RIEEEGGEQD RDRSIRLVSG
96BW15B03	VNRVRQGYSP	LSFQTLTP..	NPR.GLDRLG	RIEEEGGEQD RDRSIRLVQG
96BW16_26	VNRVRQGYSP	LSFQTLTP..	NPR.GPDRLG	RIEEEGGEQD RDRSVRLVHG
96BW17A09	VNRVRQGYSP	LSLQTLTP..	NPR.GPDGLE	RIEEGGGEQD RGRSIRLVSG
96BWM01_5	VNRVRQGYSP	LSFQTLTP..	NPR.GPDRLE	GIEEEGGEQD KDRSIRLVSG
96BWM03_2	VNRVRQGYSP	LPFQTLTP..	NPR.ELDRLG	RIEEEGGEQD RDRSIRLVSG
98BWMC12_2	VNRVRQGYSP	LSFQTLNP..	NPR.GLDRLG	RIEEEGGEQD KSTSIRLVNG
98BWMC13_4	VNRVRQGYSP	LSFQTLTP..	NPR.GPDRLE	RIEEEGGEQD RDRSIRLVNG
98BWMC14_a	VNRVRQGYSL	TSLQTHLP..	NAG.GLDRLD	RIEEEGGEQD RHRISIRLVSG
98BWM014_1	VNRVRQGYSP	LSFQTLTP..	VPR.EPDRLG	GIEEEGGEQD RDRSVRLVNG
98BWM018_d	VNRVRQGYSP	LSFQTLTP..	NPR.GPDRLG	RIEEEGGEQD RDRSIRLVSG
98BWM036_a	INRVRQGYSP	LSFQTLTP..	TPR.DPDRLR	GIEEEGGEQD RDRSIRLVSG
98BWM037_d	VNRVRQGYSL	TSFQTVIP..	NPR.GPDRPR	GIEEEGGEQD RDRSIRLVSG
99BW3932_1	VNRVRQGYSL	LSFQTLTP..	NPR.GPDRLG	GIEEEGGEQD RDRSIRLVNG
99BW4642_4	VNRVRQGYSP	LSFQTLTP..	NPR.ELDRLG	RIEEEGGEQD RDRSVRLVNG
99BW4745_8	VNRVRQGYSP	LSLQTLTP..	SPR.RPDRLG	GIEEEGGEQD RTRSVRLVNG
99BW4754_7	VNRVRQGYSP	LSFQTLTP..	NQR.GPDRLG	EIEEEGGEQD RDRSIRLVNG
99BWMC16_8	VNRVRQGYSP	LSFQTLAP..	NPG.GLDRLG	RIEEEGGEQD RGRSIRLVNG
A2_CD_97CD	VKRVRQGYSP	LSFQIPTP..	NPE.GLDRPG	RIEEEGGEQG RDRSIRLVSG
A2_CY_94CY	VNRVRQGYSP	VSFQIPTP..	SPE.GPDRPR	GTEEGGGEQG RDRSIRLVNG
A2D_97KR	VNRVRQGYSP	VSFQIPPP..	TPE.DPDRHG	RIEDGGGEQG RDRSVRLVSG
A2G_CD_97C	VNRVRQGYSP	LSFQTLTH..	HQR.EPDRPE	RIEEGGGEQD RDRSVRLVSG
A_BY_97BL0	INRARXXYSP	LSLQTLTP..	HPE.RPDRPX	RIKEEGXEQG RDRSIRLVSG
A_KE_Q23_A	INRVRQGYSP	LSFQTHTP..	NPR.GLDRPE	RIEEEDGEQG RGRSIRLVSG
A_SE_SE659	INRVRQGYSP	LSFQTHTP..	NPG.GLDRPG	RIEEEGGEQG RDRSIRLVSG
A_SE_SE725	INRVRQGYSP	LSFQTHTP..	DPR.GLDRPR	RIEEEGGEQG RGRSIRLVSG

A_SE_SE753	INRVRQGYSP	LSFQIHTP..	NPR.DPDRPG	RIEEEGGEQG	RDRSIRLASG
A_SE_SE853	INRVRQGYSP	LSFQIHTP..	NPG.DLDRPG	RIEEEGGEQD	RGRSIRLVSG
A_SE_SE889	INRVRQGYSP	LSFQIHTP..	SPG.GLDRPG	RIEEEGGEQD	RNRSIRLVNG
A_SE_UGSE8	IKRVRQGYSP	LSFQIHTP..	SPR.DPDRPG	RIEEEGGEQG	RDRSIRLVSG
A_UG_92UG0	INRVRQGYSP	LSFQTHTP..	NPR.GLDRPG	RIEEEGGEQD	RGRSIRLVSG
A_UG_U455_	INRVRQGYSP	LSFQTLAP..	IPG.GLGRPG	RIEEEGGEQG	KDRSIRLVSG
AC_IN_2130	INRVRQGYSP	LSFRTHTP..	NPG.GLDRPG	RIEEEGGEQD	KDRSIRLVSG
AC_RW_92RW	VNRVRQGYSP	LSFQTLIP..	NPR.GPDRPG	GIEEEGGEQD	RGRSIRLVSG
AC_SE_SE94	INRVRQGYSP	LSFQIHTP..	NPG.GPDRPG	RTEEEGGEQD	RDRSIRLVSG
ACD_SE_SE8	INRVRQGYSP	LSFQTHTP..	NPE.GVDRPG	RIEEEGGEQG	RDRSIRLVSG
ACG_BE_VI1	VNRVRQGYSP	LSFQTLIP..	NPR.GPDRPG	EIEEEGGEQD	RDTSTRLVSG
AD_SE_SE69	VNRVRQGYSP	LSFQTLIP..	APRGP.DRPE	GIEEEGGEQD	RGRSIRLVNG
AD_SE_SE71	INRVRQGYSP	LSFQTHTP..	NPR.DLDRPE	RIEEEGGEQD	RTRSIRLVSG
ADHK_NO_97	INRVRQGYSP	LSFQTLIP..	NPRGA.DRPE	GIEEEGGEQD	XNRSIRLVNG
ADK_CD_MAL	VNRVRQGYSP	LSLQTLIP..	TPRGPDRPE	GIEEEGGEQG	RGRSIRLVNG
AG_BE_VI11	INRVRQGYSP	LSFQILTP..	HQRDP.DRPG	RIEEEGGEQD	RDTSRRLVGG
AG_NG_92NG	VNRVRQGYSP	LSFQTLTH..	HQREP.DRPE	RIEEEGGEQD	RDRSVRLVSG
AGHU_GA_VI	VNRVRQGYSP	LSFQTLFP..	NQREP.DRPE	GIEEEGGEQG	RSRSIRLVNG
AGU_CD_Z32	INRVRQGYSP	LSFQTLTH..	HQR.EPDRPE	GIEEEGGEQD	RDRSIRLVSG
AJ_BW_BW21	VNRVRQGYSP	LSLQTLIP..	NPTEV.DRPG	GIEEEGGEQG	KTRSIRLVNG
B_AU_VH_AF	VKKVREGYSP	LSLQIRPP..	APRGP.DRPE	GIEEEGGEQD	RDKSVRLVDG
B_CN_RL42	VNRVRQGYSP	LSLQTRFP..	AQRGP.GRPE	GIEEEGGERD	RDRSERLVTG
B_DE_D31_U	VNSVRQGYSP	LSFQTRLP..	APRGP.DRPE	GIEEEGGDRD	RDRSNRLVKG
B_DE_HAN_U	VNRVRQGYSP	LSFQTLIP..	ATRGP.RQPE	EIEEEGGERD	RGRSVRLVSG
B_FR_HXB2	VNRVRQGYSP	LSFQTHLP..	TPRGP.DRPE	GIEEEGGERD	RDRSIRLVNG
B_GA_OYI	VNRVRQGYSP	LSFQTRLP..	TQRGP.DRPE	GIEEEGGERD	RDRSGRLVDG
B_GB_CAM1	VNRVRQGYSP	LSFQTRFP..	VPRGP.DRPE	GIEEEGGGRD	RDTSGRLVTG
B_GB_GB8_C	VNRVRQGYSP	LSLQTHLP..	TPRGP.DRPE	GIEEEGGEQD	RDRSIRLVNG
B_GB_MANC	VNRVRQGYPP	LSFQTHLP..	APRGP.DRPG	GIEEEGGEGD	RDRSSRLVHG
B_KR_WK_AF	VNRVRQGYSP	LSFQTHFP..	SPRGP.DRPG	GIEEGEGEGD	SGGSSHLVDG
B_NL_3202A	VNRVRQGYSP	LSFQTRLP..	APRGP.DRPE	GIEEEGGERD	RDRSGRLVNG
B_TW_TWCYS	VNRVRQGYSP	LSFQTHLP..	TPRGP.DRPE	GIDEEGGERD	RDRSERSVDG
B_US_BC_L0	VNRVRQGYSP	LSFQTHLP..	TPRGP.DRPE	GIEEEGGERD	RDRSGRLVNG
B_US_DH123	VNRVRQGYSP	LSFQTRFP..	ASRGP.DRPE	GIEEEGGDRD	RDRSSPLVDG
B_US_JRCSF	VNRVRQGYSP	LSFQTLIP..	ATRGP.DRPE	GIEEEGGERD	RDRSGQLVNG
B_US_MNCG	VNRVRQGYSP	LSLQTRPP..	VPRGP.DRPE	GIEEEGGERD	RDTSGRLVHG
B_US_P896	VNRVRQGYSP	LSFQTLIP..	ASRGP.DRPE	GTEEEGGERD	RDRSGPLVNG
B_US_RF_M1	VNRVRQGYSP	LSFQTHLP..	APRGP.DRPE	GIEEGEGGERD	RDRSGGAVNG
B_US_SF2_K	VNRVRQGYSP	LSFQTRLP..	VPRGP.DRPG	GIEEEGGERD	RDRSVRLVDG
B_US_WEAU1	VNRVRQGYSP	LSFQTHLP..	APRGP.DRPE	GIEEEGGERD	RDRSGRLVDG
B_US_WR27	XNRVRQGXSP	LSFQTLIP..	VPRGP.DRPE	GIEEEGGERD	RDRSNRLVHG
B_US_YU2_M	VNRVRQGYSP	LSFQTHLP..	AQRGP.DRPG	GIEEEGGERD	RDRSGPLVDG
BF1_BR_93B	VNRVRKGYSP	LSLQTRFP..	SQREP.DRPE	GIEEEGGEPG	KDRSVRLVNG
C_BR_92BR0	VNRVRQGYSP	LSFQTLTP..	NPR.GPDRPG	GIEEEGGEQD	RDRSIRLVSG
C_BW_96BW0	VNRVRQGYSP	LSFQTLTP..	NPR.GPDRPG	GIEEEGGEQD	RDRSIRLVSG
C_BW_96BW1	VNRVRQGYSP	LSFQTLTP..	NPR.GPDRLE	RIEEEGGEQD	RNRSIRLVSG
C_BW_96BW1	VNRVRQGYSP	LSFQTLIP..	SPR.EPDKLE	RIEEEGGEQD	RDRSIRLVSG
C_BW_96BW1	VNRVRQGYSP	LSFQTLTP..	NPR.GLDRPG	RIEEEGGEQD	RDRSIRLVQG
C_ET_ETH22	VNRVRQGYSP	LSFQTLIP..	HPR.GPDRPG	GIEEEGGEQG	RDRSIRLVNG
C_IN_93IN1	VNRVRQGYSP	LSFQTLTP..	NPR.GPDRPG	RIEEEGGEQD	KDRSIRLVNG
C_IN_93IN9	VNRVRQGYSP	LSFQTPTP..	NPG.GPDRPG	RIEEEGGEQG	KDRSIRLVNG
C_IN_93IN9	VNRVRQGYSP	LSFQTLTP..	NPG.GPDRPG	RIEEEGGEQD	KNRSIRLVNG
C_IN_94IN1	VNRVRQGYSP	LSFQTPTP..	NPG.GPDRPG	RIEEEGGGQD	NVRSIRLVNG
C_IN_95IN2	VNRVRQGYSP	LSFQTLTP..	NPG.GPDRPG	RIEEEGGEQD	KDRSIRLVSG
CRF01_AE_C	VNRVRQGYSP	LSFQTLTH..	HQR.EPDRPE	RIEEGGGEEG	KDRSIRLVSG
CRF01_AE_C	VNRVRQGYSP	LSFQTLTH..	QQR.EPDRPE	RIEEESGEQG	RDRSIRLVSG
CRF01_AE_C	VNRVRQGYSP	LSFQTLTH..	HQR.EPDRPE	RIEEGGGEQD	KDRSVRLVSG
CRF01_AE_T	VNRVRQGYSP	LSFQTPIH..	HQR.EPDRPE	RIEEGGGEQG	RDRSVRLVSG
CRF01_AE_T	VNRVRQGYSP	LSLQTPTH..	HQR.EPDRPE	RIEEGGGEQG	RDRSVRLVSG
CRF01_AE_T	VNRVRQGYSP	LSFQTPTH..	HQRGEPRPE	RIEEGGGEQG	RDRSVRLVSG

CRF01_AE_T	VNRVRQGYSP	LSFQTPLH..	HQR.EPDRPE	RIEEGGGEQG	RDRSVRLVSG
CRF01_AE_T	VNRVRQGYSP	LSFQTPSH..	HQK.EPDRPE	GIEEGGGEQG	RDRSVRLVSG
CRF01_AE_T	VNRVRQGYSP	LSFQTLTH..	HQR.DPDRPE	RIEEGGGEQG	RDRSVRLVSG
CRF02_AG_F	INRVRQGYSP	LSFQTLTH..	HQR.GPDRPE	RIEEGGGEQD	RDRSGRLVSG
CRF02_AG_F	IKRVRQGYSP	LSFQTLTH..	HQR.EPDRPE	RIEEGGGEQD	KDRSVRLVSG
CRF02_AG_G	INRVRQGYSP	LSFQILTP..	NPR.GPDRPE	GIEEGGGEQD	RDRSIRLVSG
CRF02_AG_N	INRVRQGYSP	LSFQTLTH..	HQR.EPDRPE	RIEEGGGEQD	KDRSVRLVSG
CRF02_AG_S	INRVRQGYSP	LSFQTLTH..	HQR.EPGRPE	RIEEGGGGQD	RDRSVRLVSG
CRF02_AG_S	INRVRQGYSP	LSFQTLTH..	HQR.GADRPE	GIEEGGGEQD	RDRSVRLVSG
CRF03_AB_R	VNRGRQGYSP	LSFQTRLP..	AQRGP.DRPE	GIEEEDGERD	RDTSIRLVNR
CRF03_AB_R	VNRVRQGYSP	LSFQTRLP..	TQRGP.DRPE	GIEEEGGERD	RDTSIRLVNG
CRF04_cpx_	VNRVRQGYSP	LSLQTLIPT.	TQRGL.DRPG	GTEEEGGEQD	RSRSIRLVNG
CRF04_cpx_	VNRVRQGYSP	LSFQTLIP..	TQREP.GRPE	GTEEEGGEQD	RSRSIRLVNG
CRF04_cpx_	VKRVRQGYSP	LSSQTLIPT.	TQRGP.DRPE	GTEGGGGEQD	RIESIRLVNG
CRF05_DF_B	VNRVRKGYSP	LSFQTPFP..	APRGP.DRPE	ETEEGGGEQD	RGRSIRLVNG
CRF05_DF_B	VNRVRKGYSP	LSFQTLIP..	GPRGP.DRPE	GTEEEGGEQG	RDRSVRLLTG
CRF06_cpx_	VNRVRQGYSP	LSLQTLIP..	NPTGA.DRPG	EIEEGGGEQG	RTRSIRLVNG
CRF06_cpx_	VNRVRQGYSP	LSLQTLIP..	NPTGA.DRPG	EIEEGGGEQG	RTRSIRLVNG
CRF06_cpx_	VNRVRQGYSP	LSLQTLIP..	NPAEV.DRPG	GIEEGGGEQG	RNRSIRLVNG
CRF06_cpx_	VKRVRQGYSP	LSLQTLIP..	NSAGV.DRPG	EIEGGGGEQD	RTRSIRLVNG
CRF11_cpx_	VNRCRQGYSP	LSFQTLNP..	TQQEA.DRPG	GIEEGGGEQG	RTRSIRLVSG
CRF11_cpx_	VNRCRQGYSP	LSFQALTP..	SQQEP.DRPG	GTKEGGGEQG	RTSSIRLVSG
D_CD_84ZR0	VNRVRQGYSP	LSFQTLIP..	APRGP.DRPE	GIEEGGGEQD	RGTSIRLVNG
D_CD_ELI_K	VNRVRQGYSP	LSFQTLIP..	APRGP.DRPE	GTEEEGGGERG	RDRSVRLTNG
D_CD_NDK_M	VNRVRQGYSP	LSFQTLIP..	VPRGP.DRPE	EIEEEGGGERG	RDRSIRLVNG
D_UG_94UG1	VNRVRQGYSP	LSFQTLIP..	APREP.DRPE	GIEEEGGGERD	RGRSIRLVNG
F1_BE_VI85	VNRVRKGYSP	LSLQTLIP..	SPRGP.DRPE	GIEEGGGEQG	KDRSVRLVTG
F1_BR_93BR	VNRVRKGYSP	LSFQTHIP..	SPREP.DRPE	GIEEGGGEQG	KDRSVRLVTG
F1_FI_FIN9	VNRVRKGYSP	LSLQTLIP..	APTEP.DRPE	GIEEGGGEQG	KDRSVRLVNG
F1_FR_MP41	VNRVRKGYSP	LSLQTLIP..	SPRGP.DRPE	GIEEGGGEQD	RNRSVRLVNG
F2_CM_MP25	INRVRQGYSP	LSLQTLIP..	NSRGP.ERPG	GIEEEGGEQD	KDRSIRLVSG
F2KU_BE_VI	VNRVRQGYSP	LSFQTLIP..	SPRGP.DRPE	GTEERGGEQD	RDRSTRLVSG
G_BE_DRCBL	VNRVRQGYSP	LSFQTLTH..	HQREP.DRPA	GIEEGGGEQD	RDRSIRLVSG
G_NG_92NG0	VNRVRQGYSP	LSFQTLTH..	HQREP.DRLG	KTEEGGGEQD	RDRSTRLVSG
G_SE_SE616	VNRVRQGYSP	LSFQTLTH..	HQREP.DRPE	GIEEGGGEQG	RGRSVRLVSG
H_BE_VI991	VNRVRQGYSP	LSLQTLIP..	NQRGP.DRPR	EIEEEGGEQD	RDRSIRLVNG
H_BE_VI997	VGRVRQGYSP	LSFQTLIP..	NPRGP.DRPE	GIEEEGGEQD	RGRSVRLVNG
H_CF_90CF0	VNRVRQGYSP	LSFQTLVP..	NPRGP.DRPE	GTEEGGGEQD	RDRSVRLVNG
J_SE_SE702	VNRVRQGYSP	LSFQTLIP..	NPTEA.DRPG	GIEEGGGEQG	RTRSIRLVNG
J_SE_SE788	VNRVRQGYSP	LSFQTLIP..	NPTEA.DRPG	GIEEGGGEQG	RTRSIRLVNG
K_CD_EQTB1	VNRVRQGYSP	LSFQTLTP..	SPRGP.DRPE	GIEEGGGEQD	KDRSVRLVSG
K_CM_MP535	VNRVRQGYSP	LSFQTLIP..	TSRGA.DRPE	GIEEEGGEQD	KNRSVRLVSG
N_CM_YBF30	IARVRQGYSP	LSLQTLIPT.	ARG..PDRPE	ETEGGVGEQD	RGRSVRLVSG
O_CM_ANT70	VKNIRQGYQP	LSLQIPNHH.	QEE..AGTPG	RTGGGGGEEG	RPRWIPSPQG
O_CM_MVP51	VKNIRQGYQP	LSLQIPVPH.	RQE..AETPG	RTGEEGGEGD	RPKWTALPPG
O_SN_99SE_	VKNIRQGYQP	LSFKTHIHH.	QPE..AEAPG	GTGEGGGGERG	MPTLIPWPQG
O_SN_99SE_	VRNIRHGYQP	LSFQTPTHHQ	QPE..AQAPG	GTGEGGGGERD	RLRSIPSPQG
U_CD___83C	INRVRQGYSP	LSFQTLIP..	TPR.GPDRPG	RTEEEGGGEED	NNRSVRLVNG

	851				900
00BW0762_1	FLALFWDDLR	SLCLFSYHRL	RDFILVAARA	VELLGRSSLK	GLQRGWEILK
00BW0768_2	FLALVWDDLR	RLCLFSYHRL	RDFILVATRA	VELLGHSSLR	GLQRGWEALK
00BW0874_2	FLALAWDDLR	SLCLFSYHRL	RDFILIAART	VELLGRSSLR	GLQRGWEILK
00BW1471_2	FLTLAWDDLR	SLCIFLYRLL	SDFISIAART	VNLLGQNSLR	GLQRGWEALK
00BW1616_2	FLALAWDDLR	SLCLFSYHRL	RDFTLIAARA	VETLGR....	...RGWEALK
00BW1686_8	FLALAWDDLR	SLCLFSYHQL	RDFILIVARA	VELLGRNSLR	GLQRGWEILK
00BW1759_3	FLALFWDDLR	SLCLFSYHRL	RDLILVTARA	VELLG.....	..QRGWEALK
00BW1773_2	FLALTWDDLR	SLCLFCYHRL	RDFILIAARV	VELLGRSSLR	GLQKGWEALK
00BW1783_5	FLALAWDDLR	SLCLFSYHRL	RDFILVTARA	VELLGRSSLR	GLQRGWEILK
00BW1795_6	FLALAWDDLR	SLCLFCYRRL	RDFILVTARA	VELLGRSSLK	GLQRGWEILK
00BW1811_3	FFALAWDDLR	SLCLFCYHRL	RDFILVTARA	VELLGHSSLK	GLQRGWEILK
00BW1859_5	FLALAWDDLR	SLCLFSYHRL	RDCILIAARA	VELLGHSSLR	GLQRGWEVLK
00BW1880_2	FLALAWDDLR	SLCLFSYHRL	RDFILVTARA	VELLGRSGLK	GLQKGWEILK
00BW1921_1	FLPLVWEDLR	SLCLFSYHRL	RDLILVVARA	VELLGRSSLR	GLQKGWETLK
00BW2036_1	FLALAWDDLR	NLCLFSYHQL	RDLILVTTRV	VELLGRSSLR	GLQRGWEALK
00BW2063_6	FLALAWDDLR	SLCLFCYHRL	KDFVLVTARV	VELLGLSSLK	GLQRGWEILK
00BW2087_2	FLPLFWDDLR	SLCLFSYHRL	RDLILIAARA	VELLGRSSLR	GLQRGWEILK
00BW2127_2	FLAPAWDDLR	SLCLFSYHRL	RDLILVTARV	VELLGRS...	...GWEALK
00BW2128_3	FLALFWDDLR	SLCLFSYHRL	RDFILIAARV	VELLGRSSLR	GLQRGWETLK
00BW2276_7	FLALAWDDLR	SLCLFSYHRL	RDFILVTARA	VELLGRSSLR	GLQRGWEVLK
00BW3819_3	FLALAWDDLR	SLCLFSYHRL	RDLTLVTARG	IELMGRSSLR	GLQKGWEALK
00BW3842_8	FLALAWEDLR	SLCLFSYHRL	RDLILVTARA	VELLGRSSLR	GLQRGWEALK
00BW3871_3	FLALAWDDLR	SLCLFSYHRL	RDFILIVARV	VELLGRSSLR	GLQKGWETLK
00BW3876_9	FLALAWDDPR	SLCLFSYHRL	RDFILVVVRA	VELLGRSSLK	GLKRGWEALE
00BW3886_8	FLAIAWDDLR	SLCLFSYHRL	RDFILLIARA	VELLGRSSLK	GLQRGWEALK
00BW3891_6	FLALAWEDLR	SLCLFSYHRL	RDFILVTARA	VELLGRSSLR	GLQRGWEALK
00BW3970_2	FLALAWDDLR	SLCLFSYHHL	RDFILIAARV	VELLGR....	...RGWDILK
00BW5031_1	FLALAWEDLR	SLCLFSYRHL	RDFILIVVRA	VELLGRSSLR	GIQKGWDALK
96BW01B21	FLPLVWDDLR	NLCLFSYHRL	RDFILVIARA	VELLGRSSLR	GLQRGWETLK
96BW0407	FLALAWDDLR	SLCLFSYHRL	RDFILIAARA	AELLGRSGLR	GLQKGWETLK
96BW0502	FLALAWDDLR	SLCLFSYHRL	RDFILIAARV	LELLG.....	..QRGWEALK
96BW06_J4	FLALAWDDLR	SLCLFSYHQL	RDFILVVARA	VELLGRSSLR	GLQRGWEALK
96BW11_06	FLALAWDDLR	SLCLFCYHRL	RDFTLVTARA	VELLGRSSLK	GLQRGWEILK
96BW1210	FLALAWDDLR	SLCLFSYHRL	RDSILVAART	VELLGRSSLR	GLQRGWEALK
96BW15B03	FLALAWDDLR	SLCLFSYHRL	RDLILVTARV	VELLGRSSLR	GLQRGWEALK
96BW16_26	FLALAWDDLR	SLCLFSYHRL	RDFILVAVRV	VELLGR....	...RGWEALK
96BW17A09	FLALAWDDLR	SLCIFLYHHL	RDFILIAART	VNLLGQSSLR	GLQRGWEALK
96BWM01_5	FLALAWDDLR	SLCLFCYHRL	RDFILVTARA	VELLGRSSLK	GLQRGWEILK
96BWM03_2	FLALAWDDLR	SLCLFSYHRL	RDFLLVTVRA	AELLGRSSLR	GLQRGWEALK
98BWMC12_2	FLAIAWDDLR	SLCLFSYHRL	RDFILIAARA	VELLGRSSLR	GLQRGWEALK
98BWMC13_4	FLALAWDDLR	NLCLFCYHRL	RDFILVTARA	VELLGRSSLT	GLQRGWEILK
98BWMC14_a	LLALAWDDLR	SVRLFYSYHQL	RNFILIVARA	VELLGR....	...RGWETLK
98BWM014_1	FLALFWDDLR	SLCLFSYHRL	RDLILIAVRA	VELLGRSSLW	GLQKGWEALK
98BWM018_d	FLALAWDDLR	SLCLFSYHRL	RDFILIAARA	VELLGHSLR	GLQRGWEILK
98BWM036_a	FLALAWDDLR	SLCLFSYHRL	RDFILVTARV	VELMGRSSLK	GLQRVWEILK
98BWM037_d	FLALAWDDLR	SLCLFSYHQL	RDFILLIARV	VERLGYSSLR	GLQRGWEALK
99BW3932_1	FFSLAWDDLR	SLCLFSYHRL	RDLILVTVRV	VELMGRCSLR	GLQRGWEALK
99BW4642_4	FLALAWDDLR	SLCLFSCHRL	RDCILIAVRA	VELLGRSSLK	GLQRGWEALK
99BW4745_8	FLALAWDDLR	SLCLFSYHHL	RDFILVTARA	VELLGRSSLR	GLQRVWEALK
99BW4754_7	FLAIVWDDLR	SLCLFSYHRL	RDFILIAARA	VELLGRSSLK	GLQRGWEILK
99BWMC16_8	FLAIAWEDLR	SLCLFSYHRL	RDLTLIVTRA	VELLGRSSLK	GLQRGWEALK
A2_CD_97CD	FLALAWDDLR	SLCLFSYHRL	RDCILIAARI	VELVGHSSLK	GLRLGWEGLK
A2_CY_94CY	FFALAWDDLR	SLCLFSYHRL	RDCILIAART	VELLGHCSLK	GLRLGWEGLK
A2D_97KR	FLALVWEDLR	SLCLFSYHRL	RDCISIAART	VELLGHSSLK	GLRLGWEGLK
A2G_CD_97C	FLALAWDDLR	SLCLFCYHRL	RDSILIAART	VELLRHSSLK	GLRLGWEGLK
A_BY_97BL0	FLALAXDDLX	SLCLFSYHRL	RDFISIAART	XELLKRSSLX	GLRLXXXGLK
A_KE_Q23_A	FLALAWDDLR	SLCLFSYHRL	RDFILIAART	VELLGHSSLK	GLRLGWEGLK
A_SE_SE659	FLALAWDDLR	SLCLFSYHHL	RDLILIAART	VELLGHSSLK	GLRLGWEGLK
A_SE_SE725	FLALAWDDLR	SLCLFSYHRL	RHFILIATTT	VELLGHSSLK	GLRLGWEGLK

A_SE_SE753	FLTLAWEDLR	SLCLFSYHRL	RDLILIAART	VELLGHSSLK	GLRLGWEGLK
A_SE_SE853	FLALAWDDLR	SLCLFSYHRL	RDFILIAART	VELLGQR...	....GWEGLK
A_SE_SE889	FLALAWDDLR	SLCLFCYRRL	RDFILIVART	VELLGHSSLR	GLRLGWEGLK
A_SE_UGSE8	FLALAWDDLR	SLCRFSYHRL	RDFISIATRI	VELLG.....	.....QGLK
A_UG_92UG0	FLALAWDDLR	NLCLFSYHRL	RDFILIAART	VELPGHSSLK	GLRLGWEGLK
A_UG_U455	FLAIAWDDLR	NLCLFSYHRL	RDFALIVARA	VELLGRSSLK	GLRLGWEGLK
AC_IN_2130	FLALFWDDLR	SLCLFSYHRL	RDFILIAKRT	VELLGHSSLK	GLRLGWEGLK
AC_RW_92RW	FLALAWDDLR	SLCLFSYHRL	RDLLLIAART	VELLGRSSLR	GLQRGWETLK
AC_SE_SE94	FLALAWDDLR	SLCLFSYHRL	RDFILI....	..LG.HSSLK	GLRLGWEGLK
ACD_SE_SE8	FLALAWDDLR	SLCLFSYHRL	RDLILIAARI	VELLGRR...	....GWEAIK
ACG_BE_VI1	FFALAWDDLR	SLCIFLYHHL	RDLLLIATRA	VELLG.....	..QRGWEALK
AD_SE_SE69	FSALIWDLLR	NLCLFSYHRL	RDLLLIALRI	VELLGRR...	....GWEALK
AD_SE_SE71	FLAIAWDDLR	SLCLFSYHRL	RDLILIAARI	VELLGRR...	....GWEALK
ADHK_NO_97	FLPLVWEDLR	NLCLFSYRRL	RDLLLILART	VTLLGSR...	....GWETLK
ADK_CD_MAL	FSALIWDLLR	NLCLFSYHRL	RDLLLIATRI	VELLGRR...	....GWEALK
AG_BE_VI11	FLTLVWDDLR	SLCLFSYHRL	RDLVLIAART	LELLGRSGLR	GLRLGWEGLK
AG_NG_92NG	FLALAWDDLR	NLCLFSYHRL	RDLVLIAART	AELLRRSSLQ	GLRLGWEGLK
AGHU_GA_VI	FLPLIWEDLR	NLCLFSYRHL	RDLLLIVART	VELLGKR...	....GWGALK
AGU_CD_Z32	FLPLAWDDLR	SLCLFCYHRL	RDCALIAARI	VETLIRR...	....GWETLK
AJ_BW_BW21	FLALAWEDLR	NLCLFSCHRL	RDFALIAART	VDTLGRR...	....GWEILK
B_AU_VH_AF	FLALIWDLLR	SLCLFSYHRL	RDLLLIAARI	VELLGRR...	....GWEALK
B_CN_RL42	FLSLIWEDLR	SLCLFSYHRL	RDLLLIVARI	VELLGRR...	....GWEVLR
B_DE_D31_U	FLALIWDLLS	SLCLFLYHRL	RDLLLIAARI	VELLGRR...	....GWEVLK
B_DE_HAN_U	FLALFWDDLR	SLCLFSYRRL	RDLLLIVAKI	VETLGRR...	....GWEVLK
B_FR_HXB2	SLALIWDLLR	SLCLFSYHRL	RDLLLIVTRI	VELLGRR...	....GWEALK
B_GA_OYI	FLALIWDLLR	SLCLFSYHRL	RDLILIVARI	VELLGRR...	....GWEVLK
B_GB_CAM1	FLALIWDLLR	SLCLFSYHRL	RDLLLIVARI	VELLGRR...	....GWEALK
B_GB_GB8_C	FLALFWDDLR	SLCLFSYHRL	RDLLLIVTRI	VGLLGRR...	....GWEALK
B_GB_MANC	FLALVWDDLR	SLCLFSYHRL	RDLLSIAARI	VELLGRR...	....GWEILK
B_KR_WK_AF	FLTLIWVDLR	SLCLFSYHLL	RDLLLIVTRS	VELLGLR...	....GWEILK
B_NL_3202A	FLALIWDLLR	SLCLFSYHRL	RDLLLIVTRI	VELLGRR...	....GWEVLK
B_TW_TWCYS	FLAIIWVDLR	SLCLFSYHRL	RDLLLIVTRI	VELLGRR...	....GWEALK
B_US_BC_L0	FLALFWDDLR	SLCLFSYHRL	RDLILVTRI	VELLGRR...	....GWEALK
B_US_DH123	FLAIIWVDLR	TLFLFSYHRL	RDLLLIVTRI	VELLGRR...	....GWEILK
B_US_JRCSE	FLALIWVDLR	SLFLFSYHRL	RDLLLTVTRI	VELLGRR...	....GWEILK
B_US_MNCG	FLAIIWVDLR	SLFLFSYH.H	RDLLLIAARI	VELLGRR...	....GWEVLK
B_US_P896	FLALFWVDLR	NLCLFLYHLL	RNLLIVTRI	VELLGRR...	....GWEALK
B_US_RF_M1	FLTLIWDDLR	TLCSFSYHRL	RDLLLIVVRI	VELLGRR...	....GWEALK
B_US_SF2_K	FLALIWEDLR	SLCLFSYRRL	RDLLLIAART	VEILGHR...	....GWEALK
B_US_WEAU1	FLTLIWVDLR	SLCLFLYHRL	IDLLIAKRI	VELLGRR...	.....
B_US_WR27	LLALIWDLLR	SLCLFSYHRL	RDLISIVARI	VELLGRR...	....GWEILK
B_US_YU2_M	FLAIIWVDLR	SLCLFSYHRL	RDLLLIVTRI	VELLGRR...	....GWGVLK
BF1_BR_93B	FLALVWDDLR	NLCLFSYHRL	RDFILIAARI	VDRGLKR...	....GWEALK
C_BR_92BR0	FLALAWDDLR	SLCLFSYHRL	RDLILIAARA	VELLGRSSLR	GIQRGWEILK
C_BW_96BW0	FLALVWDDLR	SLCLFSYHRL	RDFILIAARA	AELLGRSSLR	GLQKGWETLK
C_BW_96BW1	FLALAWDDLR	SLCLFCYHRL	RDFTLVAARA	VELLGRSSLK	GLQRGWEILK
C_BW_96BW1	FLALAWDDLR	SLCLFSYHRL	RDSILVAART	VELLGRSSLR	GLQRGWEALK
C_BW_96BW1	FLALAWDDLR	SLCLFSYHRL	RDLILVTARV	VELLGRSSLR	GLQRGWEALK
C_ET_ETH22	FLAIFWDDLR	SLCLFSYHRL	RDLILIAART	VELLGRSSLK	GLQRGWETLK
C_IN_93IN1	FLALAWDDLR	NLCLFSYHRL	RDFISVAARV	VELLGRS...	....SWEALK
C_IN_93IN9	FLALAWDDLR	NLCLFSYHRL	RDFILVAARV	VELLGRNSLR	GLQRGWEALK
C_IN_93IN9	FLALAWDDLR	SLCLFSYHRL	RDFILVAVRA	VELLGRSSLR	GLQRGWEALK
C_IN_94IN1	FLALAWDDLR	SLCLFSYHRL	RDFILVAARV	VELLGHNSLR	GLQRGWEALK
C_IN_95IN2	FLALFWDDLR	NLCLFSYHRL	RDFILVAARV	LELLGRRSLR	GLQRGWEALK
CRF01_AE_C	FLSLAWDDLR	SLCLFSYHRL	RDFILIAART	VELLGHSSLK	GLRRGWEGLK
CRF01_AE_C	FLALAWDDLR	SLCLFSYHRL	RDFILIAART	VELLGHSSLQ	GLRRRWEGLK
CRF01_AE_C	FLALVWDDLR	SLCLFSYHRL	RDFILIAART	VELLGHSSLE	GLRRGWEGLK
CRF01_AE_T	FLSLAWDDLR	SLCLFSYHRL	RDFILIATRT	VELLGHSSLK	GLRRGWEGLK
CRF01_AE_T	FLTLAWDDLR	SLCLFSYHRL	RDFILIAART	VELLGRSSLK	GLRRGWEGLK
CRF01_AE_T	FLALAWDDLR	SLCLFSYHRL	RDFILIAART	VELLGHSSLK	GLRRGWEGLK

CRF01_AE_T	FLALAWDDLR	SLCLFLYHRL	RDFILIAART	VELLGHSSLK	GLRRGWEGLK
CRF01_AE_T	FLALAWDDLR	SLCLFSYHRL	RDLTLIAART	VELLGHSSLK	GLRRGWEGLK
CRF01_AE_T	FLALAWDDLR	SLCLFLYHRL	RDFILIAART	VELLGHSSLK	GLRRGWEGLK
CRF02_AG_F	FLALAWDDLR	SLCLFSYHRL	RDFVLIIVRA	VELLGHSSLK	GLRLGWEALQ
CRF02_AG_F	FLALAWDDLR	SLCLFSYHRL	RDFVLIIVRA	VELLGHSSLK	GLRLGWEALQ
CRF02_AG_G	FLALAWDDLR	NLCLFSYHRL	RDLILIAART	VEILGHR...	....VWQILK
CRF02_AG_N	FLALAWDDLR	SLCLFSYHRL	RDLILIAART	VELLGHNCLK	GLRLGWGALK
CRF02_AG_S	FLALAWDDLR	SLCLFSYHRL	RDFVSIVART	VELLGHRR...	....GWEALK
CRF02_AG_S	FLALAWDDLR	SLCLFLYHRL	RDFVLIIVRA	VELLGHSSLK	GLRLGWEALQ
CRF03_AB_R	FLALIWDLLR	SLCFFIYHHL	RDLILIAART	VELLGHRR...	....GWEALK
CRF03_AB_R	FLALIWDLLR	SLCFFIYHHL	RDLILIAART	VELLGHRR...	....GWEALK
CRF04_cpx_	FLPLIWDLLR	NLCLFSYHRL	RNLILIVART	VELLGIR...	....GWEALK
CRF04_cpx_	FLPLIWDLLR	NLCLFSYHRL	RNLILIVART	VELLGIR...	....GWEALK
CRF04_cpx_	FLPLVWDDLR	NLCLFSYHRL	RNLILIVART	VELLGIR...	....GWEALK
CRF05_DF_B	FSALIWDLLR	NLCLFSYHRL	RDLTLIVVRI	VELLGHRR...	....GWEALK
CRF05_DF_B	LSTLIWDLLR	NLCLFSYHRL	RDLILIAART	VELLGHRR...	....GWEALK
CRF06_cpx_	FLALAWDDLR	SLCLFSYHRL	RDFGLIAART	VEILGRR...	....GWEILK
CRF06_cpx_	FLALAWDDLR	SLCLFSYHRL	RDFVLIIVRA	VGTLGHR...	....GWEILK
CRF06_cpx_	FLALAWDDLR	SLCLFSYHRL	RDFVLIIVRA	VETLGRR...	....GWEILK
CRF06_cpx_	FLALAWEDLR	SLCRFSYHLL	RDFVLIVLRT	VETLGHR...	....GWEILK
CRF11_cpx_	FLAIAWDDLR	NLCLFSYHRL	RDFILIVARI	VETLGHR...	....GWEILK
CRF11_cpx_	FLALAWDDLR	NLCLFLYHQL	RDFILIVARI	VETLGRR...	....GWEILK
D_CD_84ZR0	FSALIWDLLR	NLCLFSYHRL	RELILIAART	VELLGHRR...	....GWEALK
D_CD_ELI_K	FSALIWDLLR	SLCLFSYHRL	RDLILIAVRI	VELLGHRR...	....GWDILK
D_CD_NDK_M	LFALFWDDLR	NLCLFSYHRL	RDSILIAART	VELLGHRR...	....GWEALK
D_UG_94UG1	LSALIWDLLR	NLCLFSYHRL	RDLILIAART	VELLGHRR...	....GWEALK
F1_BE_VI85	FLALAWDDLR	NLCLFSYHRL	RDFILIAART	VDRGLRR...	....GWEALK
F1_BR_93BR	FLALAWDDLR	NLCLFSYHRL	RDFILIAART	VDRGLKR...	....GWEALK
F1_FI_FIN9	FLALVWDDLR	NLCLFSYHRL	RDFILIAART	VDRGLRR...	....GWEALK
F1_FR_MP41	FLSLVWDDLR	NLCLFSYHRL	RDFILIAART	VDRGLTR...	....GWETLK
F2_CM_MP25	FLALAWDDLR	SLCVFSYHCL	RNFILIAART	VDKGLKR...	....GWEVLK
F2KU_BE_VI	FLALAWDDLR	NLCLFSYHRL	RDLILIVART	LERGLRG...	....SWEILK
G_BE_DRCBL	FLALAWDDLR	SLCLFSYHRL	RDFILIAART	VELLGRNSLK	GLRLGWEALQ
G_NG_92NG0	FLALAWDDLR	SLCLFSYHRL	RDLVLIIVRA	VELLGRSSLK	GLRLGWEGLK
G_SE_SE616	FLPLIWDLLR	SLCLFSYHRL	RDSILIVART	VELLGRSSLK	GLRLGWEGLK
H_BE_VI991	FLPLVWEDLR	NLCLFSYHRL	RDLISIVART	VELLGHRR...	....GWEALK
H_BE_VI997	FLPIVWDDLR	SLCLFSYHRL	RDSLIVIVRT	VELLGHRR...	....GREALK
H_CF_90CF0	FLPVVWDDLR	SLSLFSYHRL	RDLILIVVRI	VELLGHRR...	....GREALK
J_SE_SE702	FLALAWDDLR	SLCLFSYHRL	RDFVLIIVRA	VGTLGLR...	....GWEILK
J_SE_SE788	FLALAWDDLR	NLCLFSYHRL	RDFVLIIVRA	VGTLGLR...	....GWEILK
K_CD_EQTB1	FLALAWDDLR	NLCLFSYHRL	RDLVLIIVRA	LDRGLKG...	....SWEALK
K_CM_MP535	FLALAWDDLR	NLCLFSYHRL	RNLILIVART	LERGLRG...	....GWEALK
N_CM_YBF30	FSALVWEDLR	NLILFLYHRL	TDSLILIVRT	LELLGQSLSR	GLQLLNELRT
O_CM_ANT70	FLPLLYTDLR	TIILWTYHLL	SNLASGIQKV	ISYLRGLWI	LGQKIINVCR
O_CM_MVP51	FLQQLYTDLR	TIILWTYHLL	SNLISGIRRL	IDYLRGLWI	LGQKTIEACR
O_SN_99SE_	FLPLLYTDLR	TIILWSYHLL	SNLASGIQTV	ISHLGLGLWT	LGQKIISACR
O_SN_99SE_	FLPLLYTDLR	TIILWSYHLL	SNLASGIQTV	ISHLGLGLWI	LGQKIISACR
U_CD___83C	FLALAWEDLR	SLCIFSYHRL	RDLILIVVKG	...LRR....	....GWEALK

	901				950
00BW0762_1	YLGILVQYWG	LELKKS AISL	FDTIAIAVAE	GTDR IIEAIQ	RICRAICNIP
00BW0768_2	YLG NLVLYWG	LELKKS AISL	LDSIAIAVAE	GTDRILEAVQ	RIWGAIRNIP
00BW0874_2	YLGSLVQYWG	LELKKS AISL	LDTIAIAVAE	GTDR IIELIQ	RICRAIYNIP
00BW1471_2	YLGSLGQYWG	QELKKSAINL	FDTIAIAVAE	GTDR IIEAVQ	RAVRAILHIP
00BW1616_2	YLGSLVQYWG	LELKKS AVSL	LDTIAIAVAE	GTDRILEVTQ	RICRVIRNIP
00BW1686_8	YLGSLIQYWG	LELKKS AISL	LDTIAIAVAG	GTDRFIELIQ	RIYRAIRNVP
00BW1759_3	YLGSLGQYWG	LELKKS AISL	LDTIAIAVAE	GTDR IIELIQ	TICRAIRNIP
00BW1773_2	YLG NLVQDWG	LELKKS AISL	FDAIAIAVAE	GTDR IIELIQ	RTGRAICNIP
00BW1783_5	YLGTLVQYVW	LELKKS AISL	LDATAITVAG	GTDR IIELIQ	RIGRAILSIP
00BW1795_6	YLGSLVQYWG	LELKKS AISL	LDTVAIAVAE	GTDR IIELIQ	RGYRAICNIP
00BW1811_3	YLGSLVQYWG	LELKKS AISL	LDTIAIAVGE	GTDR IIEIIQ	RICRAIRNTP
00BW1859_5	YLGSLVQYWG	LELKKS AISL	LDTIAIAVAE	GTDR IIDLIQ	RICRAILRIP
00BW1880_2	YLGSLIQYWG	LELKKS AISL	LDTIAIAVAE	GTDR IIEGIQ	RICRIARNIP
00BW1921_1	YLGSLIQYWG	LELKKS AISL	LDTIAIATAE	GTDR IIEVIQ	RICRVIRNIP
00BW2036_1	YLGSLVQYWG	LELKKS AISL	LDTIAIAVAE	GTDR IIELVQ	RIGRGIYNIP
00BW2063_6	YLGSLVQYWG	LELKKS AISL	LNTTAIAVAE	GTDRVIELLQ	RIGRAICNIP
00BW2087_2	YLGSLVQYWG	LELRKSASSL	LDTIAIAVAE	GTDR IIEVIQ	IICRAILHIP
00BW2127_2	YLG NLVLYWG	LELKKS AISL	FDTIAVAVAE	GTDRILEVIQ	RICRAIRNIP
00BW2128_3	YLGSLVQYWG	LELKKS AVSL	LNTIAIVVAE	GTDRILELIQ	RLRR AFLNIP
00BW2276_7	YLG NLAQYWG	LELKKS AISL	INTIAIAVGE	RTDR IIELIQ	TLCRAIHNIP
00BW3819_3	YLG NLVQYWG	LELKRS AISL	LDTIAIAVAE	GTDR IIEFLQ	RIFRAIRNIP
00BW3842_8	YLG NLVQYWG	LELKKS AISL	LDAIAIAVGE	GTDRILELLQ	RIGRGICNIP
00BW3871_3	YLGSLIQYWG	LELKKSAINL	LDTTAIAVAE	GTDRFIELIQ	RICRAVRNIP
00BW3876_9	YLKNLGLYWG	LELKKS AISL	LNTIAIAVAE	GTDRVIEFVL	RICRAIRHIP
00BW3886_8	YLGSLVQYWG	LELKKSATS L	LDTIAIAVAE	GTDR IIE TVL	RICRAILHIP
00BW3891_6	YLGSLVQYWG	LELKKS AISL	LDTIAIVVAE	GTDR IIELVL	GICRAIRNVP
00BW3970_2	YLASLVQYWG	LELKKG AISL	LDSIAIAVAE	GTDR IIAFIQ	RLFRAICNLP
00BW5031_1	YLGSLVQYWG	LELKKS AISL	LDTIAIAVAE	GTDR IIEVVQ	RLYRAILNIP
96BW01B21	YLG NLLLYWG	LEPKKSAINL	LDTTAIAVAE	GTDRILELVQ	GICRAIRNIP
96BW0407	FLGSLVQYWG	LELKKS AISL	LDTTAIAVAE	GTDR IIEIAQ	RICRAICNVP
96BW0502	YLGSLVQYWG	LELKKS AISL	LDTIAIAVAE	GTDR IIEFIQ	RICRAIRNIP
96BW06_J4	YLGSLIQYWG	LELKRS TISL	LDTVPIAVPE	GTDR IIELIQ	RIWRAICNIP
96BW11_06	YLGSLVQYWG	LELKKS AISL	LDTTAIAVAE	GTDR IIEVLQ	RIGRAIRNTP
96BW1210	YLGSLVQYWG	LELKKS AISL	LDTIAIAVAE	GTDR IIELTQ	RVFRAIRNIP
96BW15B03	YLGSLVQYWG	LELKKSATS L	LDSIAIAVAE	GTDR IIEVIQ	RIYRAF CNIP
96BW16_26	YLGSLVQYWG	LELKKSAINL	LDTIAIAVAE	GTDR IIDFIL	RICRAIRNIP
96BW17A09	YLGSLGQYWG	QELKKSAINL	LDTIAIAVAE	GTDR IIEVLQ	GAIRAILNIP
96BWM01_5	YLGSLVQYWG	LELKKS AISL	LDTTAIAVAE	GTDR IIEVLQ	RVGRAIRNTP
96BWM03_2	YLGSLVRYWG	LELKKS AISL	LDTIAVAVAE	GTDR IIEVIQ	GICRGIRNIP
98BWMC12_2	YLGSLVQYWG	LELKKS AISL	LDTTAIAVAE	GTDR IIEIVL	RICRAICNVR
98BWMC13_4	YLGSLVQYWG	LELKKS AISL	LDTTAIAVAE	GTDR IIELLQ	RIGRAIRNTP
98BWMC14_a	YLG NLIQYWG	LELKKSAINL	LDTLAI AVAE	GTDR IIELIQ	RVCRAILNIP
98BWM014_1	YLG NLVQYWG	LKLKKS AISL	FDTIAIAVAE	GTDR IIELIQ	IICRAIRNIP
98BWM018_d	YLGSLVQYWG	LELKKS AISL	LDTIAIAVAE	GTDR IIELVQ	RICRGVLNIP
98BWM036_a	YLGSLVQYWG	LELKKS AISL	LDTIAIATAE	GTDR IIELIQ	RICRAIYNIP
98BWM037_d	YLG NLVQYWG	LELKKS AISL	LDTIAIAVAE	GTDR IIEFIQ	RICRAIRNLP
99BW3932_1	YLGSLVQYWG	LELKKS AISL	LDATAVAVAE	GTDRILEIIQ	RIFRAICNIP
99BW4642_4	YLGSLVQYWC	LELKKSATS L	IDAIAIAVAE	GTDR IIDLIQ	RICRAIRNIP
99BW4745_8	YLGSLVQYWG	LELKKS AISL	FDTIAIAVAE	GTDR IIELVL	RICGAIRNIP
99BW4754_7	YLGSIQYWG	LKLKKS AISL	LDTTAIAVAE	GTDR IIELLR	RFCRAISIP
99BWMC16_8	YLGSLGQYWG	LELKKS AISL	LDTIAIAVAE	GTDR IIELIQ	RTFRAICNIP
A2_CD_97CD	HLWNLLVYWG	QELKTS AIRL	LDTIAVAVAE	WTD RVIEIGQ	RACRAIRNIP
A2_CY_94CY	NLWNLLLYWG	RELKNS AISL	FDTIAVAVAE	WTD RVIEIGQ	RAFRAILNIP
A2D_97KR	YLWNLLLYWG	RELKNS AISL	FNATAIAVAE	WTD RVIEIVQ	RACRAIINIP
A2G_CD_97C	YLWNLLLYWG	QELKNSASNL	LDTVAIAVAN	WTD RVIEAAQ	GACRAIRNVP
A_BY_97BL0	YXXNLXGYXG	QELKSSAINL	IDTIAIAVAX	XTDXVIEIGQ	RFCRAIRNIP
A_KE_Q23_A	YLWNLLSYWG	RELKISAINL	VDTIAIAVAG	WTD RVIEIAQ	RIGRAILHIP
A_SE_SE659	YLG NLLLYWG	RELKISAINL	LDTTAIAVAG	WTD RVIEIVQ	GIGRAFLHIP
A_SE_SE725	YLG NLLLYWG	QELKLS AISL	FDTPAIAVAG	WTD RGIELIQ	RIGRAILNIP



A_SE_SE753	YLWNLLLYWG	RELKSSAINL	VDTIAIAVAG	WTDRIIEIGL	RIGRAFLHIP
A_SE_SE853	YLWNLLVYWI	RELKISAISL	LDTIAIAVAG	WTDRVIELGQ	RLCRAILHIP
A_SE_SE889	YLKNLLSYWG	RELKLSAINL	LDTIAIVIAG	WTDRVIEIGQ	GFCRAIFHP.
A_SE_UGSE8	YLGNNLLLYWI	RELKISAISL	FDTIAIAVAG	WTDRVIEIGQ	RIGRAILHIP
A_UG_92UG0	YLGNNLLLYWG	RELKISAINL	LDTIAIAVAG	WTDRVIVTVQ	RLGRAILNIP
A_UG_U455_	YLWNLLLYWG	RELKISAITL	LDAVAVAVAG	WIDRVIEIGQ	TIGRAILNIP
AC_IN_2130	YLWNLLVYWG	RELKISAIKL	VDTIAIVVAG	WTDRIIEIGQ	GIGRAILHIP
AC_RW_92RW	YLGNLVQYWG	LELKRSAINL	LDTTAIVVAE	GTDRRIELIQ	RISRAIYNIP
AC_SE_SE94	YLWNLLLYWG	RELRSAINL	LDTIAIATAS	WTDRVIELGQ	RICRAILNIP
ACD_SE_SE8	YLWNLLQYWI	QELKNSAINL	FNTIAIAVAE	GTDRVIEIGQ	RIGRAILNTP
ACG_BE_VI1	LLGNILLYWS	QELKNSAINL	LDTIAIAVAN	WTDRVIEIGQ	RAGRAFLNIP
AD_SE_SE69	YLWNLLQYWI	QELKNSAISL	VDTTAIAVAE	GTDRVIETVQ	RAFRAVLRIIP
AD_SE_SE71	YLWNLLQYWI	QELKISAISL	VDSIAIVVAG	WTDRVIEIGQ	GIGRAILHIP
ADHK_NO_97	YLGNNLLLYWG	QELKNSAINL	LNTTAIAVAE	GTDRRIIEIVQ	RTGRAVLHIP
ADK_CD_MAL	YLWNLLQYWG	QELKNSAISL	LNTTAIAVAE	CTDRVIEIGQ	RFGRAILHIP
AG_BE_VI11	YLWNLLVYWG	QELKNSAINL	LDTVAIAVAN	WTDRVIEIGQ	RAGRAILNIP
AG_NG_92NG	YLWNLLLYWG	RELKNSAINL	IDTIAIAVAN	WTDRVIEVAQ	GACRAILNIP
AGHU_GA_VI	YLWNLLLYWG	QELKSSAISL	LDAVAIAVAN	WTDRVIEVVQ	RVGRAILNIP
AGU_CD_Z32	YLGNLVIYWG	QELKNSAINL	LDTVAIAVAD	WTDRVIEVVQ	RAGRAFLNIP
AJ_BW_BW21	YLGNLALYWG	RELKNSAISL	LDTIAITVAE	ATDRIIEIAQ	RAFRAILHIP
B_AU_VH_AF	YWWNLLQYWS	QELQNSAISL	LNATAIAVAE	GTDRVIEVVQ	RACRAILHIP
B_CN_RL42	YWWNLLQYWI	QELKNSAIGL	LNATAIAVAE	GTDRVIEVVQ	RAYRAILHIP
B_DE_D31_U	YWWNLLQYWS	QELKNSAVSL	LNATAIAVAE	GTDRVIEVVQ	RAWRAILHIP
B_DE_HAN_U	YWWNLLQYWS	QELKNSAVSL	FNTIAIAVAE	GTDRVIEVVQ	RACRAILHIP
B_FR_HXB2_	YWWNLLQYWS	QELKNSAVSL	LNATAIAVAE	GTDRVIEVVQ	GACRAIRHIP
B_GA_OYI_	YWWNLLQYWS	QELKNSVISL	LNATAIAVAE	GTDRVIEIVQ	RAYRAFLNIP
B_GB_CAM1_	YWWNLLQYWS	QELRNSAVSL	FDTIAIAVAE	GTDRVIEVVQ	RACRAILHIP
B_GB_GB8_C	YWWNLLQYWI	QELKNSAISL	LNTTAIAVAE	GTDRVIEVVQ	RAYRAILHIP
B_GB_MANC_	YWWNLLQYWS	QVLKNSAVSL	LNVTIAIAVAE	GTDRRIIEVVQ	RVGRAILHIP
B_KR_WK_AF	YLWNLLQYWS	QELKNSAVSL	LNATAVAVAE	GTDRRIIEILQ	RAYRAILNIP
B_NL_3202A	YWWNLLQYWS	QELKNSAVSL	LNATAIAVAE	GTDRVIEVVQ	RACRAVLHIP
B_TW_TWCYS	YLWNLLQYWI	QELKNSAVSL	FNAIAIAVAE	GTDRVIEVVQ	RVFRAILHIP
B_US_BC_L0	YWWNLLQYWS	QELKNSAVNL	LNVTIAIAVAE	GTDRVIEVVQ	RTYRAILHIP
B_US_DH123	YLWNLLQYWS	QELKNSAVSL	LNATAIAVGE	GTDRRIIEILQ	RAGRAILNIP
B_US_JRCSF	YWWNLLQYWS	QELKNSAVSL	LNATAIAVAE	GTDRRIIEVVQ	RVYRAILHIP
B_US_MNCG_	YWWNLLQYWS	QELKSSAVSL	LNATAIAVAE	GTDRVIEVLQ	RAGRAILHIP
B_US_P896_	YWWNLLQYWS	QELKNSAVSL	LNATAIAVAE	GTDRVIKIVQ	RACRAIRNIP
B_US_RF_M1	YWWNLLQYWS	QELKNSAVSL	LNTTAIAVAE	GTDRRIIEVAQ	RILRAFLHIP
B_US_SF2_K	YWWNLLQYWI	QELKNSAVSW	LNATAIAVTE	GTDRVIEVAQ	RAYRAILHIH
B_US_WEAU1	.....	.....	.....	.....	.....
B_US_WR27	YWGNNLLQYWG	QELRNSAISL	LNATAIAVAE	GTDRVIEVGQ	RIFRAILHIP
B_US_YU2_M	YWWNLLQYWI	QELKNSAVSL	LNATAIAVAE	GTDRVIEILQ	RAFRAVLHIP
BF1_BR_93B	LLGNLALYWS	QELKNSAISL	LNTTAIVVAE	GTDRVIEALQ	RAGRAVLNVP
C_BR_92BR0	YLGGLVQYWS	LELKKS AISL	FDTIAIAVAE	GTDRRIIEVIQ	GIWRAICNIP
C_BW_96BW0	FLGSLVQYWG	LELKKS AISL	LDTTAIAVAE	GTDRRIIEIAQ	RICRAICNIP
C_BW_96BW1	YLGSLVQYWG	LELK MSTISL	LDTTAIAIAE	GTDRRIELIQ	RIGRAIRNTP
C_BW_96BW1	YLGSLVQYWG	LELKKS AISL	LDTIAIAVAE	GTDRRIELTQ	RVFRAIRNIP
C_BW_96BW1	YLGSLVQYWG	LELKKSATS	LDSIAIAVAE	GTDRRIIEVIQ	RIYRAFCNIP
C_ET_ETH22	YLGSLVQYWG	LELKKSAINL	LNTTAIVVGE	GTDRFIELIQ	RIWRAFCNIP
C_IN_93IN1	YLGSLVQYWG	LELKKS AISL	FDSIAIVVAE	GTDRRIELVQ	GFCRAIRNIP
C_IN_93IN9	YLGSLVQYWG	LELKKS AISL	LDIIAIAVAE	GTDRRIELIQ	RTCRAIRNIP
C_IN_93IN9	YLGSLVQYWG	IELKRS AISL	LDTAIAVAE	GTDRRIELVL	RICRAIRNIP
C_IN_94IN1	YLGSLVQYWG	LELKKS AIRL	LDIIAIAVAE	GTDRRIEIIQ	GTCRAIRNIP
C_IN_95IN2	YLGSLVQYWG	LELKKSAINL	LDRIAIAVAE	GTDRILELVQ	RICRAIRNIP
CRF01_AE_C	YLGNNLLSYWG	QELKTSAITL	FDAIAVAVAG	WTDRVIEVVQ	RAWRALIHIP
CRF01_AE_C	YLGNNLLSYWV	QELRISAITL	LDATAITVAG	WTDRVIEIVQ	RAWRAILHIP
CRF01_AE_C	YLGSLLSYWG	QELKTSAITL	LDATAITVAG	WTDRAIEIAQ	RACRAILHIP
CRF01_AE_T	YLGNNLLLYWG	QELKISAISL	LNTTAIAVAG	WTDRVIEVAQ	GAWRAILHIP
CRF01_AE_T	YLGNNLLLYWG	QELKISAISL	LDATAIAVAG	WTDRVIEVAQ	GAWRAILHIP
CRF01_AE_T	YLGNNLLLYWG	QELKISAISL	FDALAVVAG	WTDRVIEVAQ	GAWRAILHIP

CRF01_AE_T	YLGNNLLLYWG	QELKISAIISL	LDAIAIAVAG	WTDRVIKVAQ	RAWRAILHIP
CRF01_AE_T	YLGNNLLLYWG	QELKISAIISL	LDATAIAAAG	WTDRVIEVAQ	GAWRAILHIP
CRF01_AE_T	YLWNLLLYWG	QELKISVISL	LNATAIVVAG	WTDRVIEVAQ	GAWRAILHIP
CRF02_AG_F	YLGNNLLLYWG	QELKNSAINL	LDTIALAVAN	WTDRVIEIGQ	RVGRAILNIP
CRF02_AG_F	YLGNNLLTYWG	QELKNSAINL	LDTIAIAVAN	WTDRVIEIGQ	RVGRAIRNIP
CRF02_AG_G	YLGNNLAQYWG	LELKNSAISL	LNTTAIVVAE	QTDRLLEFLQ	RAGRAILHIP
CRF02_AG_N	YLWNLLISYV	QELKNSAINL	LNTIAIVVAN	WTDRAIEIGQ	RVGRAIRNIP
CRF02_AG_S	YLWNLLSYWG	QELKNSAISL	LDTIAIVVAN	WTDRVIELVQ	RAGRAILNIP
CRF02_AG_S	HLWNLLSYWG	QELKNSAINL	LDTTAVAVAN	WTDRVIEIVQ	RTGRAICNIP
CRF03_AB_R	YWWNLLQYWI	QELKSSAINL	IGTIAIAVAG	WTDRVIEIGQ	RFCRAMRNIP
CRF03_AB_R	YWWNLLQYWI	QELKSSAINL	INTIAIAVAG	WTDRVIEIGQ	RFCRAIRNIP
CRF04_cpx_	YLWNFLLYWG	QELKNSAINL	FNTTAIAVAE	GTDRIEEAVQ	RACRAICNIP
CRF04_cpx_	YLWNLLLYWG	QELRNSAINL	LDTTAIAVAE	GTDRILEAVQ	RACRAIRNIP
CRF04_cpx_	YLWNLLLYWG	QEIRSSAISL	LDTTAVAVAE	GTDRIEEAVQ	RICRAILNIP
CRF05_DF_B	YLWSLPQYWS	RELKNSAISL	LNTTAVVVAE	GTDRVIEALQ	RAGRAILNIP
CRF05_DF_B	YLWSLLQYWS	QELKNSAISL	LNTTAVVVAE	GTDRILEALQ	RAGRAVLNIP
CRF06_cpx_	YLGNNLCYWG	QELQNSAISL	FDAIAIAVAN	WTDRVAEVVQ	RIFRAFLNVP
CRF06_cpx_	YLGSLVWYWG	QELKNSAINL	LDTTAIAVAN	GTDRVIEIVQ	RAFRAVLNIP
CRF06_cpx_	YLWNLVQYWG	QELKNSAISL	IDTTAIAVAN	WTDRVIEVVQ	RAFRAVLNIP
CRF06_cpx_	YLGNNLVQYWG	QELKNSAISL	LDTTAIAVAN	WTDRVIEIVQ	RVFRAFLNVP
CRF11_cpx_	YLGNNLTQYWG	QELKNSAINL	LNTTAIAVAE	GTDRIEEIVQ	RVLRGILHIP
CRF11_cpx_	YLGNNLAQYWG	QELKSSAISL	LNATAIAVAE	GTDRIEEVAH	RALRAILNIP
D_CD_84ZR0	YLWNLLQYWS	RELKNSAISL	VDAIAIAVAE	GTDRIIDIVR	RACKAVLHIP
D_CD_ELI_K	YLWNLLQYWS	QELRNSASSL	FDAIAIAVAE	GTDRVIEIIQ	RACRAILNIP
D_CD_NDK_M	YLWNLLQYWS	QELRNSASSL	LDTIAIAVAE	RTDRVIEVVQ	RACRAILNVP
D_UG_94UG1	YLWNLLQYWI	QELKNSAVSL	FNTIAIAVAE	GTDRAIELVQ	RAVRAILNIP
F1_BE_VI85	YLGNNLTRYWS	QELKNSAISL	FNTTAIVVAE	GTDRIEEVLQ	RAGRAVLNIP
F1_BR_93BR	YLGNNLTQYWG	QELKNSAISL	LNATAIAVAE	WTDRVIEALQ	RAGRAILNIP
F1_FI_FIN9	YLGNNIIQYWS	QELKNSAISL	FNTTAIVVAE	GTDRVIEALQ	RAVRAVLNIP
F1_FR_MP41	YLWNLAQYWS	QELKNSAISL	LNTTAIVVAE	GTDRVIEVLQ	RAGRAVLNVP
F2_CM_MP25	YLWNLAQYWG	QELKNSAISL	LDRTAIAVAE	GTDRIEEILQ	RAGRAVLNIP
F2KU_BE_VI	YLWSLVQYWG	QELKNSAINL	LNTTAIAVAE	GTDRIEEVFQ	RAGRAVLNIP
G_BE_DRCBL	YLWNLLLYWA	RELKNSAINL	LDTIAIAVAN	WTDRVIEVAQ	RAGRAVLNIP
G_NG_92NG0	YLWNLLLYWG	RELKNSAINL	LDTIAIATAN	GTDRVIEVAQ	RAYRAILNVP
G_SE_SE616	YLWNLLLYWG	RELKNSAISL	LDTVAIAVAN	WTDRVIEVAQ	RACRAILNIP
H_BE_VI991	LLGNLLLYWG	QELKNSAISL	LNTTAIAVAE	GTDRIEELVQ	RAWRAILHIP
H_BE_VI997	YLWNLLQYWG	QELKNSAINL	LNTTAIVVAE	GTDRIEEIVQ	RAWRAVLHIP
H_CF_90CF0	YLWNLLQYWG	QELKNSAIDL	LNTTAIAVAE	GTDGIIIVIVQ	RAWRAILHIP
J_SE_SE702	YLVNLVWYWG	QELKNSAISL	LNTTAIAVAE	GTDRIEEIAQ	RAFRAILHIP
J_SE_SE788	YLVNLVWYWG	QELKNSAISL	LNTTAIAVAE	GTDRIEEIAQ	RAFRAILHIP
K_CD_EQTB1	YLWNLLLYWG	QELKNSAINL	LNTTAIAVAE	GTDRIEEIVY	RAFRALLHIP
K_CM_MP535	YLWNLVQYWS	QELKNSAISL	LNTTAIAVAG	GTDRIEEIGQ	RAFRALLHIP
N_CM_YBF30	HLWGILAYWG	KELRDSAISL	LNTTAIVVAE	GTDRIEELAQ	RIGRGILHIP
O_CM_ANT70	ICAAVTQYWL	QELQNSATS	LDTLAVAVAN	WTDGIIAGIQ	RIGTGIRNIP
O_CM_MVP51	LCGAVMQYWL	QELKNSATNL	LDTIAVSVAN	WTDGIIILGLQ	RIGQGFLHIP
O_SN_99SE_	LCIAVIQYWL	QELQNSATS	LDTIAVAVAN	WTVTIIILGIQ	RIGRGILNIP
O_SN_99SE_	ICIAVIQYWL	QELQNSATS	LDTLAVAVAN	WTDGIIILGLQ	RIGRGILNIP
U_CD___83C	YLGNNLVLYWG	QELKNSAISL	LNATAIVVAE	GTDRIEEVGQ	RICRAILNIP

	951	962
00BW0762_1	RRIRQGFEEA	LQ
00BW0768_2	RRIRQGFEEA	LQ
00BW0874_2	RRIRQGFEEA	LQ
00BW1471_2	RRIEQTFEPP	LL
00BW1616_2	RRIRQGVEEA	LQ
00BW1686_8	RRIRQGFETA	LL
00BW1759_3	RRIRQGFEEA	LQ
00BW1773_2	RRIRQGFEEA	LQ
00BW1783_5	RRIRQGFEEA	LQ
00BW1795_6	TRIRQGFEEA	LQ
00BW1811_3	RRIRQGFEEA	LL
00BW1859_5	RRIRQGFEEA	LL
00BW1880_2	TRIRQGFEEA	LQ
00BW1921_1	TRIRQGFEEA	LQ
00BW2036_1	RRIRQGFEEA	LQ
00BW2063_6	RRVRQGFETA	LL
00BW2087_2	RRIRQGFEEA	LL
00BW2127_2	TRIRQGFEEA	LL
00BW2128_3	SSIRQGFEEA	LQ
00BW2276_7	RRIRQGFEEA	LL
00BW3819_3	TRIRQGFEEA	LL
00BW3842_8	RRIRQGFEEA	LQ
00BW3871_3	RRLRQGFEEA	LL
00BW3876_9	RRIRQGFEEA	LL
00BW3886_8	RRIRQGFEEA	LL
00BW3891_6	TRIRQGFEEA	LQ
00BW3970_2	RRIRQGFEEA	LL
00BW5031_1	RRIRQGFEEA	LQ
96BW01B21	RRIRQGFEEA	LQ
96BW0407	TRIRQGFEEA	LQ
96BW0502	RRIRQGFEEA	LQ
96BW06_J4	RRIRQGFEEA	LL
96BW11_06	RRIRQGFETA	LL
96BW1210	RRIRQGFEEA	LQ
96BW15B03	RRVRQGFEEA	LQ
96BW16_26	RRLRQGFEEA	LQ
96BW17A09	TRIRQGLEAA	LQ
96BWM01_5	RRIRQGFEEA	LL
96BWM03_2	RRIRQGFEEA	LL
98BWMC12_2	.....GFEEA	LQ
98BWMC13_4	RRIRQGFETA	LL
98BWMC14_a	RRVRQGFEEA	LQ
98BWM014_1	TRIRQGLEAA	LL
98BWM018_d	RRIRQGFEEA	LQ
98BWM036_a	TRIRQGFEEA	LL
98BWM037_d	RRIRQGFEEA	LL
99BW3932_1	RRIRQGFETA	LL
99BW4642_4	RRIRQGFEEA	LQ
99BW4745_8	TRIRQGFEEA	LQ
99BW4754_7	RRIRQGFEEA	LQ
99BWMC16_8	RRIRQGFETA	LL
A2_CD_97CD	RRIRQGLERA	LL
A2_CY_94CY	RRIRQGLERA	LL
A2D___97KR	RRIRQGLERA	LL
A2G_CD_97C	RRIRQGLERA	LL
A_BY_97BL0	RRIRXGAEKA	LQ
A_KE_Q23_A	VRIRQGLERA	LL
A_SE_SE659	RRIRQGFEEA	LL
A_SE_SE725	RRIRQGFEEA	LL

A_SE_SE753	RRIRQGFERA	LL
A_SE_SE853	VRIRQGFERA	LL
A_SE_SE889	RRSKQGLKRA	LQ
A_SE_UGSE8	RRIRQGFER.	..
A_UG_92UG0	RRIRQGFERA	LL
A_UG_U455_	RRIRQGLERA	LL
AC_IN_2130	RRIRQGLERA	LL
AC_RW_92RW	SRIRQGFEEA	LQ
AC_SE_SE94	RRIRQGFERA	LL
ACD_SE_SE8	RRIRQGLERA	LL
ACG_BE_VI1	RRIRQGFERA	LL
AD_SE_SE69	ARIRQGLERV	LL
AD_SE_SE71	RRIRQGLERA	LL
ADHK_NO_97	RRIRQGFERX	LL
ADK_CD_MAL	RRIRQGFERA	LL
AG_BE_VI11	RRIRQGLERA	LL
AG_NG_92NG	RRIRQGLERA	LL
AGHU_GA_VI	RRIRQGLERA	LI
AGU_CD_Z32	RRIRQGLERA	LL
AJ_BW_BW21	VRIRQGFERA	LL
B_AU_VH_AF	RRIRQGLERL	LL
B_CN_RL42_	TRIRQGLERA	LL
B_DE_D31_U	VRIRQGLERA	LL
B_DE_HAN_U	RRVRQGLERA	LL
B_FR_HXB2_	RRIRQGLERI	LL
B_GA_OYI_	RRIRQGLERA	LL
B_GB_CAM1_	RRIRQGLERL	LL
B_GB_GB8_C	TRIRQGLERA	LQ
B_GB_MANC_	VRIRQGLERA	LL
B_KR_WK_AF	RRIRQGLERA	LL
B_NL_3202A	VRIRQGLERA	LL
B_TW_TWCYS	TRIRQGLERA	LL
B_US_BC_L0	RRIRQGLERL	LL
B_US_DH123	TRIRQGLERA	LL
B_US_JRCSF	TRIRQGLERA	LL
B_US_MNCG_	TRIRQGLERA	LL
B_US_P896_	TRIRQGLERA	LL
B_US_RF_M1	RRIRQGLERA	LL
B_US_SF2_K	RRIRQGLERL	LL
B_US_WEAU1	.....	..
B_US_WR27_	RRIRQGLERV	LL
B_US_YU2_M	VRIRQGLERA	LL
BF1_BR_93B	RRIRQGLERA	LL
C_BR_92BR0	RRIRQGFEEA	LQ
C_BW_96BW0	TRIRQGFEEA	LQ
C_BW_96BW1	RRIRQGFETA	LL
C_BW_96BW1	RRIRQGFEEA	LQ
C_BW_96BW1	RRVRQGFEEA	LQ
C_ET_ETH22	RRIRQGLEAA	LQ
C_IN_93IN1	TRIRQGFEEA	LQ
C_IN_93IN9	RRIRQGFEEA	LQ
C_IN_93IN9	TRIRQGFEEA	LQ
C_IN_94IN1	RRIRQGLEAA	LQ
C_IN_95IN2	RRIRQGFEEA	LQ
CRF01_AE_C	RRIRQGLERA	LL
CRF01_AE_C	RRIRQGLERA	LL
CRF01_AE_C	RRIRQGLERA	LL
CRF01_AE_T	RRIRQGLERT	LL
CRF01_AE_T	RRIRQGLERA	LL
CRF01_AE_T	RRIRQGLERA	LL

CRF01_AE_T	RRIRQGLERA	LL
CRF01_AE_T	RRIRQGLERT	LL
CRF01_AE_T	RRIRQGLERA	LL
CRF02_AG_F	RRIRQGLERA	LL
CRF02_AG_F	VRIRQGLERA	LL
CRF02_AG_G	RRIRQGFERA	LL
CRF02_AG_N	RRIRQGFERA	LL
CRF02_AG_S	RRIRQGFERA	LL
CRF02_AG_S	RRIRQGLERA	LQ
CRF03_AB_R	RRIRQGAEKA	LQ
CRF03_AB_R	RRIRQGAEKA	LQ
CRF04_cpx_	RRIRQGLERA	LL
CRF04_cpx_	RRIRQGFeka	LL
CRF04_cpx_	RRIRQGLERA	LL
CRF05_DF_B	RRIRQGLERA	LL
CRF05_DF_B	RRIRQGLERA	LL
CRF06_cpx_	RRIRQGFERA	LL
CRF06_cpx_	TRIRQGFERA	LL
CRF06_cpx_	RRIRQGAERA	LI
CRF06_cpx_	RRIRQGFERA	LL
CRF11_cpx_	RRIRQGLERA	LL
CRF11_cpx_	RRIRQGFERA	LL
D_CD_84ZR0	TRIRQGLERA	LL
D_CD_ELI_K	RRIRQGLERS	LL
D_CD_NDK_M	RRIRQGLERL	LL
D_UG_94UG1	VRIRQGLERA	LL
F1_BE_VI85	RRIRQGAERA	LL
F1_BR_93BR	RRIRQGLERA	LL
F1_FI_FIN9	RRIRQVERA	LI
F1_FR_MP41	RRIRQGLERS	LL
F2_CM_MP25	RRIRQGLERA	LL
F2KU_BE_VI	RRIRQGFERA	LL
G_BE_DRCBL	RRIRQGLERA	LL
G_NG_92NG0	TRIRQGLERA	LL
G_SE_SE616	TRIRQGLERA	LL
H_BE_VI991	RRIRQGFERA	LL
H_BE_VI997	RRIRQGLERI	LL
H_CF_90CF0	RRIRQGFERS	LL
J_SE_SE702	RRIRQGLERA	LL
J_SE_SE788	RRIRQGLERA	LL
K_CD_EQTB1	RRIRQGFERL	LL
K_CM_MP535	RRIRQGLERA	LL
N_CM_YBF30	RRIRQGLERA	LI
O_CM_ANT70	RRIRQGLERS	LL
O_CM_MVP51	RRIRQGAERI	LV
O_SN_99SE_	RRIRQGLERS	LL
O_SN_99SE_	RRIRQGLERA	LL
U_CD___83C	RRIRQGFERA	LL

Table 13. HIV Nef Sequence Alignment  
 GCG Multiple Sequence File.  
 Written by Omiga 1.1

Name: 00BW0762_1	<u>SEQ ID NO: 636</u>	Len: 232	Check: 3461	Weight: 1.00
Name: 00BW0768_2	<u>SEQ ID NO: 637</u>	Len: 232	Check: 5650	Weight: 1.00
Name: 00BW0874_2	<u>SEQ ID NO: 638</u>	Len: 232	Check: 3483	Weight: 1.00
Name: 00BW1471_2	<u>SEQ ID NO: 639</u>	Len: 232	Check: 9491	Weight: 1.00
Name: 00BW1616_2	<u>SEQ ID NO: 640</u>	Len: 232	Check: 1504	Weight: 1.00
Name: 00BW1686_8	<u>SEQ ID NO: 641</u>	Len: 232	Check: 1380	Weight: 1.00
Name: 00BW1759_3	<u>SEQ ID NO: 642</u>	Len: 232	Check: 5319	Weight: 1.00
Name: 00BW1773_2	<u>SEQ ID NO: 643</u>	Len: 232	Check: 156	Weight: 1.00
Name: 00BW1783_5	<u>SEQ ID NO: 644</u>	Len: 232	Check: 8063	Weight: 1.00
Name: 00BW1795_6	<u>SEQ ID NO: 645</u>	Len: 232	Check: 3123	Weight: 1.00
Name: 00BW1811_3	<u>SEQ ID NO: 646</u>	Len: 232	Check: 4460	Weight: 1.00
Name: 00BW1859_5	<u>SEQ ID NO: 647</u>	Len: 232	Check: 9116	Weight: 1.00
Name: 00BW1880_2	<u>SEQ ID NO: 648</u>	Len: 232	Check: 4302	Weight: 1.00
Name: 00BW1921_1	<u>SEQ ID NO: 649</u>	Len: 232	Check: 2737	Weight: 1.00
Name: 00BW2036_1	<u>SEQ ID NO: 650</u>	Len: 232	Check: 4558	Weight: 1.00
Name: 00BW2063_6	<u>SEQ ID NO: 651</u>	Len: 232	Check: 1020	Weight: 1.00
Name: 00BW2087_2	<u>SEQ ID NO: 652</u>	Len: 232	Check: 7532	Weight: 1.00
Name: 00BW2127_2	<u>SEQ ID NO: 653</u>	Len: 232	Check: 3425	Weight: 1.00
Name: 00BW2128_3	<u>SEQ ID NO: 654</u>	Len: 232	Check: 5136	Weight: 1.00
Name: 00BW2276_7	<u>SEQ ID NO: 655</u>	Len: 232	Check: 3623	Weight: 1.00
Name: 00BW3819_3	<u>SEQ ID NO: 656</u>	Len: 232	Check: 993	Weight: 1.00
Name: 00BW3842_8	<u>SEQ ID NO: 657</u>	Len: 232	Check: 6030	Weight: 1.00
Name: 00BW3871_3	<u>SEQ ID NO: 658</u>	Len: 232	Check: 3547	Weight: 1.00
Name: 00BW3876_9	<u>SEQ ID NO: 659</u>	Len: 232	Check: 1951	Weight: 1.00
Name: 00BW3886_8	<u>SEQ ID NO: 660</u>	Len: 232	Check: 3786	Weight: 1.00
Name: 00BW3891_6	<u>SEQ ID NO: 661</u>	Len: 232	Check: 3655	Weight: 1.00
Name: 00BW3970_2	<u>SEQ ID NO: 662</u>	Len: 232	Check: 8913	Weight: 1.00
Name: 00BW5031_1	<u>SEQ ID NO: 663</u>	Len: 232	Check: 2223	Weight: 1.00
Name: 96BW01B21	<u>SEQ ID NO: 664</u>	Len: 232	Check: 2176	Weight: 1.00
Name: 96BW0407	<u>SEQ ID NO: 665</u>	Len: 232	Check: 5261	Weight: 1.00
Name: 96BW0502	<u>SEQ ID NO: 666</u>	Len: 232	Check: 333	Weight: 1.00
Name: 96BW06_J4	<u>SEQ ID NO: 667</u>	Len: 232	Check: 5784	Weight: 1.00
Name: 96BW11_06	<u>SEQ ID NO: 668</u>	Len: 232	Check: 4950	Weight: 1.00
Name: 96BW1210	<u>SEQ ID NO: 669</u>	Len: 232	Check: 6118	Weight: 1.00
Name: 96BW15B03	<u>SEQ ID NO: 670</u>	Len: 232	Check: 5089	Weight: 1.00
Name: 96BW16_26	<u>SEQ ID NO: 671</u>	Len: 232	Check: 3957	Weight: 1.00
Name: 96BW17A09	<u>SEQ ID NO: 672</u>	Len: 232	Check: 1945	Weight: 1.00
Name: 96BWM01_5	<u>SEQ ID NO: 673</u>	Len: 232	Check: 5827	Weight: 1.00
Name: 96BWM03_2	<u>SEQ ID NO: 674</u>	Len: 232	Check: 2303	Weight: 1.00
Name: 98BWMC12_2	<u>SEQ ID NO: 675</u>	Len: 232	Check: 2423	Weight: 1.00
Name: 98BWMC13_4	<u>SEQ ID NO: 676</u>	Len: 232	Check: 4043	Weight: 1.00
Name: 98BWMC14_a	<u>SEQ ID NO: 677</u>	Len: 232	Check: 3568	Weight: 1.00
Name: 98BWM014_1	<u>SEQ ID NO: 678</u>	Len: 232	Check: 4909	Weight: 1.00
Name: 98BWM018_d	<u>SEQ ID NO: 679</u>	Len: 232	Check: 3505	Weight: 1.00
Name: 98BWM036_a	<u>SEQ ID NO: 680</u>	Len: 232	Check: 6393	Weight: 1.00
Name: 98BWM037_d	<u>SEQ ID NO: 681</u>	Len: 232	Check: 1912	Weight: 1.00
Name: 99BW3932_1	<u>SEQ ID NO: 682</u>	Len: 232	Check: 19	Weight: 1.00
Name: 99BW4642_4	<u>SEQ ID NO: 683</u>	Len: 232	Check: 6848	Weight: 1.00
Name: 99BW4745_8	<u>SEQ ID NO: 684</u>	Len: 232	Check: 938	Weight: 1.00
Name: 99BW4754_7	<u>SEQ ID NO: 685</u>	Len: 232	Check: 1379	Weight: 1.00
Name: 99BWMC16_8	<u>SEQ ID NO: 686</u>	Len: 232	Check: 4222	Weight: 1.00
Name: A2_CD_97CD	<u>SEQ ID NO: 687</u>	Len: 232	Check: 2359	Weight: 1.00
Name: A2_CY_94CY	<u>SEQ ID NO: 688</u>	Len: 232	Check: 5163	Weight: 1.00
Name: A2D___97KR	<u>SEQ ID NO: 689</u>	Len: 232	Check: 9468	Weight: 1.00
Name: A2G_CD_97C	<u>SEQ ID NO: 690</u>	Len: 232	Check: 4189	Weight: 1.00
Name: A_BY_97BL0	<u>SEQ ID NO: 691</u>	Len: 232	Check: 2590	Weight: 1.00

Name: A_KE_Q23	<u>SEQ ID NO: 692</u>	Len: 232	Check: 2652	Weight: 1.00
Name: A_SE_SE659	<u>SEQ ID NO: 693</u>	Len: 232	Check: 9245	Weight: 1.00
Name: A_SE_SE725	<u>SEQ ID NO: 694</u>	Len: 232	Check: 985	Weight: 1.00
Name: A_SE_SE753	<u>SEQ ID NO: 695</u>	Len: 232	Check: 1638	Weight: 1.00
Name: A_SE_SE853	<u>SEQ ID NO: 696</u>	Len: 232	Check: 2503	Weight: 1.00
Name: A_SE_SE889	<u>SEQ ID NO: 697</u>	Len: 232	Check: 2327	Weight: 1.00
Name: A_SE_UGSE8	<u>SEQ ID NO: 698</u>	Len: 232	Check: 9538	Weight: 1.00
Name: A_UG_92UG0	<u>SEQ ID NO: 699</u>	Len: 232	Check: 2621	Weight: 1.00
Name: A_UG_U455	<u>SEQ ID NO: 700</u>	Len: 232	Check: 2084	Weight: 1.00
Name: AC_IN_2130	<u>SEQ ID NO: 701</u>	Len: 232	Check: 2406	Weight: 1.00
Name: AC_RW_92RW	<u>SEQ ID NO: 702</u>	Len: 232	Check: 3441	Weight: 1.00
Name: AC_SE_SE94	<u>SEQ ID NO: 703</u>	Len: 232	Check: 3488	Weight: 1.00
Name: ACD_SE_SE8	<u>SEQ ID NO: 704</u>	Len: 232	Check: 3016	Weight: 1.00
Name: ACG_BE_VI1	<u>SEQ ID NO: 705</u>	Len: 232	Check: 5006	Weight: 1.00
Name: AD_SE_SE69	<u>SEQ ID NO: 706</u>	Len: 232	Check: 3362	Weight: 1.00
Name: AD_SE_SE71	<u>SEQ ID NO: 707</u>	Len: 232	Check: 2262	Weight: 1.00
Name: ADHK_NO_97	<u>SEQ ID NO: 708</u>	Len: 232	Check: 8765	Weight: 1.00
Name: ADK_CD_MAL	<u>SEQ ID NO: 709</u>	Len: 232	Check: 6397	Weight: 1.00
Name: AG_BE_VI11	<u>SEQ ID NO: 710</u>	Len: 232	Check: 6471	Weight: 1.00
Name: AG_NG_92NG	<u>SEQ ID NO: 711</u>	Len: 232	Check: 2880	Weight: 1.00
Name: AGHU_GA_VI	<u>SEQ ID NO: 712</u>	Len: 232	Check: 9053	Weight: 1.00
Name: AGU_CD_Z32	<u>SEQ ID NO: 713</u>	Len: 232	Check: 523	Weight: 1.00
Name: AJ_BW_BW21	<u>SEQ ID NO: 714</u>	Len: 232	Check: 3842	Weight: 1.00
Name: B_AU_VH	<u>SEQ ID NO: 715</u>	Len: 232	Check: 8468	Weight: 1.00
Name: B_CN_RL42	<u>SEQ ID NO: 716</u>	Len: 232	Check: 9366	Weight: 1.00
Name: B_DE_D31	<u>SEQ ID NO: 717</u>	Len: 232	Check: 3989	Weight: 1.00
Name: B_DE_HAN	<u>SEQ ID NO: 718</u>	Len: 232	Check: 563	Weight: 1.00
Name: B_FR_HXB2	<u>SEQ ID NO: 719</u>	Len: 232	Check: 3184	Weight: 1.00
Name: B_GA_OYI	<u>SEQ ID NO: 720</u>	Len: 232	Check: 5511	Weight: 1.00
Name: B_GB_CAM1	<u>SEQ ID NO: 721</u>	Len: 232	Check: 4779	Weight: 1.00
Name: B_GB_GB8	<u>SEQ ID NO: 722</u>	Len: 232	Check: 1128	Weight: 1.00
Name: B_GB_MANC	<u>SEQ ID NO: 723</u>	Len: 232	Check: 2885	Weight: 1.00
Name: B_KR_WK	<u>SEQ ID NO: 724</u>	Len: 232	Check: 9915	Weight: 1.00
Name: B_NL_3202A	<u>SEQ ID NO: 725</u>	Len: 232	Check: 3135	Weight: 1.00
Name: B_TW_TWCYS	<u>SEQ ID NO: 726</u>	Len: 232	Check: 2211	Weight: 1.00
Name: B_US_BC	<u>SEQ ID NO: 727</u>	Len: 232	Check: 3145	Weight: 1.00
Name: B_US_DH123	<u>SEQ ID NO: 728</u>	Len: 232	Check: 7019	Weight: 1.00
Name: B_US_JRCFSF	<u>SEQ ID NO: 729</u>	Len: 232	Check: 4099	Weight: 1.00
Name: B_US_MNCG	<u>SEQ ID NO: 730</u>	Len: 232	Check: 4137	Weight: 1.00
Name: B_US_P896	<u>SEQ ID NO: 731</u>	Len: 232	Check: 4405	Weight: 1.00
Name: B_US_RF	<u>SEQ ID NO: 732</u>	Len: 232	Check: 450	Weight: 1.00
Name: B_US_SF2	<u>SEQ ID NO: 733</u>	Len: 232	Check: 5413	Weight: 1.00
Name: B_US_WEAU1	<u>SEQ ID NO: 734</u>	Len: 232	Check: 5335	Weight: 1.00
Name: B_US_WR27	<u>SEQ ID NO: 735</u>	Len: 232	Check: 3720	Weight: 1.00
Name: B_US_YU2	<u>SEQ ID NO: 736</u>	Len: 232	Check: 9943	Weight: 1.00
Name: BF1_BR_93B	<u>SEQ ID NO: 737</u>	Len: 232	Check: 3598	Weight: 1.00
Name: C_BR_92BR0	<u>SEQ ID NO: 738</u>	Len: 232	Check: 3908	Weight: 1.00
Name: C_BW_96BW0	<u>SEQ ID NO: 739</u>	Len: 232	Check: 3880	Weight: 1.00
Name: C_BW_96BW1	<u>SEQ ID NO: 740</u>	Len: 232	Check: 4542	Weight: 1.00
Name: C_BW_96BW1	<u>SEQ ID NO: 741</u>	Len: 232	Check: 6118	Weight: 1.00
Name: C_BW_96BW1	<u>SEQ ID NO: 742</u>	Len: 232	Check: 5089	Weight: 1.00
Name: C_ET_ETH22	<u>SEQ ID NO: 743</u>	Len: 232	Check: 744	Weight: 1.00
Name: C_IN_93IN1	<u>SEQ ID NO: 744</u>	Len: 232	Check: 943	Weight: 1.00
Name: C_IN_93IN9	<u>SEQ ID NO: 745</u>	Len: 232	Check: 1241	Weight: 1.00
Name: C_IN_93IN9	<u>SEQ ID NO: 746</u>	Len: 232	Check: 9885	Weight: 1.00
Name: C_IN_94IN1	<u>SEQ ID NO: 747</u>	Len: 232	Check: 6448	Weight: 1.00
Name: C_IN_95IN2	<u>SEQ ID NO: 748</u>	Len: 232	Check: 5597	Weight: 1.00
Name: CRF01_AE_C	<u>SEQ ID NO: 749</u>	Len: 232	Check: 1052	Weight: 1.00
Name: CRF01_AE_C	<u>SEQ ID NO: 750</u>	Len: 232	Check: 744	Weight: 1.00
Name: CRF01_AE_C	<u>SEQ ID NO: 751</u>	Len: 232	Check: 1265	Weight: 1.00

Name:	CRF01_AE_T	SEQ ID NO: 752	Len:	232	Check:	697	Weight:	1.00
Name:	CRF01_AE_T	SEQ ID NO: 753	Len:	232	Check:	8468	Weight:	1.00
Name:	CRF01_AE_T	SEQ ID NO: 754	Len:	232	Check:	9246	Weight:	1.00
Name:	CRF01_AE_T	SEQ ID NO: 755	Len:	232	Check:	8105	Weight:	1.00
Name:	CRF01_AE_T	SEQ ID NO: 756	Len:	232	Check:	9948	Weight:	1.00
Name:	CRF01_AE_T	SEQ ID NO: 757	Len:	232	Check:	9460	Weight:	1.00
Name:	CRF02_AG_F	SEQ ID NO: 758	Len:	232	Check:	925	Weight:	1.00
Name:	CRF02_AG_F	SEQ ID NO: 759	Len:	232	Check:	9559	Weight:	1.00
Name:	CRF02_AG_G	SEQ ID NO: 760	Len:	232	Check:	399	Weight:	1.00
Name:	CRF02_AG_N	SEQ ID NO: 761	Len:	232	Check:	2782	Weight:	1.00
Name:	CRF02_AG_S	SEQ ID NO: 762	Len:	232	Check:	538	Weight:	1.00
Name:	CRF02_AG_S	SEQ ID NO: 763	Len:	232	Check:	6700	Weight:	1.00
Name:	CRF03_AB_R	SEQ ID NO: 764	Len:	232	Check:	6784	Weight:	1.00
Name:	CRF03_AB_R	SEQ ID NO: 765	Len:	232	Check:	3106	Weight:	1.00
Name:	CRF04_cpx	SEQ ID NO: 766	Len:	232	Check:	1551	Weight:	1.00
Name:	CRF04_cpx	SEQ ID NO: 767	Len:	232	Check:	5866	Weight:	1.00
Name:	CRF04_cpx	SEQ ID NO: 768	Len:	232	Check:	7925	Weight:	1.00
Name:	CRF05_DF_B	SEQ ID NO: 769	Len:	232	Check:	3625	Weight:	1.00
Name:	CRF05_DF_B	SEQ ID NO: 770	Len:	232	Check:	5585	Weight:	1.00
Name:	CRF06_cpx	SEQ ID NO: 771	Len:	232	Check:	3770	Weight:	1.00
Name:	CRF06_cpx	SEQ ID NO: 772	Len:	232	Check:	4202	Weight:	1.00
Name:	CRF06_cpx	SEQ ID NO: 773	Len:	232	Check:	5376	Weight:	1.00
Name:	CRF06_cpx	SEQ ID NO: 774	Len:	232	Check:	1869	Weight:	1.00
Name:	CRF11_cpx	SEQ ID NO: 775	Len:	232	Check:	3479	Weight:	1.00
Name:	CRF11_cpx	SEQ ID NO: 776	Len:	232	Check:	3712	Weight:	1.00
Name:	D_CD_84ZR0	SEQ ID NO: 777	Len:	232	Check:	1380	Weight:	1.00
Name:	D_CD_ELI	SEQ ID NO: 778	Len:	232	Check:	4418	Weight:	1.00
Name:	D_CD_NDK	SEQ ID NO: 779	Len:	232	Check:	4588	Weight:	1.00
Name:	D_UG_94UG1	SEQ ID NO: 780	Len:	232	Check:	2178	Weight:	1.00
Name:	F1_BE_VI85	SEQ ID NO: 781	Len:	232	Check:	4350	Weight:	1.00
Name:	F1_BR_93BR	SEQ ID NO: 782	Len:	232	Check:	7703	Weight:	1.00
Name:	F1_FI_FIN9	SEQ ID NO: 783	Len:	232	Check:	5036	Weight:	1.00
Name:	F1_FR_MP41	SEQ ID NO: 784	Len:	232	Check:	84	Weight:	1.00
Name:	F2_CM_MP25	SEQ ID NO: 785	Len:	232	Check:	2622	Weight:	1.00
Name:	F2KU_BE_VI	SEQ ID NO: 786	Len:	232	Check:	2193	Weight:	1.00
Name:	G_BE_DRCBL	SEQ ID NO: 787	Len:	232	Check:	2548	Weight:	1.00
Name:	G_NG_92NG0	SEQ ID NO: 788	Len:	232	Check:	3608	Weight:	1.00
Name:	G_SE_SE616	SEQ ID NO: 789	Len:	232	Check:	2716	Weight:	1.00
Name:	H_BE_VI991	SEQ ID NO: 790	Len:	232	Check:	1561	Weight:	1.00
Name:	H_BE_VI997	SEQ ID NO: 791	Len:	232	Check:	663	Weight:	1.00
Name:	H_CF_90CF0	SEQ ID NO: 792	Len:	232	Check:	1804	Weight:	1.00
Name:	J_SE_SE702	SEQ ID NO: 793	Len:	232	Check:	1615	Weight:	1.00
Name:	J_SE_SE788	SEQ ID NO: 794	Len:	232	Check:	1704	Weight:	1.00
Name:	K_CD_EQTB1	SEQ ID NO: 795	Len:	232	Check:	4783	Weight:	1.00
Name:	K_CM_MP535	SEQ ID NO: 796	Len:	232	Check:	2033	Weight:	1.00
Name:	N_CM_YBF30	SEQ ID NO: 797	Len:	232	Check:	6419	Weight:	1.00
Name:	O_CM_ANT70	SEQ ID NO: 798	Len:	232	Check:	8742	Weight:	1.00
Name:	O_CM_MVP51	SEQ ID NO: 799	Len:	232	Check:	5835	Weight:	1.00
Name:	O_SN_MP129	SEQ ID NO: 800	Len:	232	Check:	8625	Weight:	1.00
Name:	O_SN_MP130	SEQ ID NO: 801	Len:	232	Check:	8793	Weight:	1.00
Name:	U_CD_83C	SEQ ID NO: 802	Len:	232	Check:	1586	Weight:	1.00

SEQ ID NO	1	50
<u>636</u>	00BW0762_1 MGGKWSKSS. IVGWPAVRER IR....RTDP .....	AAEGVG
<u>637</u>	00BW0768_2 MGGKWSKSSI V.GWPEVRER IRR..TEP.. .....	AAEGVG
<u>638</u>	00BW0874_2 MGGKWSKSS. LTGWPAVRER IR....RTEP .....	AAEGVG
<u>639</u>	00BW1471_2 MGGKWSKSS. IVGWPAVKER IRR..TNPR. ....	TERAAVG
<u>640</u>	00BW1616_2 MGKWSKSS. IVGWPAVRDR MRR..AEP.. ....	AAEGVG



641	00BW1686_8	MGGKWSKRS.	KADWPAVREK	LR....TTEP	.....	....AAEGVG
642	00BW1759_3	MGNKWSKS..	...WPAVRER	IRR..TRPAR	.....	GNEPAAEGVG
643	00BW1773_2	MGSKWSKSSI	V.GWPKVRET	IRR..TEP..	.....	....AAEGVG
644	00BW1783_5	MGNKWSKS..	...WPAIRER	IRR..TNPAA	.....	ERTRAAEGVG
645	00BW1795_6	MGGKWSKSS.	VVGWPAIRER	MRR.....	.....	.TEPAAEGVG
646	00BW1811_3	MGGKWSKSC.	KIGWPAVRER	MRR.....	.....	.TEPAVEGVG
647	00BW1859_5	MGGKWSKSG.	KVGWPEVRER	MRR..TRPAA	EGG.....	..DSAAEGVG
648	00BW1880_2	MGGKWSKSS.	LVGWPAVRER	IRT..TAP..	.....	.....
649	00BW1921_1	MGGKWSKSS.	IVGWPAVRER	MR....KTEP	.....	....AAEGVG
650	00BW2036_1	MGGKWSKSS.	IVGWPAVRER	IRR.....	.....	.TEPAAEGVG
651	00BW2063_6	MGGKWSKSSI	I.GWPAVRER	MRK..AEP..	.....	....AAEGVG
652	00BW2087_2	MGSKWSKSS.	IVGWPAVRER	IRR..T....	.....	RTEPAAEGVG
653	00BW2127_2	MGGKWSKSSI	I.GWPAIRER	IRR..TEP..	.....	....AAEGVG
654	00BW2128_3	MGSKWSKCSI	I.GWPAVRER	IRR..AEP..	.....	....AAVGVG
655	00BW2276_7	MGSKWSKC..	.SGWPDVRER	MRR..ATPAA	EAGRA...AP	AAEGAAPGVG
656	00BW3819_3	MGSKWSKCSI	V.GWPDVRER	MRR..ARPAV	RERRRQTEPA	AEGVAAEGVG
657	00BW3842_8	MGGKWSKGR.	IVGWPAVRER	MRR.....	.....	.TEPAAEGVG
658	00BW3871_3	MGSKWSKRS.	IVEWPAVRER	LR....KTEP	.....	....AAEGVG
659	00BW3876_9	MGGKWSKSS.	IVGWPAVRER	IRQ..TGAR.	.....	....AAEGV G
660	00BW3886_8	MGGKWSKSS.	IVGWSAVRER	MK....RTEP	.....	....AAEGVG
661	00BW3891_6	MGGKWSKSS.	IVGWPTVRER	MRR..TQP..	.....	....AAEGVG
662	00BW3970_2	MGSKWSKRS.	TAGWPAVRER	MRR..TQPAA	EG.....	.TQSAAEGVG
663	00BW5031_1	MGGKWSKSS.	LVGWPEVRDR	IRR..TDP..	.....	....AAEGVG
664	96BW01B21	MGGKWSKSSI	V.GWPAVRER	IRR..TEP..	.....	....AAEGVG
665	96BW0407	MGGKWSKSSI	V.GWPAVRER	MRR..AEP..	.....	....AAEGVG
666	96BW0502	MGGKWSK...	CSGWPAVRER	MRR..TRPAV	EGR.....	.TESAAEGVG
667	96BW06_J4	MGGKWSKSS.	IVGWPAVRER	IR....RTDP	.....	....PAEGVR
668	96BW11_06	MGGKWSKSSI	I.GWPAIRER	IRR..TEPAA	ER.....V	..GAAAEGVG
669	96BW1210	MGNKWSKG..	...WPAVRDR	IRR..TEPAT	.....	..EPAAEGVG
670	96BW15B03	MGGKWSKSS.	IVGWPAVRER	IRR.....	.....	.TEPAAEGVG
671	96BW16_26	MGGKWSK...	...WPAVRER	MRR..TR...	.....	.....VG
672	96BW17A09	MGXKWSKRS.	IVGWPNVRER	IRR..TNPLT	ER.....	EAERAAGVG
673	96BWM01_5	MGSKWSKSSI	I.GWPAVRER	IRK..TEPRK	.....	.TEPAAEGVG
674	96BWM03_2	MGGKWSKSS.	IVGWPAVRER	MRR..TRPGA	AE.....	.....GVG
675	98BWMC12_2	MGSKWSKSS.	IIGWPAVRER	MR....RTEP	.....	....AAEGVG
676	98BWMC13_4	MGGKWSKSS.	IIGWPAVRER	MRR.....	.....	.TEPAAEGVG
677	98BWMC14_a	MGGKWSKSS.	LVGWPDVRER	IR....KPRP	KP.....	....AAEGVG
678	98BWM014_1	MGSKLSKSK.	IVGWPAIRER	LR.....	.....	RTEPAAEGVG
679	98BWM018_d	MGGKWSKSS.	IVGWPAVRER	IRQ..TDPRE	RI.....R	QTEPAAEGVG
680	98BWM036_a	MGGKWSKSSI	V.GWPAVRER	IRR..TEPRR	.....	.AEPAAEGVG
681	98BWM037_d	MGGKWSKSS.	IVGWPEVRER	LR....RTAP	.....	....AAEGVG
682	99BW3932_1	MGGKWSKRKI	V.QWPTVRER	LRR..TEP..	.....	....AEGVG
683	99BW4642_4	MGGKWSKSS.	IVGWPAVRER	IRR..TQPAA	EG.....	.....VG
684	99BW4745_8	MGSKLSKSC.	TAGWPTVRER	IRQ..AEP..	.....	....AAEGVG
685	99BW4754_7	MGGKWSKSS.	IVGWANVRER	MRR.....	.....	.TEPAAGVG
686	99BWMC16_8	MGNKWSKS..	...WPAVRER	IRR..TEPAV	RV.....R	RTEPAAEGVG
687	A2_CD_97CD	MGGKWSKRT.	IVGWPEIRER	MRR..TPPAA	EG.....VR	PTPPAAEGVG

688	A2_CY_94CY	MGGKWSKRS.	IPGWPAIRER	MRRTPTAQR	TE.....	AVSPAAPGVG
689	A2D__97KR	MGGKWSKRS.	LPGWPAIRER	MRRTPPAAER	TP.....	PAA.AAEGVG
690	A2G_CD_97C	MGSKWSKSS.	IVGWPAVRAR	IR...QTPP.	.....	AAEGVG
691	A_BY_97BL0	XXGKWSKSS.	IXXWPQVXER	IRRAPAP...	.....	AARXVG
692	A_KE_Q23	MGGKWSKSS.	IVGWPEIRER	MRRAPP....	.....	AAPGVG
693	A_SE_SE659	MGGKWSKSS.	IVGWPEIRER	MRRAPS....	.....	AAAPGVG
694	A_SE_SE725	MGSKWSKSS.	IVGWREVRER	LRQTLAAARG	.....	VG
695	A_SE_SE753	MGGRWSKSR.	IVGWPEVRER	IRRAPP....	.....	AATGVG
696	A_SE_SE853	MGGKWSKRS.	KEGWSEVREK	IRQT.....	.....	PPAAKGVG
697	A_SE_SE889	MGGKWSKSS.	IVGWPKVRER	MARTPP....	.....	AAKGVG
698	A_SE_UGSE8	MGNKWSK... .	GWPEVRER	IRQARAPAHT	.....	PAPTAATGVG
699	A_UG_92UG0	MGNKWSKSC.	IVGWPEVRER	IRQTPTAARE	RTR.....	QAPTAAGVG
700	A_UG_U455	MGGKWSKKS.	RVEWPEVRKR	MRETPA....	.....	AAKGVG
701	AC_IN_2130	MGGKWPKSS.	VVGWPEVRER	IRRTPA....	.....	AAPGVG
702	AC_RW_92RW	MGSKWSKCSP	V.GWPAVRER	LRQ..TEP..	.....	AAEGVG
703	AC_SE_SE94	MGGKWSKSS.	IIGWPQIRER	IRRTPP....	.....	AATGVG
704	ACD_SE_SE8	MGGKWLKSSI	V.GWPAVRER	IRR..TEP..	.....	AAEGVG
705	ACG_BE_VI1	MGGKWSKRS.	KVEWPQVRER	MRQ..TPIAA	EA.....EG	AAAEGVG
706	AD_SE_SE69	MGGKWSKSS.	IVGWPAVRER	IKR..T....	.....	DPAAEGVG
707	AD_SE_SE71	MGGKWSKSS.	IVGWPEVRER	MRRARAP...	.....	SAAPGVG
708	ADHK_NO_97	MGGKWSKSS.	IVGWPAIRER	MRR..AEP..	.....	AAEGVG
709	ADK_CD_MAL	MGGKWSKSS.	IVGWPKIRER	IRRTPTTETG	.....	VGAVSQD
710	AG_BE_VI11	MGGKWSKSS.	PVGWSRVRER	MRR..TPPAA	EG.....	AAAEGVG
711	AG_NG_92NG	IGGKWSKSS.	IVGWPAVRER	IR...QTP..	.....	PAEGVG
712	AGHU_GA_VI	MGGEWSRSS.	IVGWSTIRER	MRRAP....	.....	AAAGVG
713	AGU_CD_Z32	MGNKWSKG..	WPAVRER	IRQ..TPPAP	P.....	AAEGVG
714	AJ_BW_BW21	MGSNWSKS.S	IIGWPQVRER	MKR.....AP	A.....P	AAEGVG
715	B_AU_VH	MGGKGSKRI.	RSEWPTVRER	IIQ..AEPAA	AG.....	VG
716	B_CN_RL42	MGGKWSKHS.	MFGWPSVRER	MKR..AEPAA	DG.....	VG
717	B_DE_D31	MGGKWSKSS.	VVGWPAIRER	MK.....	.....	RAEPAAEGVG
718	B_DE_HAN	MGGKWSK... .	CSGWPTVRER	MKQAEP....	.....	EPAADGVG
719	B_FR_HXB2	MGGKWSKSS.	VIGWPTVRER	MR.....	.....	RAEPAADRVG
720	B_GA_OYI	MGGKWSKCS.	MKGWPTIRER	MKR..AELQP	PE.....	PAAEGVG
721	B_GB_CAM1	MGGKWSKRS.	LGGWSAVRER	MQR..AEP..	.....	RAEPAAEGVG
722	B_GB_GB8	MGGKLSKRS.	MFGWSRVRDR	MQQ..AEP..	.....	AAEGVG
723	B_GB_MANC	MGGKWSKSR.	KIGWPTVRER	MKQ..VDPAB	EGR....KK	QAEPAAGVG
724	B_KR_WK	MGGKWSKRS.	VPGWNTIRKR	MRR..AEPAA	EG.....	VG
725	B_NL_3202A	MGGKWSKSS.	VVGWPAIRER	MK.....	.....	RAEPAADGVG
726	B_TW_TWCYS	MGGKWSKRS.	IPGWSNIRER	IRQ..AEP..	.....	AADGVG
727	B_US_BC	MGGKWSKRM.	EGGWHAVRER	MR.....	.....	RAEPAADGVG
728	B_US_DH123	MGGKLSKCG.	GVGWSTVRER	MRR..AEPAA	DR.....	EP.AVGVG
729	B_US_JRCSF	MGGKWSKHS.	VPGWSTVRER	MRR..AEPAT	DR.....VR	QTEPAAGVG
730	B_US_MNCG	MGGKWSKR..	VTGWPTVRER	MRR..AEP..	.....	AELAADGVG
731	B_US_P896	MGGKWSKRR.	AEGWQTIRER	MRRAP....	.....	EPAADGVG
732	B_US_RF	MGGKWSKSK.	MGGWPAVRER	MQK..AEPAA	DG.....	VG
733	B_US_SF2	MGGKWSKRS.	MGGWSAIRER	MRR..AEP..	.....	RAEPAADGVG
734	B_US_WEAU1	MGGIWSKRS.	GSGWPAIRER	MKR..AEPAA	EG.....	VG

735	B_US_WR27	MGGKWSKRS.	VGGWPAIRER	MX.....	RAEPAAEGVG
736	B_US_YU2	MGGKWSKRS.	MAGWPTVRER	MRR..AEPAA ER.....MR	RAEPAADGVG
737	BF1_BR_93B	MGSKWSKSS.	IVGWPAIRER	LRQ..TP...	...PAAEGVG
738	C_BR_92BR0	MGNKWSKCST	V.GRPAIRER	MRR...AP..	....AAEGVG
739	C_BW_96BW0	MGGKWSKSSI	V.GWPAVRER	MRR..TEP..	....AAEGVG
740	C_BW_96BW1	MGGKWSKRSK	I.EWPTIRDR	MRR..TEPAA EG.....V	..GAAAEGVG
741	C_BW_96BW1	MGNKWSKG..	...WPAVRDR	IRR..TEPAT	...EPAAEGVG
742	C_BW_96BW1	MGGKWSKSS.	IVGWPAVRER	IRR.....	..TEPAAEGVG
743	C_ET_ETH22	MGGTMSKCSP	V.GWPAIRER	IRR..AAP..	....AAEGVG
744	C_IN_93IN1	MGGKWSKCSI	V.GWPAIRER	MRR..AEP..	....AAEGVG
745	C_IN_93IN9	MGGKWSKCSI	V.GWPDIRER	MRR..TQP..	....AAEGVG
746	C_IN_93IN9	MGGKWSKCSI	V.GWPAVRER	MRR..TEP..	....AAEGVG
747	C_IN_94IN1	MGGKWSKCSI	V.GWPEIRER	MRR..TQP..	....AADGVG
748	C_IN_95IN2	MGGKWSKCSI	V.GWPDIRER	MRR..TEP..	....AAEGVG
749	CRF01_AE_C	MGGKWSKN.R	IVGWQVRER	IRR..TPAAA	.....EGVG
750	CRF01_AE_C	MGGKWSKSC.	IVGWQVRER	IRQ..TPVAE E.....R	QTPAAAEGVG
751	CRF01_AE_C	MGNKWSKS..	..WPQIRER	IRQ..TPVAT	.....EGVG
752	CRF01_AE_T	MGGKWSKS.S	IVGWQVREK	IKQ..TPPAA	.....EGVG
753	CRF01_AE_T	MGGKWSKS.S	IVGWQVREK	IKQ..TPPAA	.....EGVG
754	CRF01_AE_T	MGGKWSKS.S	IVGWQVRER	IKQ..TPPAA	.....EGVG
755	CRF01_AE_T	MGAKWSKRG.	...WPQVRER	IRQ..TPPAA	.....EGVG
756	CRF01_AE_T	MGSKWSKS.S	IVGWQVREK	IKQ..TPPAT	.....EGVG
757	CRF01_AE_T	MGNKWSKS..	...WPRVRER	IKQ..TPPAA	.....EGVG
758	CRF02_AG_F	MGGKWSKSS.	IVGWPKVRER	IR...QTPP.	....AATGVG
759	CRF02_AG_F	MGGKWSKSS.	LVGWPKVRER	II...QTPP.	....AATGVG
760	CRF02_AG_G	MGGKWSKSS.	IVGWQVRER	IR...QTPT.	....AAKGVG
761	CRF02_AG_N	MGGKWSKSS.	IVGWPKVMKR	MR...QTPT.	....AATGVG
762	CRF02_AG_S	MGGKWSKSS.	IVGWQIRDR	IR...QTPP.	....AARGVG
763	CRF02_AG_S	MGGKWSKSS.	LVGWQVRER	IRRTQPTPS.	....AAIGVG
764	CRF03_AB_R	MGGKWSKSS.	IVGWQVRER	IRRAPAP...	....AARGVG
765	CRF03_AB_R	MGGKWSKSS.	IVGWQIRER	IRRAPAP...	....AARGVG
766	CRF04_cpx_	MGGKWSKSS.	IVGWPEIRER	MRR..ARAEP ERM.....RA	QAEPAAGVG
767	CRF04_cpx_	MGGKWSKSS.	LVGWPAIRER	MRR..ARAEP .....	AA QAEPAAGVG
768	CRF04_cpx_	MGNKWSKS..	...WPAVRER	MRR..ARAEP .....	A RAEPAAGVG
769	CRF05_DF_B	MGGKWSKSS.	VVGWPAIREK	MRR..TP...	...PAAEGVG
770	CRF05_DF_B	MGGKWSKNR.	IVGWPAIRER	MRR..TPPAA	....GAAAEGVG
771	CRF06_cpx_	MGNKWSK...	..GWSQVRER	MRR..TPPTE R.....	....AAEGVG
772	CRF06_cpx_	MGSKWSKS.S	IVGWQVRER	IRQ..TPPTE G.....	....AAKGVG
773	CRF06_cpx_	MGGKWSKS.S	LVGWQVRER	IRQ..TPPTE G.....	....AAEGVG
774	CRF06_cpx_	MGGKWSKS.S	IVGWPKVRER	MRQ..TPPAA E.....R	QTPPAAGVG
775	CRF11_cpx_	MGGKWSKS.S	IVGWPEIRER	LRR.....	...T PPAAADGVG
776	CRF11_cpx_	MGGNWSKS.S	IVGWPEIRER	LRR.....	...T PPTAAAGVG
777	D_CD_84ZR0	MGGKWSKSS.	IVGWPAIRER	IRK..TDPRE RR.....	RPEPAADGVG
778	D_CD_ELI	MGGKWSKSS.	IVGWPAIRER	IRR..T....	..NPAADGVG
779	D_CD_NDK	MGGKWSKSS.	LVGWPAIRER	IRK..T....	..DPAADGVG
780	D_UG_94UG1	MGGKWSKSS.	IVGWPAVRER	MRR..T....	..EPAAEGVG
781	F1_BE_VI85	MGGKWSKSS.	IVGWPAVGER	MRQ..TP...	...TAAEGVG

782	F1_BR_93BR	MGGKWSKSS.	IVGWPAIRER	MRR..TPPT.	.....	..PPAAEGVG
783	F1_FI_FIN9	MGGKWSKSS.	IVGWPAIRER	MRR..PP...	.....	..PAAAGVG
784	F1_FR_MP41	MGGKWSKSS.	IVGWPAVRER	MRR..TP...	.....	...PAAEGVG
785	F2_CM_MP25	MGGKWSKSS.	IVGWPAIRER	IRR..TP...	.....	...VAAEGVG
786	F2KU_BE_VI	MGGKWSK...	..GWPSVRER	IRR..TPPAA	P.....	....AADGVG
787	G_BE_DRCBL	MGNKWSKRK.	VAGWPEVRER	LR...QHPA.	.....	....AAEGVG
788	G_NG_92NG0	MGGKWSKSS.	IVGWQIRER	IR...QTPV.	.....	....AAEGVG
789	G_SE_SE616	MGGKWSKSS.	IVGWPEVRER	IR...NTPT.	.....	....AAEGVG
790	H_BE_VI991	MGGKWSKGC.	ISGWPAVRER	IRQ..TEP..	.....	....AAEGVG
791	H_BE_VI997	MGGKWSKSS.	IVGWPAVRER	IRR..AQP..	.....	....AADGVG
792	H_CF_90CF0	MGGKWSKSR.	MGGWSTIRER	MRR..AEP..	.....	....VAEGVG
793	J_SE_SE702	MGNKWSKS..	...WPQVRDR	MRR..A..AP	A.....P	....AADGVG
794	J_SE_SE788	MGNKWSKS..	...WPQVRER	MRR.....AP	A.....P	....AADGVG
795	K_CD_EQTB1	MGGKWSKS.S	IVGWSTVRER	MR.....	.....	KTPPAADGVG
796	K_CM_MP535	MGGKWSKS.S	IVGWPAIRER	MRR..ARPA	DR.....V	GTQPAADGVG
797	N_CM_YBF30	MGKIWSKSS.	LVGWPEIRER	MRRQTQEP..	.....	..AVEPAVGAG
798	O_CM_ANT70	MGNALRKKGK.	FEGWAAVRER	MRRTRTF...	.....P	ESEPCAPGVG
799	O_CM_MVP51	MGNAWSKSK.	FAGWSEVRDR	MRRSSS....	.....D	PQQPCAPGVG
800	O_SN_MP129	MGNVLGKDI.	FKGWSAVRER	MRGTS.....	.....P	DPEPCAPGVG
801	O_SN_MP130	MGNVLGKDK.	FKGWSAVRER	MRKTS.....	.....P	EPEPCAPGVG
802	U_CD___83C	MGNKWSKQ..	...WPAIRER	MRR..ARPA	E.....P	....AADGVG

	51					100
00BW0762_1	AASQDLDRHG	AITSSNTPTT	NAACAWLEAQ	EEDE...VGF	PVRPQVPLRP	
00BW0768_2	AASQDLDKYG	ALTSSNTANT	NAACAWLEAQ	EKEE.E.VGF	PVRPQVPLRP	
00BW0874_2	EASQDLDKHG	ALTSSNTAAN	NADCAWLQAH	EEEG..EVGF	PVRPQVPLRP	
00BW1471_2	AASQDLDKYG	ALTANNTPAN	NADCARLQAA	EEDN..EVGF	PVRPQVPLRP	
00BW1616_2	PASQDLGRHG	ALTSSNTAHN	NADCAWLEAQ	EEEG.G.VGF	PVRPQVPLRP	
00BW1686_8	AASQDLAKHG	ALTSSNTAHN	NADCAWLEAQ	EEEE...VGF	PVRPQVPLRP	
00BW1759_3	AASQDLDKYG	ALTSSNTPTT	NAACAWLEAQ	EEAE.E.VGF	PVRPQVPLRP	
00BW1773_2	AASQDLDKYG	ALTSSNTDTN	NADCAWLKAA	EEEG.E.VGF	PVRPQVPLRP	
00BW1783_5	AASRDLDKHG	ALTSSNTPAT	NADCAWLEAQ	EEEE.E.VGF	PVRPQVPVPR	
00BW1795_6	AASQDLDKYG	ALTSSNTATN	NADCAWLEAQ	EEAD..DVGF	PVRPQVPLRP	
00BW1811_3	AASQDLDRHG	ALTSSNTATN	NADCAWLEAQ	EEGE..EVGF	PVRPQVPLRP	
00BW1859_5	AASRDLARHG	ALTSSNTATT	NAACAWLEAQ	EEAD..EVGS	PVRPQVPLRP	
00BW1880_2	.....	.....AAT	NDACARLKEQ	EEEG.E.VGF	PVRPQVPVPR	
00BW1921_1	AASRDLDKYG	ALTSSNTVTT	NAACAWLEAQ	EKEG..GVGF	PVRPQVPLRP	
00BW2036_1	AASQDLDKHG	ALTSSNTSST	NDACAWLEAQ	EEAD..DVGF	PVRPQVPLRP	
00BW2063_6	AASQDLDKHG	ALTSSNTANN	NADCAWLEAQ	EEEE...VGF	PVKPQVPLRP	
00BW2087_2	AASQDLDKHG	ALTPSNTAGN	NSTCAWLQAA	EEEE..EVGF	PVRPQVPLRP	
00BW2127_2	AASQDLDKHG	ALTSSNTATN	NADCAWLQAA	EEES.EGVGF	PVRPQVPLRP	
00BW2128_3	AASQDLDKYG	ALTSSNTDTN	NAACAWLRAQ	EEEE.E.VGF	PVX....TS	
00BW2276_7	AASRDLDHRG	ALTSSNTPTN	NADCAWLQAA	EEEE.EEVGF	PVRPQVPLRP	
00BW3819_3	TASQDLAKHG	ALTSSNTPAN	NAACAWLQAA	EEEE.D.VGF	PVRPQVPLRP	
00BW3842_8	AASRDLDKHG	ALTSSNTAEN	NADCAWLEAQ	EETE..EVGF	PVRPQVPLRP	
00BW3871_3	AASQDLDKHG	ALTSSNTAQN	NAACAWLEAQ	EEAE.GEVGF	PVRPQVPLRP	
00BW3876_9	AASQDLDRHG	ALTSSNTGAT	NSDVAVLEAQ	EEEG.E.VGF	PVRPQVPLGP	
00BW3886_8	AASQDLDKHG	ALTSSNTPAN	NADCAWLETQ	EEAD..EVGF	PVRPQVPLRP	
00BW3891_6	AASQDLDKYG	ALTSSNTADT	NADCAWLQAA	EEEG.E.VGF	PVRPQVPLRP	
00BW3970_2	AASQDLDKHG	ALTSSNTAAT	NADCAWLEAQ	EEDG..DVGF	PVRPQVPLRP	
00BW5031_1	AASQDLDKHG	ALTSSNTAAT	NKDCAWLEAQ	EEEG.E.VGF	PVRPQVPLRP	
96BW01B21	AASQDLDKYG	ALTSSNTDPN	NAACAWLRAQ	EEEG.E.VGF	PVRPQVPLRP	
96BW0407	TASRDLDKYG	ALTSSNTPTN	NAACAWLEPQ	EEEE.E.VGF	PVRPQVPLRP	
96BW0502	AASQDLDKYG	ALTSSNTSTN	NADCAWLEAQ	EEEG..DVGF	PVRPQVPLRP	

96BW06_J4	APSQDLDKHG	ALTSSNTPAN	NADVAWLEPQ	EEEG..AVGF	PLRPQVPLKP
96BW11_06	AASQDLDKHG	ALTSSNTAAN	NADCAWLEAQ	EEEE...VGF	PVRPQVPLRP
96BW1210	SASKDLEKHG	ALTTSNTAAN	NPHCAWLEAQ	EEEE.E.VGF	PVRPQVPLRP
96BW15B03	AASQDLDKYG	AFTSSNTASN	NADCAWLEAQ	EEAD..EVGF	PVRPQVPLRP
96BW16_26	AEYQDLDKDR	ALTSSNTDTN	NAACAQ...Q	EEEE.E.VGF	PVRPQVPLRP
96BW17A09	AASQDLDKHG	ALTSSNTPAN	NADCAWLQAQ	EEDE..EVGF	PVRPQVPLRP
96BWM01_5	AVSQDLQDHG	AITSSNTATN	.ADCACLEAQ	EEEE.E.LGF	PVRPQMPLKP
96BWM03_2	AASQDLDKYG	ALTSSNTASN	NADCAWLEAQ	EEAN..EVGF	PVRPQVPLRP
98BWMC12_2	AASQDLDKYG	AMTTSNTAHN	NGDCAWLQAQ	EEEE..EVGF	PVRPQVPLRP
98BWMC13_4	AASQDLDKHG	ALTSSNTATT	NADCAWLEAQ	AEAE..KVGF	PVRPQVPLRP
98BWMC14_a	AASQDLDKYG	ALTSSNTATN	NAACAWLEAQ	EEAG..EVGF	PVKPQVPLRP
98BWM014_1	AASQDLDKHG	ALTTSNTASN	NAACAWLQAQ	EEDN.GDVGF	PVRPQVPLRP
98BWM018_d	AASRDLEKRG	AITTSNTAAN	NPACAWLEAQ	EEDG.D.VGF	PVRPQVPLRP
98BWM036_a	AASQDLDKHG	ALTTSNTASN	NADCAWLEAQ	EEEE.E.VGF	PVKPQVPLRP
98BWM037_d	AASQDLAKHG	AITSSNTATT	NADCAWLEAQ	EEGE..EVGF	PVRPQVPLRP
99BW3932_1	AASQDLANHG	ALTTSNTATN	NADCAWLQAQ	EEEE...VGF	PVRPQVPLRP
99BW4642_4	AASQDLDRHG	AITSSNTAAT	NADCAWLEAQ	EEAD..EVGF	PVRPQX...P
99BW4745_8	AASKDLDKHG	ALTSSNTAGT	NADCAWLQAQ	EEEG.E.VGF	PVRPQVPLRP
99BW4754_7	AASQDLDKYG	ALTSSNTAAT	NADCARLEAQ	EETE..EVGF	PVRPQVPLRP
99BWMC16_8	AASKDLEKHG	ALTTSNTVHN	NPDCAWLEAQ	EEEE.E.VGF	PVRPQVPLRP
A2_CD_97CD	AVSQDLARHG	AVTSSNTAAN	NPDCAWLEAQ	EEE...EVGF	PVRPQVPLRA
A2_CY_94CY	AVSQDLATHG	AVTSSNTAAT	NPDCAWVEAQ	EEES..EVGF	PVRPQVPLRP
A2D_97KR	AVSQDLATRG	AVTINNTAAT	NADSAWLEAQ	EEEE..EVGF	PVRPQVPLRP
A2G_CD_97C	AVSQDLARHG	AITSSNTAAN	NPDCAWLEAQ	QEDS..EVGF	PVRPQVPLRP
A_BY_97BL0	PVSQDXDKHG	AVTSSNTAAN	NADCAXLEAQ	X...EXEVGF	PVRPQVPLRP
A_KE_Q23	AVSQDLDKHG	AVTSKNINH.	.PSYAWLEAQ	E...DEDVGF	PVRPQVPLRP
A_SE_SE659	AVSQDLAKHG	AVTSSNINN.	.PSCVWLEAQ	E...EEEVGF	PVRPQVPLRP
A_SE_SE725	AVSQDLEKYG	AVTSSNVNH.	.PSCAWLEAQ	E...EEEVGF	PVRPHVPLRP
A_SE_SE753	AVSQDLDKYG	AITSSNINH.	.PSCVWLEAQ	E...DEGVGF	PVRPQVPLRP
A_SE_SE853	AVSQDLDRHG	AITSSNINH.	.PSCTWLEAQ	E...DEEVGF	PVKPQVPLRP
A_SE_SE889	AVSQDLDKHG	AVTSSNINH.	.PSCAWVEAQ	E...EEEVGF	PVRPQVPLRP
A_SE_UGSE8	AVSQDLEKHG	AITSSNINH.	.PSCTWLEAQ	AQE.DEEVGF	PVRPQVPLRP
A_UG_92UG0	AVSQDLDKHG	AVTSSNVNH.	.PSCVWLEAQ	E...EEEVGF	PVRPQVPLRP
A_UG_U455	AVSQDLDKYG	AVTSSNTSST	NASCWLEAQ	E...EGDVGF	PVRPQVPLRP
AC_IN_2130	AVSQDLDKHG	AVTSSNVNH.	.PSCVWLDAQ	E...EEEVGF	PVRPQVPLRP
AC_RW_92RW	AASQDLDKYG	ALTSSNTPSN	NADCAWLAAQ	EEEN.E.VGF	PVRPQVPLRP
AC_SE_SE94	AVSQDLDKHG	AITSSNINH.	.PSNTWLAAQ	E.E.EEEVGF	PVRPQVPLRP
ACD_SE_SE8	AASQDLDKYG	ALTSSNTVTN	NPDCAWLEAQ	KEEE.E.VGF	PVRPQVPLRP
ACG_BE_VI1	AVSQDLARHG	AVTSRNTSAT	NADCAWLEAQ	EDE...EVGF	PVRPQVPLRP
AD_SE_SE69	AASRDLEKRG	AITSSNTAQT	NPDCAWLEAQ	EED..GEVGF	PVRPQVPLRP
AD_SE_SE71	AVSQDLDKHG	AITSSNINH.	.PSCVWLEAQ	E...DEDVGF	PVRPQVPLRP
ADHK_NO_97	AASRDLEKRG	AIXINNLPNS	NSDSAWLEAQ	EE...EEVGF	PVRPQVPLRP
ADK_CD_MAL	AVSQDLDKCG	AAASSSPAAN	NASCEPPEEE	EE....VGF	PVRPQVPLRP
AG_BE_VI11	AVSRDLAKHG	AITSSNTVAT	NADCAWLEAQ	KEG...EEVGF	PVRPQVPLRP
AG_NG_92NG	AAPQDLARHG	AITSSNTAQT	NPDCAWLEAQ	QENS..EVGF	PVRQQVPLRP
AGHU_GA_VI	AVSQDLDKRG	AITTNNTVKT	NADCAWLEAQ	EDE...EVGF	PVRPQLPLRP
AGU_CD_Z32	AASQDLAKHG	AISSSNTATN	NPDCAWLEAQ	EESE..EVGF	PVRPQVPLRP
AJ_BW_BW21	AVSRDLDKHG	AITSSNTPTT	NADCAWLEAQ	TEAE.DEVGF	PVKPQVPLRP
B_AU_VH	AASRDLEKHG	AITSSN..IN	NADCVWLQAQ	EEE...EVGF	PVRPQVPLRP
B_CN_RL42	AVSRDLEKHG	AITSSNTAAT	NAACAWLEAQ	EEE...EVGF	PVRPQVPLRP
B_DE_D31	AVSRDLEKHG	AITSSNTPAT	NAACAWLEAQ	EEE...EVGF	PVKPQVPLRP
B_DE_HAN	AASRDLEKHG	AITSSNTATN	NAACAWLEAQ	EEE...EEGF	PVRPQVPLRP
B_FR_HXB2	AASRDLEKHG	AITSSNTAAT	NAACAWLEAQ	EEE...EVGF	PVTPQVPLRP
B_GA_OYI	AASRDLEKHG	AITSSNTAAT	NADCAWLEAQ	EDE...EVGF	PVRPQVPLRP
B_GB_CAM1	AVSRDLEKHG	AITSSNTAAT	NADCAWLEAQ	EEE...EVGF	PVRPQVPLRP
B_GB_GB8	AVSRDLEKHG	AITSSNTAAT	NADCAWLEAQ	EEE...EVGF	PVRPQVPLRP
B_GB_MANC	AVSRDLEKHG	AITSSNTAAT	NADCAWLEAQ	EEE...EVGF	PVRPQVPLRP
B_KR_WK	AASRDLEQRG	AITTSNTASN	NAACAWQEAQ	EEE...EVGF	PVRPQVPLRP
B_NL_3202A	AVSRDLEKHG	AITSSNTAAT	NADCAWLEAQ	EDE...EVGF	PVKPQVPLRP
B_TW_TWCYS	AVSRDLEKHG	AITSSNTAAT	NADCAWLEAQ	EEE...EVGF	PVRPQVPLRP

B_US_BC	AVSRDLEKHG	AITSSNTAAN	NADCAWLEAQ	EEE...EVGF	PVRPQVPLRP
B_US_DH123	AASRDLEKHG	AITSSNTAAT	NADCAWLEAQ	QEE...EEVGF	PVRPQIPLRP
B_US_JRCSF	AVSRDLEKHG	AITSSNTAAT	NADCAWLEAY	EDE...EVGF	PVRPQVPLRP
B_US_MNCG	AASRDLEKHG	ALTSSNTAAT	NADCAWLEAQ	EEE...EVGF	PVKPQVPLRP
B_US_P896	AVSRDLARHG	AITSSN..TN	NADIAWLEAQ	EEG...EVGF	PVRPQVPLRP
B_US_RF	AASRDLEKHG	TITSSNTAAN	NAACTWLEAQ	EDED.EEVGF	PVRPQVPLRP
B_US_SF2	AVSRDLEKHG	AITSSNTAAT	NADCAWLEAQ	EEE...EVGF	PVRPQVPLRP
B_US_WEAU1	AVSRDLAKHG	AITSSN..EN	NADCVWLKAQ	EDE...EVGF	PVRPQVPLRP
B_US_WR27	AVSRDLEKHG	AITSSNTAAT	NADCAWLEAQ	EEE...EVGF	PVRPQVPLRP
B_US_YU2	AVSRDLERHG	AITSSNTAAT	NADCAWLEAQ	EEE...EVGF	PVRPQVPLRP
BF1_BR_93B	AVSQDLERRG	AITSSNTGAN	NPDLAWLEAQ	EEEE...VGF	PVRPQVPLRP
C_BR_92BR0	PASQSDKYG	ALTSSSTPAN	NADCAWLEAQ	QEEE.E.VGF	PVRPQVPLRP
C_BW_96BW0	TASQDLDKHG	ALTSSNTAAN	NAACAWLEAQ	EEEE.E.VGF	PVRPQVPLRP
C_BW_96BW1	AASQDLDKHG	ALTSSNTAAN	NADCAWLEAQ	EEEE...VGF	PVRPQVPLRP
C_BW_96BW1	SASKDLEKHG	ALTSSNTAAN	NPHCAWLEAQ	EEEE.E.VGF	PVRPQVPLRP
C_BW_96BW1	AASQDLDKYG	AFTSSNTASN	NADCAWLEAQ	EEAD..EVGF	PVRPQVPLRP
C_ET_ETH22	AASRDLDKYG	ALTSSNTPAN	NPDCAWLEAQ	EEEE.E.VGF	PVRPQVPLRP
C_IN_93IN1	AASQDLDKHG	ALTSSNTDTT	NADCAWLRAQ	EEEG.E.VGF	PVTPQVPLRP
C_IN_93IN9	AASQDLDKYG	ALTSSNTDIT	NPDCAWLKAQ	EEEE.E.VGF	PVRPQVPLRP
C_IN_93IN9	AASQDLDKYG	ALTSSNTDTT	NADCAWLRAQ	EEEE.E.VGF	PVRPQVPLRP
C_IN_94IN1	AASQDLDKYG	ALTSSNTDTT	NADCAWLRTQ	EEEE.E.VGF	PVRPQVPLRP
C_IN_95IN2	AASQDLDRYG	ALTSSNTDTT	NTE.....	.EEE.G.VGF	PVRPQVPLRP
CRF01_AE_C	AASQDLDKHG	AITSSNMNN.	.ADCAWLEAQ	EE...EEVGF	PVRPQVPLRP
CRF01_AE_C	AVSQDLDKHG	AVTSSNINN.	.ADNVWLEAQ	EE...EEVGF	PVRPQVPLRP
CRF01_AE_C	AVSQDLDKHG	AVTSSNMNS.	.AASVWLEAQ	ED...EEVGF	PVRPQVPLRP
CRF01_AE_T	TVSQDLDKHG	AVTSSNMNN.	.DDCVWLGAQ	EE...EEVGF	PVRPQVPLRP
CRF01_AE_T	AVSQDLDKHG	AVTSSNMNN.	.ADCEWLRAQ	EE...EEVGF	PVRPQVPLRP
CRF01_AE_T	AVSQDLDKHG	AVTSSNMNN.	.ADCVWLRAQ	EE...EGVGF	PVRPQVPLRP
CRF01_AE_T	AVSRDLDKHG	AVTSSNMNN.	.ADSVWLRAQ	EED...EEVGF	PVRPQVPLRP
CRF01_AE_T	AVSQDLDKHG	AITSSNIDN.	.ADCVWLRAQ	ED...EEVGF	PVMPQVPLRP
CRF01_AE_T	AVSQDLDKHG	AVTSTNMDN.	.ADSVWLRAQ	EED...EEVGF	PVEPQVPLRP
CRF02_AG_F	AASQDLDRHG	AITSSNTADT	NADCAWLEAQ	EEE...EVGF	PVRPQVPLRP
CRF02_AG_F	AASQDLDRHG	AITSSNTAET	NADCAWLEAQ	EDE...EVGF	PVKPQVPLRP
CRF02_AG_G	AASQDLDKYG	AITSSNTAFT	NADCAWLEAQ	EEE...EVGF	PVRPQVPLRP
CRF02_AG_N	AASQDLDRHG	AITSSNTAQT	NPDCAWLEAQ	EDE...NVGF	PVRPQVPLRP
CRF02_AG_S	AASQDLDRHG	AITSSNTAAT	NAACAWLEAQ	EEE...EVGF	PVRPQVPLRP
CRF02_AG_S	AVSQDLDRHG	AITSRNTAHT	NADCAWLEAQ	EEE...EVGF	PVRPQVPLRP
CRF03_AB_R	PVSQDLDKYG	AVTSSNTAAN	NADCAWLEAQ	E...EEEVGF	PVRPQVPLRP
CRF03_AB_R	PVSQDLDKYG	AVTSSNTAAN	NADCAWLEAQ	K...EEEVGF	PVRPQVPLRP
CRF04_cpx_	AVSQDLDKHG	AITINNTAAT	NPDKTWLEAQ	EEEE...EVGF	PVRPQVPLRP
CRF04_cpx_	AVSRDLDKHG	AITSSNTAAT	NPDKAWLEAQ	EEDE...EVGF	PVRPQVPLRP
CRF04_cpx_	AVSQDLDKYG	AITSSNTAAT	NPDKAWLEAQ	EEEE...EVGF	PVRPQVPLRP
CRF05_DF_B	AVFQDLDRNG	AVTIRNTVAT	NPDMAWVEAQ	EEEE...VGF	PVKPQVPLRP
CRF05_DF_B	SVSQDLERRG	AITSSNTAAT	NADLAWVEAQ	EEEE...VGF	PVRPQVPLRP
CRF06_cpx_	AVSQDLDKHG	AITSSNTATT	NAACAWVEAQ	TEE...EVGF	PVRPQVPLRP
CRF06_cpx_	AVSQDLDKHG	AITSSNTPPT	NAACAWLEEQ	TED...EVGF	PVRPQVPLRP
CRF06_cpx_	AVSQDLDTHG	AITSSNTVTT	NAACAWLEAQ	TED...EVGF	PVRPQVPLRP
CRF06_cpx_	AASQDLAKHG	AITSSNTAAT	NADCAWLEAQ	SEDN.EEVGF	PVRPQVPLRP
CRF11_cpx_	AVSKDLEKFG	AITSSNTAHT	NDTCAWLEAQ	ED...EEVGF	PVRPQVPLRP
CRF11_cpx_	AASKDLERHG	AITSSNTSQN	NAACAWLEAQ	ED...EGVGF	PVRPQVPLRP
D_CD_84ZR0	AVSRDLERHG	AITSSNTATT	NAACAWVEAQ	EED...EEVGF	PVRPQVPLRP
D_CD_ELI	AVSRDLEKHG	AITSSNTAST	NADCAWLEAQ	EES...DEVGF	PVRPQVPLRP
D_CD_NDK	AVSRDLEKHG	AITSSNTAST	NDTCAWLEAQ	EES...EEVGF	PVRPQVPLRP
D_UG_94UG1	AASRDLEKHG	AITSSNTAQT	NDACAWLEAQ	EE...EEVGF	PVRPQVPLRP
F1_BE_VI85	AVSRDLDRRG	AITSSNTRTT	NPDLAWLEAQ	EEEE...VGF	PVRPQVPLRP
F1_BR_93BR	AVSQDLERRG	AITSSNTRAN	NPDLAWLEAQ	EEDE...VGF	PVRPQVPLRP
F1_FI_FIN9	AVSQDLERRG	AITSSNTGAT	NPDLAWLEAQ	EDEE...VGF	PVRPQVPLRP
F1_FR_MP41	AVSQDLDRRG	AVTSSNTAAT	NPDLAWLEAQ	EDEE...VGF	PVRPQVPLRP
F2_CM_MP25	AVSQDLDKRG	AITSSNTGAT	NADLAWLEAQ	EDEE...VGF	PVRPQVPLRP
F2KU_BE_VI	AVSQDLAKHG	AITSSNTSST	NPDCAWLEAQ	EEE...EVGF	PVGPQVPLRP

G_BE_DRCBL	AVSQDLDRHG	AITSRNTAGT	NPDCAWLEAQ	EEDS..EVGF	PVRPQVPLRP
G_NG_92NG0	AVSQDLARHG	AITSSNTATN	NPDCAWLEAQ	EEDS..DVGF	PVRPQVPLRP
G_SE_SE616	AVSQDLDRHG	AITSSNTAAN	NPDCAWLEAQ	EEDS..EVGF	PVRPQVPLRP
H_BE_VI991	AVSQDLDRRG	AVTINNIAASN	NADSAWLEAQ	EEE..EEVGF	PVRPQVPLRP
H_BE_VI997	AVSRDLDRRG	AVTINNTAAT	NPDVAWLEAQ	EEA..EEVGF	PVRPQVPLRP
H_CF_90CF0	AVSRDLDRRG	AVTINNTAST	NRDAAWLEAQ	EDG..EEVGF	PVRPQVPLRP
J_SE_SE702	AVSQDLAKHG	AITSSNTAAT	NDDCAWLEAQ	T..E.EEVGF	PVRPQXPLRP
J_SE_SE788	AVSQDLAKHG	AITSSNTAAT	NADCAWLEAQ	T..E.EEVGF	PVKPQIPLRP
K_CD_EQTB1	AVSQDLDKHG	AVTSSNTAFN	NPDCAWLEAQ	ED...EDVGF	PVRPQVPLRP
K_CM_MP535	AVSQDLARHG	AVTSSNTSHN	NPDCAWLEAQ	EE...EEVGF	PVRPQVPLRP
N_CM_YBF30	AASQDLANRG	AITIRNTRDN	NESIAWLEAQ	EEEE..EVGF	PVRPQVPLRP
O_CM_ANT70	QISRELAARG	GIPSSHTPQN	NAALAFLESH	QEEE...VGF	PVAPQVPLRP
O_CM_MVP51	AVSRELATRG	GISSSHTPQN	NAALAFLDHSH	KDED...VGF	PVRPQVPLRP
O_SN_MP129	QISRELAARG	GIPSSYTPQN	NAALAFLESH	QDEE...VGF	PVRPQVPLRP
O_SN_MP130	QISRELAARG	GISNSHTPQN	NAALAFLESH	QDED...VGF	PVRPQVPLRP
U_CD___83C	AASRDLEKYG	AITSSNTAET	NEACAQLEAA	QE.D.GEVGF	PVRPQVPLRP

101

150

00BW0762_1	MTYKGALDLG	FFLK.EKGGL	EGLIYSTKRK	EILDLWVYHT	QGYFPDWQNY
00BW0768_2	MTYKGAVDLS	WFLK.EKGGL	EGLIYSKKRQ	EILDLWVYNT	QGYFPDWQNY
00BW0874_2	MTFKGAFDLG	FFLK.EKGGL	EGLIWSQKRQ	DILDLWVYHT	QGYFPDWQNY
00BW1471_2	MTYKGAFDLG	FFLK.EKGGL	DGMIYSKKRQ	DILDLWVYNT	QGYFPDWQNY
00BW1616_2	MTYKAAFDLS	FFLK.EKGGL	DGLIYSKKRK	EILDLWVYHT	QGFFPDWQCY
00BW1686_8	MTYKGAFDLG	FFLK.EKGGL	EGLIYSKKRQ	EILDLWVYHT	QGYFPDWQNY
00BW1759_3	MTYKAAFDLG	FFLK.EKGGL	EGLIHSKQRQ	DILDLWVYHT	QGYFPDWQNY
00BW1773_2	MTYKAAFDLS	FLLK.EXGGL	EGLIYSKKRQ	EILDLWVYHT	QGFFPDWQNY
00BW1783_5	MTYKAAFDLS	FFLK.EKGGL	EGLIHSKQRQ	DILDLWVYNT	QGYFPDWQNY
00BW1795_6	MTYKAAFDLS	FFLK.EKGGL	DGLIYSRKRQ	EILDLWVYHT	QGFFPDWQNY
00BW1811_3	MTYKAAFDLS	FFLK.EKGGL	DGLIHSKKRQ	DILDLWVYHT	QGYFPDWQNY
00BW1859_5	MTYKAAFDLG	FFLK.EKGGL	DGLIYSKKRQ	EILDLWVYHT	QGFFPDWQNY
00BW1880_2	MTYKAAFDLS	FFLK.EKGGL	DGLIYSKKRQ	EILDLWVYNT	QGFFSDWQNY
00BW1921_1	MTYKAAFDLG	FFLK.EKGGL	EGLIYSKKRQ	EILDLWVYHT	QGYFPDWQNY
00BW2036_1	MTYKAAIDLS	FFLK.EKGGL	DGLIYSAKRQ	EILDLWVYHT	QGFFPDWQNY
00BW2063_6	MTMKGAVDLS	FFLK.EKGGL	EGLIYSKKRQ	EILDLWVYHT	QGFFPDWQNY
00BW2087_2	MTYKAAFDLS	FFLK.EKGGL	DGLIYSKQRQ	DILDLWVYNT	QGFFPDWQNY
00BW2127_2	MTYKAAFDLS	FFLK.EKGGL	EGLIYSKKRQ	EILDLWVYHT	QGFFPDWQNY
00BW2128_3	GTFKAAFDLS	FFLK.EKGGL	EGLIYSKKRQ	EILDLWVYHT	QGFFPDWQNY
00BW2276_7	MTYKAAFDLS	FFLK.EKGGL	EGLIYSRKRQ	EILDLWVYHT	QGYFPDWQNY
00BW3819_3	MTYKGAFDLS	FFLK.EKGGL	EGLIYSKKRQ	DILDLWVYNT	QGYFPDWQSY
00BW3842_8	MTYKGAVDLS	FFLK.EKGGL	DGLIYSQKRQ	DILDLVHHT	QGYFPDWQNY
00BW3871_3	MTYKGAFDLG	FFLK.EKGGL	EGLIYSKKRQ	EILDLWVYHT	QGYFPDWQNY
00BW3876_9	MTYKGAVDLS	FFLK.EKGGL	ERLIYSKKRQ	EILDLWVYHT	QGYFPDWQNY
00BW3886_8	MTYKGAFDLG	FFLK.EKGGL	EGLIYSKKRQ	EILDLWVYHT	QGYFPDWQNY
00BW3891_6	MTYKGAVDLS	FFLKXEKGGL	EGLIYSKKRQ	EILDLWVYHI	QGYFPDWQNY
00BW3970_2	MTYKGAFNLG	FFLK.EKGGL	DGLIYSKKRQ	EILDLWVYHT	QGFFPDWQNY
00BW5031_1	MTYKGAFDLG	WFLK.EKGGL	DGLIYSKKRQ	EILDLWVYHT	QGYFPDWQNY
96BW01B21	MTYKGAFDLG	FFLK.EKGGL	EGLIYSKKRQ	EILDLWVYNT	QGVFPDWQNY
96BW0407	MTYKAAVDLS	FFLK.EKGGL	GGLIYSNKRQ	DILDLWVYNT	QGYFPDWQNY
96BW0502	MTYKGAFDLG	FFLK.EKGGL	EGLVYSKKRQ	EILDLWVYHT	QGFFPDWQNY
96BW06_J4	MTYKGAVDLG	FFLK.EKGGL	EGLIYSKKRQ	EILDLWVYHT	QGYFPDWQNY
96BW11_06	MTYKAAFDLS	FFLK.EKGGL	EGLIYSRKRQ	EILDLWVYHT	QGFFPDWHNY
96BW1210	MTYKGAFDLS	FFLK.EKGGL	DGLIYSKKRQ	EILDLWVYNT	QGYFPDWQCY
96BW15B03	MTYKGAVDLS	FFLK.EKGGL	DGLIYSPKRQ	EILDLWVYHT	QGFFPDWHNY
96BW16_26	MTYKEAFDLS	FFLK.EKGGL	DGLIYSKKRQ	DILDLWVYNT	QGFLPDWQNY
96BW17A09	MTYKAAFDLS	FFLK.EKGGL	DGLIYSKKRQ	EILDLWVYHT	QGFFPDWQNY
96BWM01_5	VTYKAAFDLS	FFLK.KKGGL	EGLIYSKKRQ	NILDLWVYHT	QGFFPDWHNY
96BWM03_2	MTQKGAFDLG	FFLK.EKGGL	DGLIYSRKRQ	EILDLWVYHT	QGYFPDWQNY
98BWMC12_2	MTFKGALDLG	FFLK.EKGGL	DGLIHSKRRQ	DILDLWVYHT	QGYFPDWQNY
98BWMC13_4	MTYKGAVDLS	FFLK.EKGGL	DGLIYSKQRQ	DILDLWVYNT	QGYFPDWQNY
98BWMC14_a	MTYKAAFDLG	FFLK.EKGGL	EGLIYSKKRQ	EILDLWVYHT	QGFFPDWQNY

98BWM014_1	MTYKAAFDLG	FFLK.EKGGL	DGLIYSKKRQ	DILDLWVYNT	QGFFPDWQNY
98BWM018_d	MTYKAAFDLS	FFLK.EKGGL	DGLIYSKKRQ	DILDLWVYNT	QGFFPDWQNY
98BWM036_a	ITYKAAFDLS	FFLK.EKGGL	EGLIYSKKRQ	EILDLWVYNT	QGYFPDWQNY
98BWM037_d	MTYKGAFDLG	FFLK.EKGGL	DGLIHSKKRQ	DILDLWVYHT	QGYFPDWQNY
99BW3932_1	MTYKAAFDLS	FFLK.EKGGL	EGLIYSKQRQ	DILDLWVYNT	QGFFPDWHNY
99BW4642_4	MTYKAAFDLS	FFLK.EKGGL	DGLIYSRKRQ	DILDLWVYHT	QGFFPDWQNY
99BW4745_8	MTYKSAFDLS	FFLK.EKGGL	EGLIYSKKRQ	EILDLWVYHT	QGFFPDWQNY
99BW4754_7	MTYKAAFDLS	FFLK.EKGGL	DGLIHSKKRQ	EILDLWVHHT	QGFFPDWQNY
99BWMC16_8	MTYKAAVDLS	WFLK.EXGGL	DGLIHSQKRQ	EILDLWVYNT	QGYFPDWQNY
A2_CD_97CD	MTYKGAVDLS	HFLK.EKGGL	DGLIYSQRRQ	DILDLWVYNT	QGYFPDWQNY
A2_CY_94CY	MTFKGAFDLS	FFLK.EKGGL	DGLIYSQKRQ	DILDMWVYHT	QGYFPDWQNY
A2D_97KR	MTYKGAFDLS	HFLR.EKGGL	DGLIHSQKRQ	DILDLWVYHT	QGFFPDWQGY
A2G_CD_97C	MTYKSAFDLS	FFLK.EKGGL	DGLIYSKQRQ	DILDLWVYNT	QGFFPDWQNY
A_BY_97BL0	MTXXXXDXS	HFXK.EKGGL	DGLIYSKKRQ	XILDLXVYHT	QGYFPDWQNY
A_KE_Q23	MTYKGAVDLS	HFLK.KKGGL	DGLVYSRKRQ	EILDLWVYHT	QGYFPDWQNY
A_SE_SE659	MTYKAAVDLS	HFLK.EKGGL	DGLIYSRKRQ	EILDLWVHHT	QGFFPDWQNY
A_SE_SE725	MTYKGALDLS	HFLK.EKGGL	DGLIYSRRRQ	EILDLWVYNT	QGYFPDWQNY
A_SE_SE753	MTYKGALDLS	HFLK.EKGGL	DGLVYSKKRQ	EILDLWVHHT	QGYFPDWQNY
A_SE_SE853	MTYKGAFDLS	HFLK.EKGGL	DGLIYSRKRQ	EILDLWVYNT	QXYFPDWQNY
A_SE_SE889	MTYKGAVDLS	HFLK.EKGGL	DGLIYSRRRQ	EILDLWVYNT	QGYFPDWQNY
A_SE_UGSE8	MTYKGALDLS	HFLK.EKGGL	EGLIYSRKRQ	EILDLWVYHT	QGYFPDWHNY
A_UG_92UG0	MTYKAAFDLG	FFLK.EKGGL	DGLIYSKKRQ	EILDLWVYHT	QGYFPDWQNY
A_UG_U455	MTYKAAFDLS	FFLK.EKGGL	DGLIHSQKRQ	EILDLWVYHT	QGFFPDWQNY
AC_IN_2130	MTYKGALDLS	FFLK.EKGGL	DGLIYSRKRQ	EILDLWVYHT	QGFFPDWHNY
AC_RW_92RW	MTYKAAVDLS	FFLK.EKGGL	EGLIYSKKRQ	DILDLWVYNT	QGYFPDWQNY
AC_SE_SE94	MTYKGALDLS	HFLK.EKGGL	DGLIYSQQRQ	DILDLWVYNT	QGYFPDWQNY
ACD_SE_SE8	MTYKAAVDLS	FFLK.EKGGL	EGLIYSKKRQ	DILDLWVYNT	QGFFPDWQNY
ACG_BE_VI1	MTFKGALDLS	HFLK.EKGGL	DGLIYSRKRQ	EILDLWVYHT	QGYFPDWQNY
AD_SE_SE69	MTYKGAVDLS	HFLK.EKGGL	EGLVWSPKRQ	EILDLWVYHT	QGYFPDWQNY
AD_SE_SE71	MTYKAAVDLS	HFLK.EKGGL	DGLIYSRKRQ	DILDLWVYHT	QGFFPDWQCY
ADHK_NO_97	MTYKAAVDLS	HFLK.EKGGL	DGLIYSKKRQ	EILDLWVHNT	QGFFPDWQNY
ADK_CD_MAL	MTYKGAFDLS	HFLK.EKGGL	DGLVWSPKRQ	EILDLWVYHT	QGYFPDWQNY
AG_BE_VI11	MTYKAALDLS	HFLK.EKGGL	EGLIYSQQRQ	DILDLWVYNT	QGYFPDWQNY
AG_NG_92NG	MTYKAAFDLS	FFLK.EKGGL	DGLIYSKKRQ	DILDLWVYNT	QGYFPDWQNY
AGHU_GA_VI	MTFKGAFDLG	FFLK.EKGGL	DGLIHSQKRQ	DILDLWVYHT	QGYFPDWQNY
AGU_CD_Z32	MTFKGAFDLS	FFLK.EKGGL	DGLIYSKKRQ	EILDLWVYHT	QGFFPDWHNY
AJ_BW_BW21	MTYKGAFDLS	FFLK.EKGGL	DGLIYSKKRQ	EILDLWVYNT	QGFFPDWQNY
B_AU_VH	MTFKAAHDLS	FFLK.EQGGL	EGLIYSQRRQ	DILDLWIYHT	QGYFPDWQNY
B_CN_RL42	MTYKGALDLS	HFLR.EKGGL	EGLIYSQRRQ	DILDLWVYHT	QGYFPDWQNY
B_DE_D31	MTYKAAVDLS	HFLK.EKGGL	EGLVHSQKRQ	DILDLWVYHT	QGYFPDWQNY
B_DE_HAN	MTYKGALDLS	HFLK.EKGGL	EGLIYSPKRQ	EILDLWVYHT	QGYFPDWQNY
B_FR_HXB2	MTYKAAVDLS	HFLK.EKGGL	EGLIHSQRRQ	DILDLWIYHT	QGYFPD.QNY
B_GA_OYI	MTYKGALDLS	HFLK.EKGGL	EGLIYSQKRQ	DILDLWVYHT	QGYFPDWQNY
B_GB_CAM1	MTYKAALDIS	HFLK.EKGGL	EGLIYSQRRQ	DILDLWIYHT	QGYFPDWQNY
B_GB_GB8	MTYKAAVDLS	HFLK.EQGGL	DGLIYSPKRQ	EILDLWVYHT	QGYFPDWQNY
B_GB_MANC	MTFKGALDLS	HFLR.EKGGL	EGLVYSQKRQ	DILDLWVYHT	QGYFPDWQNY
B_KR_WK	MTYKSALDLS	HFLK.EKGGL	EGLVYSQKRQ	DILDLWVYHT	QGFFPDWQNY
B_NL_3202A	MTYKGALDLS	HFLK.EKGGL	EGLIYSQRRQ	DILDLWIYHT	QGYFPDWQNY
B_TW_TWCYS	MDYKGALDLS	HFLR.KEGGL	EGLVYSQKKE	DILDLWIYHT	QGFFPDWQNY
B_US_BC	ITYKAAVDIS	HFLK.EKGGL	EGLIFSQRRQ	DILDLWTYHT	QGYFPDWQNY
B_US_DH123	MTYKAALDLS	HFLK.EKGGL	EGLIYSQKRQ	DILDLWVYNT	QGYFPDWQNY
B_US_JRCSE	MTYKAAIDLS	HFLK.EKGGL	EGLIYSQKRQ	DILDLWIYHT	QGYFPDWQNY
B_US_MNCG	MTYKAALDLS	HFLK.EKGGL	DGLIYSQKRQ	DILDLWVYHT	QGYFPDWQNY
B_US_P896	MTYKAAVDLS	HFLK.EKGGL	EGLVHSQKRQ	DILDLWVYHT	QGFFPDWQNY
B_US_RF	MTFKAAVDLS	HFLK.EKGGL	DGLVFSQKRQ	DILDLWVYHT	QGYFPDWQNY
B_US_SF2	MTYKAALDIS	HFLK.EKGGL	EGLIWSQRRQ	EILDLWIYHT	QGYFPDWQNY
B_US_WEAU1	MTYKAAHDLS	HFK..EKGGL	EGLIYSQKRQ	DILDLWVYHT	QGFFPDWQNY
B_US_WR27	MTYKAAVDLS	HFLK.EKGGL	EGLIYSQKRQ	DILDLWVYHT	QGYFPDWQNY
B_US_YU2	MTHKAAMDLS	HFLK.EKGGL	EGLIHSQQRQ	DILDLWVYHT	QGYFPDWQNY
BF1_BR_93B	MTYKGALDLS	HFLK.EKGGL	EGLIYSKKRQ	EILDLWVYHT	QGYFPDWQNY



C_BR_92BR0	MTYKAVVDLS	FFLE.EKGGL	EGLIYSKKRQ	DILDLWVYNT	QGYFPDWQNY
C_BW_96BW0	MTYKAAVDLS	FFLK.EKGGL	EGIIYSKKRQ	DILDLWVYNT	QGYFPDWQNY
C_BW_96BW1	MTYKAAFGLS	FFLK.EKGGL	EGLIYSRKRQ	EILDLWVYHT	QGFFPDWHNY
C_BW_96BW1	MTYKGAFDLS	FFLK.EKGGL	DGLIYSKKRQ	EILDLWVYNT	QGYFPDWQCY
C_BW_96BW1	MTYKGAVDLS	FFLK.EKGGL	DGLIYSPKRQ	EILDLWVYHT	QGFFPDWHNY
C_ET_ETH22	MTYKAAFGLS	LFLK.EKGGL	EGLIYSKKRQ	EILDLWVYNT	QGFFPDWQNY
C_IN_93IN1	MTYKSAFDLS	FFLK.EKGGL	EGLIYSKKRQ	EILDLWVYHT	QGFFPDWQNY
C_IN_93IN9	MTFKEAVDLS	FFLK.EKGGL	EGLIYSKKRQ	EILDLWVYHT	QGYFPDWQNY
C_IN_93IN9	MTFKGAFDLS	FFLK.EKGGL	EGLIYSKKRQ	EILDLWVYHT	QGFFPDWQNY
C_IN_94IN1	MTFKGAFDLS	FFLK.EKGGL	EGLIYSKKRQ	EILDLWVYHT	QGYFPDWQNY
C_IN_95IN2	MTFKGALDLS	FFLK.EKGGL	EGLIYSKKRQ	EILDLWVYHT	QGYFPDWQNY
CRF01_AE_C	MTYKGAFDLS	FFLK.EKGGL	DGLIYSKKRQ	EILDLWVYHT	QGYFPDWQNY
CRF01_AE_C	MTYKGAFDLS	FFLK.EKGGL	DGLIHSKRRQ	EILDLWVHNT	QGYFPDWQNY
CRF01_AE_C	MTYKGAFDLG	FFLK.EKGGL	DGLIYSKKRQ	EILDLWVYNT	QGFFPDWQNY
CRF01_AE_T	MTYKGAFDLS	FFLK.EKGGL	DGLIYSKKRQ	EILDLWVYNT	QGFFPDWHNY
CRF01_AE_T	MTFKGAFDLS	FFLK.EKGGL	DGLIYSKKRQ	EILDLWVYNT	QGFFPDWQNY
CRF01_AE_T	MTYKGAFDLS	FFLK.EKGGL	EGLVYSKKRQ	EILDLWVYHT	QGFFPDWHNY
CRF01_AE_T	MTFKEAFDLS	FFLK.EKGGL	DGLIYSKKRQ	EILDLWVYNT	QGFFPDWQNY
CRF01_AE_T	MTYKGAFDLS	FFLK.EKGGL	DGLIYSKKRQ	EILDLWVYNT	QGFFPDWQNY
CRF01_AE_T	MTYKGAFDLS	FFLE.EKGGL	DGLVYSKKRQ	EILDLWVYNT	QGFFPDWQNY
CRF02_AG_F	MTYKAAFGLG	FFLK.EKGGL	DGLVYSKKRQ	EILDLWVYHT	QGFFPDWQNY
CRF02_AG_F	MTYKGAFDLG	FFLK.EKGGL	DGLIYSKKRQ	EILDLWVYHT	QGFFPDWQNY
CRF02_AG_G	MTYKGALDLS	HFLK.EKGGL	EGLIYSRKRQ	EILDLWVYHT	QGFFPDWHNY
CRF02_AG_N	MTYKGAVDLS	HFLK.EKGGL	DGLIYSKKRQ	EILDLWVYNT	QGFFPDWQNY
CRF02_AG_S	MTYKAAVDLS	HFLK.EKGGL	EGLIYSKKRQ	EILDLWVYHT	QGFFPDWQNY
CRF02_AG_S	MTYKAAVDLS	HFLK.EQGG	EGLIYSKKRQ	EILDLWVYHT	QGFFPDWQNY
CRF03_AB_R	MTYKGAFDLS	HFLK..KGGL	DGLIYSKKRQ	EILDLWVYHT	QGYFPDWQ..
CRF03_AB_R	MTYKGAFDLS	HFLK.EKGGL	DGLIYSKKRQ	EILDLWVYHT	QGYFPDWQNY
CRF04_cpx_	MTFKGALDLS	HFLK.EKGGL	DGLIYSKKRQ	EILDLWVYHT	QGFFPDWDNY
CRF04_cpx_	MTFKAALDLS	HFLK.EKGGL	DGLIYSKQRQ	DILDLWVYNT	QGYFPDWQNY
CRF04_cpx_	MTYKAAVDLS	HFLK.EKGGL	EGLIYSKKRQ	EILDLWVYNT	QGYFPDWQNY
CRF05_DF_B	MTYKAAVDLS	HFLK.EKGGL	EGLIYSKKRQ	DILDLWVYNT	QGYSPDWQNY
CRF05_DF_B	MTFKGALDLS	HFLK.EKGGL	DGLIWSRKRQ	KILDLWVYNT	QGYFPDWQNY
CRF06_cpx_	MTYKAAFGLS	FFLK.EKGGL	DGLIYSKKRQ	EILDLWVYNT	QGFFPDWQNY
CRF06_cpx_	MTFKGAFDLG	FFLK.EKGGL	DGLIYSKKRQ	EILDLWVYHT	QGYFPDWQNY
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CRF06_cpx_	MTYKAAFGLG	FFLK.EKGGL	DGLIYSKKRQ	EILDLWVYHT	QGFFPDWQNY
CRF11_cpx_	MTYKAAFGLG	FFLK.EKGGL	DGLIYSQKRK	EILDLWVYHT	QGFFPDWQY
CRF11_cpx_	MTYKGAFDLS	FFLK.EKGGL	DGLIYSKKRQ	EILDLWVHNT	QGFFPDWQNY
D_CD_84ZR0	MTYKAAVDLS	HFLR.KKGGL	EGLVYSQKRQ	DILDLWVYHT	QGFFPDWQNY
D_CD_ELI	MTYKEALDLS	HFLK.EKGGL	EGLIWSKKRQ	EILDLWVYNT	QGIFFPDWQNY
D_CD_NDK	MTYKEAVDLS	HFLK.EKGGL	EGLIWSKKRQ	EILDLWVYNT	QGIFFPDWQNY
D_UG_94UG1	MTYKEAVDLS	HFLK.EKGGL	EGLVWSPKRQ	EILDLWVYHT	QGFFPDWQNY
F1_BE_VI85	MTYKAAVDLS	HFLK.EKGGL	EGLIYSKKRG	DTLWVYHT	QGYFPDWQNY
F1_BR_93BR	MTYKGAVDLS	HFLK.EKGGL	EGLIYSKRRQ	EILDLWVYHT	QGYFPDWQNY
F1_FI_FIN9	MTYKGAFDLS	QFXX.EKGGL	EGLXYSKKRQ	EILDLWLYHT	QGYFPDWQNY
F1_FR_MP41	MTFKAARDLS	HFLK.EKGGL	EGLIYSKKRQ	EILDLWVYHT	QGFFPDWQNY
F2_CM_MP25	MTYKAALDLS	HFLK.EKGGL	EGLIYSRKRQ	EILDLWVYHT	QGYFPDWQNY
F2KU_BE_VI	MTYKGAFDLS	HFIK.EKGGL	DGLIYSKKRQ	EILDLWVYNT	QGYFPDWHNY
G_BE_DRCBL	MTYKAAFGLS	FFLK.EKGGL	DGLVYSKKRQ	EILDLWVYHT	QGFFPDWQNY
G_NG_92NG0	MTYKAAFGLS	FFLK.EKGGL	DGLIYSKRRQ	DILDLWVYNT	QGYFPDWQNY
G_SE_SE616	MTFKGAFDLS	FFLK.EKGGL	DGLIYSKKRQ	EILDLWVYNT	QGYFPDWQNY
H_BE_VI991	MTYKGAFDLS	HFLK.EKGGL	EGLIYSKKRQ	EILDLWVYNT	QGYFPDWHNY
H_BE_VI997	MTYKAALDLS	HFLK.EKGGL	DGLIYSKKRQ	EILDLWVYNT	QGYFPDWQNY
H_CF_90CF0	MTYKGAFDLS	HFLK.EKGGL	DGLIYSKQRQ	DILDLWVYNT	QGYFPDWQNY
J_SE_SE702	MTYKGAFDLS	FFLK.EKGGL	DGLIYSKKRQ	EILDLWVHNT	QGYFPDWQNY
J_SE_SE788	MTYKGAVDLS	FFLK.EKGGL	DGLIYSKKRQ	EILDLWVHNT	QGYFPDWQNY
K_CD_EQTB1	MTFKGAFDLG	FFLK.EKGGL	DGLIYSKRRQ	EILDLWVYHT	QGFFPDWQNY
K_CM_MP535	MTYKAAFGLG	FFLK.EKGGL	DGLIYSKKRQ	EILDLWVYHT	QGFFPDWQNY
N_CM_YBF30	ITYKQAFDLS	FFLK.DKGGL	EGLVWSRKRQ	DILDLWVYHT	QGILPDWHNY

O_CM_ANT70	MTYKGAFDLS	FFLK.EKGGL	EGLIYSHKRA	EILDLWVYNT	QGFFPDWQNY
O_CM_MVP51	MTFKAAFDLS	FFLK.EKGGL	DGLIYSHKRA	EILDLWIYHT	QGFFPDWQCY
O_SN_MP129	MTYKGAFDLS	FFLK.EKGGL	DGLIYSHKRA	EILDLWVYHT	QGFFPDWQGY
O_SN_MP130	MTYKGAFDLS	FFLK.EKGGL	DGLIYSPERA	EILDLWVYHT	QGFFPDWQNY
U_CD___83C	MTYKAAFDLG	FFLK.EKGGL	DGLIYSKKRQ	EILDLWVYNT	QGYFPDWQNY

	151			200
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96BW11_06	TPGPGVRYPL	TFGWCFKLVP	VD.PGEVEEA	NEGENNCLLH PMAQHGMEDD
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96BW16_26	TPGPGVRYPL	TFGWCFKLVP	VD.PREVEEA	TEGEDNCLLH PMNQHGMEDE
96BW17A09	TPGPGVRYPL	TFGWCFKLVP	VD.PREVEEA	NEGENNCLLH PMSQHGMEDD
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A2_CY_94CY	TPGPGVRYPL	TFGWCFKLVP	VE.PSEVEEA	TQGENNCLLH PICQHGMEDE

A2D__97KR	TPGPGIRYPL	TFGWCFKLVP	VS.PAEVEEA	TEGETNSLLH	PICQHGIEDP
A2G_CD_97C	TPGPGVRYPL	TFGWCFKLVP	MD.PAEVEEA	NKEENSSLLH	PICQHGMEDD
A_BY_97BL0	TPGPXIRFPL	TFXXCYKLVP	VD.PAEVEEA	TXGENNSLLH	PICQHGMDDDE
A_KE_Q23	TPGPGTRFPL	TFGWCFKLVP	VD.PDEVEKA	TEGENNSLLH	PICQHGMDDDE
A_SE_SE659	TPGPGIRFPL	TFGWCFKLVP	VD.PDEVEKD	TEGENNSLLH	PICQHGMDDDE
A_SE_SE725	TPGPGVRYPL	TFGWCFKLVP	VD.PDEVEQA	NEGENNSLLH	PMCQHGMDDDE
A_SE_SE753	TPGPGIRYPL	TFGWCFKLVP	VD.PDEVKKD	TEGENNSLLH	PMCQHGMDDDE
A_SE_SE853	TPGPGVRYPL	TFGWCFKLVP	VE.PEEVEKA	NEGENNSLLH	PICQHGMDDDE
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A_SE_UGSE8	TPGPGIRYPL	TFGWCFKLVP	VD.PDEVEKA	TEGENNSLLH	PMCQHGMDDDE
A_UG_92UG0	TPGPGIRYPL	TFGWCFKLVP	VD.EDEVEEA	TGGENNSLLH	PICQHGMDDDE
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AC_IN_2130	TPGPGVRYPL	TFGWCFKLVP	VD.PREVEEA	TGGEDNCLLH	PVCQHGMEDDE
AC_RW_92RW	TPGPGVRYPL	TFGWCFKLVP	VD.PREVEEA	NEGEDNCLLH	PLSQHGMEDDE
AC_SE_SE94	TPGPGIRYPL	TFGWCFKLVP	VN.PDEVEEA	TKGENNSLLH	PMCQHGMDDDK
ACD_SE_SE8	TPGPGTRYPL	TFGWCFKLVP	VD.PREVEEA	NEGENNCLLH	PMSQHGIEDDE
ACG_BE_VI1	TPGPGTRFPL	TFGWCFKLVP	MD.PTEVEEA	NEGENNCLLH	PISQHGMEDDE
AD_SE_SE69	TPGPGIRYPL	IFGWCFELVP	VD.PKEVEED	IG.ENSSLLH	PMHQHGMEDT
AD_SE_SE71	TPGPGTRFPL	TFGWCFKLVP	VD.PDEVEKA	TEGETNTLLH	PICQHGMDDDE
ADHK_NO_97	TPGPGERFPL	TFGWCFKLVP	VD.PQEVEKA	NDGENNCLLH	PMCQHGMEDDE
ADK_CD_MAL	TPGPGIRFPL	TFGWCFKLVP	MS.PEEVEEA	NEGENNCLLH	PISQHGMEDDA
AG_BE_VI11	IPGPGTRFPL	TFGWCFKLVP	MD.PAGIEKA	NEGENNSLLH	PICQHGMGDT
AG_NG_92NG	TPGPGTRFPL	TFRWCFKLVP	MD.PAEIEEA	NKGENNSLLH	PICQHGLEDA
AGHU_GA_VI	TPGPGIRYPL	CFGWCYKLVP	VD.PKEVEEA	TEGENNCLLH	PICQQGMDDG
AGU_CD_Z32	TPGPGTRYPL	CFGWCYKLVP	VD.PREVEEA	NTGENNCLLH	PMSQHGMDDDD
AJ_BW_BW21	TPGPGTRFPL	TFGWCFKLVP	VD.PKEVEEA	NEGENNCLLH	PLCQHGMEDDE
B_AU_VH	TPGPGTRYPL	TFGWCFKLVP	VE.PDQVEKA	NEGENISLLH	PMSLHGMEDK
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B_DE_HAN	TPGPGVRYPL	TFGWCFKLVP	VE.PDEEENS	.....SLLH	PASLHGTEDT
B_FR_HXB2	TPGPGVRYPL	TFGWCFKLVP	VE.PDKIEEA	NKGENTSLLH	PVSLHGMDDP
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B_GB_GB8	TPGPGTRFPL	TFGWCFKLVP	VE.PEEVEKA	NEGENNCLLH	PMSQHGIEDP
B_GB_MANC	TRGPGIRYPL	AFGWCFKLVP	VD.PEQVEEA	NEGENNSLLH	PMSLHGMDDP
B_KR_WK	TPGPGTRFPL	TFGWCFKLVP	VE.PEKVEEA	TVGKNNCLLH	PMNLHGMDDP
B_NL_3202A	TPGPGIRYPL	TFGWCFKLVP	VE.QEKIEEA	NEGENNSLLH	PMSQHGMDDP
B_TW_TWCYS	TPGPGVRYPL	TFGWCFKLVP	VE.PEQVEKA	NEGENXCLLH	PMSQHGMDDP
B_US_BC	TPGPGIRYPL	TFGWCFKLVP	VD.PEKIEEA	NEGENNSLLH	PMSQHGMDDP
B_US_DH123	TPGPGIRYPL	TFGWCFKLVP	VD.PEKVEEA	NEGENNCLLH	PISLHGMEDP
B_US_JRCSF	TAGPGVRFPL	TFGWCFKLVP	VD.PEKVEEA	NEGENNCLLH	PMSQHGMDDP
B_US_MNCG	TPGPGIRYPL	TFGWCFKLVP	VE.PEKIEEA	NKGENNCLLH	PMSQH.MDDP
B_US_P896	TPGPGIRYPL	TFGWCFKLVP	VE.PDEGENN	RE..DNSLLH	PANQHGVEDS
B_US_RF	TPGPGTRYPL	TFGWCFKLVP	VE.PDKVEEA	TEGENNSLLH	PICLHGMDDP
B_US_SF2	TPGPGIRYPL	TFGWCFKLVP	VE.PEKVEEA	NEGENNSLLH	PMSLHGMEDDA
B_US_WEAU1	TPGPGTRYPL	CFGWCYKLVP	VE.PEKVEEA	NEGENNSLLH	PMSLHGMDDH
B_US_WR27	TPGPGTRYPL	TFGWCFKLVP	LE.PDQVEEA	NKGENNCLLH	PMSQHGMDDP
B_US_YU2	TPG.GTRWPL	TFGWCFKLVP	VE.PEKIEEA	NAGENNCLLH	PMSQHGMDDP
BF1_BR_93B	TPGPGTRYPL	TLGWCFKLVP	VD.PEEVEKA	NEGENNCLLH	PMSQHGMEDDE
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C_BW_96BW1	TPGPGVRYPL	TFGWCFKLVP	VD.PGEVEEA	NEGEN.CLLH	PIAQHGMEDDE
C_BW_96BW1	TPGPGVRYPL	TFGWCFKLVP	VD.PGEVEEA	NGGEDNCLLH	PMSQHGIEDA
C_BW_96BW1	TPGPGVRYPL	TFGWCFKLVP	VD.PREVEEN	NQGENHCLLH	PMSQHGMNDP
C_ET_ETH22	TPGPGVRYPL	TFGWCFKLVP	VD.PSEVEEI	NEGENNCLLH	PASLHGMEDDE
C_IN_93IN1	TPGPGVRYPL	TFGWCFKLVP	VD.PREVEEA	NEGEDNCLLH	PVCQHGMEDDE
C_IN_93IN9	TPGPGVRYPL	TFGWCFKLVP	VD.PREVEEA	NEGEDNCLLH	PVCQHGMDDDE
C_IN_93IN9	TPGPGVRFPL	TFGWCFKLVP	VD.PREVEEA	NEGENNCLLH	PVCQHGMEDDE
C_IN_94IN1	TPGPGTRFPL	TFGWCFKLVP	VD.PREVEEA	NEGEDNCLLH	PVCQHGMEDD
C_IN_95IN2	TPGPGVRFPL	TFGWCFKLVP	VD.PREVEEA	NKGEDNCLLH	PVCQHGMEDD

CRF01_AE_C	TPGPGIRYPL	CFGWCYKLVP	VD.	PKEVEED	NKDESNCLLH	PMSQHGVDDE
CRF01_AE_C	TPGPGVRYPL	CFGWCFKLVP	VD.	PREVEED	NKGENNCLLH	PMSQHGIDDD
CRF01_AE_C	TPGPGTRYPL	CFGWCYKLVP	VD.	PREVEED	NKGENNCLLH	PMSQHGIEDE
CRF01_AE_T	TPGPGIRYPL	CFGWCFKLVP	VD.	PREVEED	NKGENNCLLH	PLSQHGIEDE
CRF01_AE_T	TPGPGIRYPL	CFGWCFKLVP	VD.	PREVEED	NKEENNCLLH	PMSQHGIDDE
CRF01_AE_T	TPGPGIRYPL	CFGWCFKLVP	VD.	PREVEED	NKGENNCLLH	PMSQHGIEDE
CRF01_AE_T	TPGPGIRFPL	CFGWCFKLVP	VD.	PREVEED	NKGENNCLLH	PMSQHGMGDG
CRF01_AE_T	TPGPGIRFPL	CFGWCFKLVP	VD.	QREVEED	NKGENNCLLH	PMSQHGIEDE
CRF01_AE_T	TPGPGVRLPL	CFGWCFKLVP	VD.	PREVEED	NKGENNCLLH	PMSQHGIEDE
CRF02_AG_F	TPGPGTRYPL	TFGWCFNLEP	ID.	PAEIEEA	NKEENNCLLH	PICQHGMEDE
CRF02_AG_F	TPGPGTRYPL	TFGWCFKLEP	MD.	PAEVEEA	NKGENNCLLH	PICQHGMEDE
CRF02_AG_G	TPGPGTRFPL	TFGWCFKLVP	MD.	PAVEEA	TEGENNSLLH	PICQHGIEDE
CRF02_AG_N	TPGPGTRFPL	TFGWCFKLVP	MD.	PAVEEA	NEGENNSLLH	PICQHGMEDE
CRF02_AG_S	TPGPGIRYPL	TFGWCFKLVP	MD.	PADIEKD	TEGENNSLLH	PICQHGMEDE
CRF02_AG_S	TPGPGIRYPL	TFGWCFKLVP	MD.	PAVEEA	NQGENNSLLH	PICQHGMEDE
CRF03_AB_R	...PGIRFPL	TFGWCFKLVP	VD.	PAVEEA	TEGENNSLLH	PICQHGMDDE
CRF03_AB_R	TPGPGIRFPL	TFGWCFKLVP	VD.	PDEVEEA	TEGENNSLLH	PICQHGMDDE
CRF04_cpx_	TPGPGERFPL	CFGWCFKLVP	VD.	PQEVEEA	TEGENTCLLH	PISQHGMEDE
CRF04_cpx_	TPGPGERFPL	CFGWCFKLVP	VD.	PQEVEEA	NEGENNSLLH	PISQHGMEDE
CRF04_cpx_	TPGPGTRFPL	CFGWCFKLVP	VD.	PQEVEEI	TAGEDNCLLH	PISQHGMEDE
CRF05_DF_B	TPGPGIRYPL	TLGWCFKLVP	VN.	PEEVEKA	NEGEDNCLLH	PMSLHGMEDD
CRF05_DF_B	TPGPGTRYPL	TFGWCFKLVP	VD.	PEEVEKA	NEGENKCLLH	PMHQHGMDDE
CRF06_cpx_	TPGPGTRFPL	TFGWCFKLVP	VD.	PEEVEEL	TKGENNSLLH	PICQHGAEDE
CRF06_cpx_	TPGPGIRYPL	TFGWCFKLVP	VD.	PREVEEE	TKGENNSLLH	PICQHGAEDE
CRF06_cpx_	TPGPGIRYPL	TFGWCFKLVP	VD.	PREVEED	TKGENNSLLH	PMSQHGMEDE
CRF06_cpx_	TPGPGIRYPL	TFGWCFKLVP	VD.	PKEVEEE	TKGENXSLLH	PMCQHGVDDE
CRF11_cpx_	TPGPGVRYPL	CFGWCYKLVP	VD.	PREVEEA	NEGENNSLLH	PMSQHGMDDE
CRF11_cpx_	TPGPGIRYPL	CFGWCYKLVP	VD.	PREVEEA	NEGENNSLLH	PMSQHGIEDE
D_CD_84ZR0	TPGPGIRYPL	TFGWCFKLVP	VD.	PEVVEKA	TEGEDNCLLH	PICQHGMEDE
D_CD_ELI	TPGPGIRYPL	TFGWCFKLVP	VD.	PQEVEED	TEGETNSLLH	PICQHGMEDE
D_CD_NDK	TPGPGIRYPL	TFGWCFKLVP	VD.	PQEVEEA	TEREDNCLLH	PMCQQGMEDP
D_UG_94UG1	TPGPGIRYPL	TFGWCFKLVP	ME.	PKEVEEN	TEGEDNCLLH	PINQHGMEDE
F1_BE_VI85	TPGPGIRYPL	TLGWCFKLVP	VD.	PEEVEKA	NEGENNSLLH	PMSQHGMEDE
F1_BR_93BR	TPGPGIRYPL	TMGWCFKLVP	VD.	PEEVEKA	NEGENNSLLH	PMSQHGMEDE
F1_FI_FIN9	TPGPGVRYPL	TFGWCFKLVP	VE.	PEEVEKA	NEGENNSLLH	PMSQHGMEDE
F1_FR_MP41	TPGPGIRFPL	TFGWCFKLVP	VD.	PDEVEKA	NEGENNSLLH	PMSQHGMDDE
F2_CM_MP25	TPGPGPRFPL	TFGWCFKLVP	VD.	PEEVEKA	NEGENNSLLH	PMSLHGMEDD
F2KU_BE_VI	TPGPGIRYPL	CFGWCFKLVP	MD.	PQEVEEA	NVGENNSLLH	PICQHGIDDT
G_BE_DRCBL	TPGPGTRVPL	TFGWCFKLVP	ME.	PSEVEEA	NKGENNCLLH	PICQHGMEDE
G_NG_92NG0	TPGPGTRLPL	TFGWCFKLVP	MD.	PAEIEEA	NKGENNCLLH	PICQHGMEDE
G_SE_SE616	TPGPGTRFPL	TFGWCFKLVP	MD.	PAVEEA	NKGENNCLLH	PICQHGMEDE
H_BE_VI991	TPGPGERYPL	TFGWCFKLVP	VD.	PQDVEKA	NEGENNSLLH	PMCQHGIEDP
H_BE_VI997	TPGPGEGYPL	TFGWCFKLIP	VD.	PQEVEEA	NEGENNSLLH	PICQHGMEDE
H_CF_90CF0	TPGPGERFPL	TFGWCFKLVP	VN.	PQEVEQA	NEGENNSLLH	PMSLHGMEDD
J_SE_SE702	TPGPGTXYPL	TFGWCFKLVP	VD.	PSEVEEA	NEGENNSLLH	PACQHGIEDE
J_SE_SE788	TPGPGIRYPL	TFGWCFKLVP	VD.	PSEVEEA	NEGENNSLLH	PICQHGIEDE
K_CD_EQTB1	TPGPGIRYPL	TFGWCFKLVP	VD.	PREVEEA	TEGENNSLLH	PVNQHGMEDE
K_CM_MP535	TPGPGIRYPL	TFGWCFKLVP	VD.	PAVEEET	TEGEDNCLLH	PINQHGMEDE
N_CM_YBF30	TPGPGIRYPL	TFGWCFKLVP	LS.	AAVEEA	NEGDNNCLLH	PICQHGADDD
O_CM_ANT70	TPGPGTRFPL	TFGWLFKLVP	VSEEEAERLG	NTCERANLLH	PACAHGFEDT	
O_CM_MVP51	TPGPGPRFPL	TFGWLFKLVP	VSAEEAERLG	NTNEDASLLH	PACNHGAEDA	
O_SN_MP129	TPGPGTRFPL	TFGWLFKLVP	VSEAAEELG	NKCDRASLLH	PACNHGFEDN	
O_SN_MP130	TPGPGTRFPL	TFGWLFKLVP	VSEAAEELG	NKCDRASLLH	PVCNHGFEDP	
U_CD_83C	TPGPGIRYPL	TFGWPFKLVP	VD.	PKEVEEA	NEGENNSLLH	PICQHGMDDE

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00BW0762_1	HREVLWKF	SSLARRHVAR	E.	LHPEYYKD	C.
00BW0768_2	EREVLWKF	SSLARRHVAR	E.	LHPEYYKD	C.
00BW0874_2	DREVLWQFD	SSLVRRHVAR	E.	LHPEYYKD	C.
00BW1471_2	DREVLWVFD	SSLARRHVAR	E.	LHPEYYKD	C.

00BW1616_2	DREVLRWKFD	SSLARRHLAR	E.LHPEYYKD	C.
00BW1686_8	DREVLWKFD	SHLAYRHMAR	E.LHPEYYKD	C.
00BW1759_3	HGEVLMWKFD	SALARRHMAR	E.LHPEYYKD	C.
00BW1773_2	HGEVLKWKFD	SSLARRHLAR	E.KHPEFYKD	C.
00BW1783_5	DKEVLQWKFD	SSLARRHMAR	E.LHPEYYKD	C.
00BW1795_6	DREVLWKFD	SHLARRHTAR	E.LHPEFYKD	CR
00BW1811_3	HGEVLEWKFD	SMLARRHMAR	E.LHPEYYKD	C.
00BW1859_5	EREVLRWKFD	SQLARRHMAR	E.LHPEYYKD	C.
00BW1880_2	HKEVLRWKFD	SSLARRHLAR	E.LHPEYYKD	C.
00BW1921_1	DREVLWKFD	SQLAHRHLAR	E.KHPEWYKD	C.
00BW2036_1	HKEVLTWKFD	SHLARRHMAR	E.LHPEYYKD	C.
00BW2063_6	HREVLQWKFD	SQLARRHIAR	E.RHPEYYKD	C.
00BW2087_2	DREVLKWVFD	SSLARRHLAR	E.KHPEFYKD	C.
00BW2127_2	EREVLQWKFD	SLLSRRHLAR	IXIHAEYYKD	C.
00BW2128_3	HGEVLMWKFD	SHLAYRHMAR	E.KHPEFYKD	C.
00BW2276_7	EREVLKWKFD	SSLARRHMAR	E.LHPEYYKA	C.
00BW3819_3	EGEVLQWKFD	SLLAYRHMAR	E.QHPEYYKD	C.
00BW3842_8	DREVPMWKFD	SLLAHRHMAR	E.LHPGYKD	C.
00BW3871_3	DREVLWKFD	SHLVHRHMAR	E.LHPEYYKG	C.
00BW3876_9	DREVLRWKFD	S.LARRHIAR	E.LHPEYYKN	C.
00BW3886_8	EREVLKWKFD	SQLAYRHMAR	E.IHPEYYKD	C.
00BW3891_6	DREVLRWKFD	SHLARRHMAR	E.LHPEWYKD	C.
00BW3970_2	DREVLKWQFD	ISLARRHMAR	E.LHPEWYKD	..
00BW5031_1	DREVLRWKFD	SELARRHIAR	E.RHPEFYKD	C.
96BW01B21	HREVLKWKFD	SQLARRHMAR	E.LHPEYYKD	C.
96BW0407	DREVLRWKFD	SSLAHRHMAR	E.LHPEYYKD	C.
96BW0502	HGEVLKWKFD	SQLARRHMAR	E.LYPEYYKD	C.
96BW06_J4	EREVLTWKFD	SHLVHRPMAR	E.IHPEYYKD	C.
96BW11_06	HKEVLKWKFD	SQLARRHLAR	E.LHPEFYKD	C.
96BW1210	DREVLKWKFD	SSLARRHLTR	E.KHPEYYKD	C.
96BW15B03	DKEVLMWKFD	SHLARRHMAR	E.LHPEYYKD	C.
96BW16_26	ERGVLKWKFD	SHLARRHMAR	E.LHPEYYKD	C.
96BW17A09	DREVLKWVFD	SHLARKHMAR	E.LHPEYYKN	C.
96BWM01_5	HREVLKWKFD	SSLARRHMAR	E.LHPEFYKD	C.
96BWM03_2	HGEVLMWKFD	SQLARRHMAR	E.LHPEYYKD	C.
98BWMC12_2	EREVLKWQFD	SSLARRHMAR	E.LHPEYYKD	C.
98BWMC13_4	GKEVLIWKFD	SHLARRHMAR	E.LHPEFYKD	C.
98BWMC14_a	DREVLWKFD	SQLARRHIAR	E.IHPEYYKD	C.
98BWM014_1	EKEVLKWVFD	SSLARRHVAR	E.LHPEFYKD	C.
98BWM018_d	DREVLRWKFD	SSLARRHMAR	E.LHPEYYKD	C.
98BWM036_a	DREVLKWEFD	IRLAHTHMAR	Q.LHPEFYKN	C.
98BWM037_d	DREVLKWQFD	SSLAHRHVAR	E.LHPEYYKD	C.
99BW3932_1	DREVLKWKFD	SMLARRHMAR	E.LHPEFYKD	C.
99BW4642_4	DREVLWKYD	SQLARRHMAR	E.LHPDYYKD	C.
99BW4745_8	DREVLRWKFD	SHLARRHMAR	E.LHPEFYKD	C.
99BW4754_7	HKEVLKWKFD	SHLARRHMAR	E.LHPEFYKD	C.
99BWMC16_8	DREVLKWQFD	SSLARRHMAR	E.LHPEYYKD	C.
A2_CD_97CD	EREVLKWKFD	SRLALRHLAR	E.QHPEFYKD	C.
A2_CY_94CY	EREVLWEFD	RSLARRHRAR	E.LHPEYYKD	C.
A2D_97KR	EREVLKWVFD	SHLALVHKAR	E.LHPEFYKD	C.
A2G_CD_97C	DKQVLGWRFD	SSLARRHIAR	E.KHPEYYKD	C.
A_BY_97BL0	EKEVLMWKFD	SRLALKHRAR	E.LHPEFYKD	C.
A_KE_Q23	EREVLKWKFD	SRLALKHRAR	E.LHPEWYKD	C.
A_SE_SE659	EKEVLKWKFD	SRLALKHLAC	E.KHPEFYKD	C.
A_SE_SE725	EKETLRWRFD	SRLALRHRAQ	E.MHPEFYKD	C.
A_SE_SE753	EREVLKWKFD	SRLALKHRAQ	E.LHPEFYKD	C.
A_SE_SE853	ERETLMWKFD	SKLALKHRAH	E.LHPEYFKN	C.
A_SE_SE889	ERETLMWKFD	SRLALTHRAR	E.LHPEFYKD	C.
A_SE_UGSE8	ERETLMWKFD	PHLAFKHRAR	E.LHPEYYKN	..
A_UG_92UG0	EKETLRWKFD	SSLARVHKAR	E.LHPEFYKD	C.

A_UG_U455	EKEVLMWKFD	STLALKHRAY	E.LHPEFYKD	..
AC_IN_2130	YGEVLQWKFD	SHLAYKHQAR	E.RHPEFYKD	C.
AC_RW_92RW	DREVLKWKFD	SHLAHRHMAR	E.LHPEYYKD	C.
AC_SE_SE94	ERETLVWRFD	SRLALKHLAR	E.KHPEFYKD	C.
ACD_SE_SE8	DKEVLRWKFD	SQLARRHMAR	E.MHPEYYKD	C.
ACG_BE_VI1	DREVLVWRFD	SRLALKHIAK	E.KHPEYFKD	C.
AD_SE_SE69	EREVLMWRFN	SRLAFEHKAH	Q.LHPEYYKD	C.
AD_SE_SE71	EKEVLKWQFD	SRLALKHLAR	E.KHPEFYKD	C.
ADHK_NO_97	EXEVLMWRFD	SRLAFKHRAR	E.LHPEFYKD	C.
ADK_CD_MAL	EREVLKWKFD	SSLALRHRAR	E.QHPEYYKD	C.
AG_BE_VI11	EREVLVWKFD	SMLAFKHRAR	E.LHPEYYKD	C.
AG_NG_92NG	DREVLVWRFD	SSLARRHIAR	E.QHPEYYKD	C.
AGHU_GA_VI	EREVLMWKFD	SSLAREHVAR	K.LYPEFFKD	C.
AGU_CD_Z32	EREVLMWKFD	SSLARKHLAR	E.MHPEFYKD	..
AJ_BW_BW21	DREVLMWKFD	SSLARRHLAR	E.KHPEFYKD	C.
B_AU_VH	EKEVLMWKFD	SRLAVHHMAR	E.LHPEYYKN	..
B_CN_RL42	EREVLMWKFD	SRLAIHHMAR	E.MHPEYHKD	C.
B_DE_D31	EREVLVWRFD	SRLAFKHMAR	E.LHPEYYKN	..
B_DE_HAN	EREVLKWKFD	SHLAFHHKAR	E.LHPEYYKD	C.
B_FR_HXB2	EREVLEWRFD	SRLAFHHVAR	E.LHPEYFKN	C.
B_GA_OYI	EKEVLVWKFD	SRLAFRHMAR	E.VHPEYYKD	C.
B_GB_CAM1	EKEVLMWKFD	SRLAFHHMAR	E.KHPEFYKD	C.
B_GB_GB8	EKEVLVWKFN	SRLAFHHMAR	E.LHPEFYKD	C.
B_GB_MANC	EKEVLVWKFD	SRLAFHHVPD	E.LHPEYYKD	C.
B_KR_WK	EGEVLVWRFD	SRLAFHHMAR	E.KHPEYYKD	C.
B_NL_3202A	EREVLEWRFD	SRLAFHHMAR	E.LHPEYYKD	C.
B_TW_TWCYS	EKEVLVWRFD	STLAFHHRAR	E.LHPEYYKX	C.
B_US_BC	EREVLEWRFD	SRLAFHHMAR	E.LHPEYYKN	R.
B_US_DH123	EKEVLLWKFD	SRLAYHHMAR	E.LHPEYYKN	C.
B_US_JRCSF	EKEVLVWKFD	SKLALHHVAR	E.LHPEYYKD	C.
B_US_MNCG	EREVLVWKS	SHLAFQHYAR	E.LHPEYYKN	C.
B_US_P896	ERQVLVWRFD	SRLAFHHVAR	E.LHPEYFKN	..
B_US_RF	EKEVLVWKFD	SRLAFHHVAR	E.KHPEYYKD	C.
B_US_SF2	EKEVLVWRFD	SKLAFHHMAR	E.LHPEYYKD	C.
B_US_WEAU1	EKEVLMWKFD	SKLAFHHVAR	E.LHPEYFKD	C.
B_US_WR27	EKEVLVWKFD	SRLAFHHKAR	E.LHPEYYKN	..
B_US_YU2	EREGLEWRFD	SRLAFHHVAR	E.LHPEYYKN	..
BF1_BR_93B	DREILQWRFD	SRLAFHHMAR	E.LHPEYYKD	C.
C_BR_92BR0	HREVLQWKFD	SLLARRHMAR	E.LHPEYYKD	C.
C_BW_96BW0	DGEVLRWKFD	SHLAHRHMAR	E.LHPEYYKD	C.
C_BW_96BW1	HKEVLKWKFD	SQLARRHLAR	E.LHPEFYKD	C.
C_BW_96BW1	DREVLKWKFD	SSLARRHLTR	E.KHPEYYKD	C.
C_BW_96BW1	DKEVLKWKFD	SHLARRHMAR	E.LHPEYYKD	C.
C_ET_ETH22	DREVLKWKFD	SHLARRHMAR	E.LHPEYYKD	C.
C_IN_93IN1	HREVLKWKFD	SQLARRHMAR	E.LHPEFYKD	C.
C_IN_93IN9	HREVLQWKFD	SLLAHRHRAR	E.LHPEFYKD	C.
C_IN_93IN9	HREVLQWKFD	SHLAHRHMAR	E.LHPEYYKD	C.
C_IN_94IN1	HREVLWK..	QLAHRHIAR	E.LHPEFYKD	C.
C_IN_95IN2	HNEVLVWKFD	SQLAHKHRAR	E.LHPEFYNK	DC
CRF01_AE_C	EREVLMWKFD	SSLARRHIAR	E.LRPEYYKD	C.
CRF01_AE_C	EREVLMWKFD	SSLARRHIAR	E.LHPEYYKD	..
CRF01_AE_C	EREVLMWKFD	SSLARRHIAR	E.LHPEYYKD	C.
CRF01_AE_T	EREVLMWKFD	SALARKHTAR	E.LHPEYYKD	C.
CRF01_AE_T	EREVLMWKFD	STLARKHIAR	E.QHPEFYKD	C.
CRF01_AE_T	EREVLIWKFD	SALARRHIAR	E.LRPEFYKD	C.
CRF01_AE_T	EREVLMWKFD	SALARKHIAR	E.MHPEYYKD	C.
CRF01_AE_T	EREVLMWKFD	SALARKHVAR	E.QHPEYYKD	C.
CRF01_AE_T	EREVLIWKFD	SSLARKHLAR	E.LHPEYYKD	C.
CRF02_AG_F	DREVLVWRFD	SSLARTHVAR	E.LHPEYYKD	C.
CRF02_AG_F	DREVLVWRFD	SSLARRHIAR	E.RHPEFYKD	C.

CRF02_AG_G	DREVLVWRFD	SSLAFTHRAR	E.MHPEFYKD	C.
CRF02_AG_N	DREVLWRFD	SRLAFRHTAR	E.LHPEYYKD	C.
CRF02_AG_S	DREVLVWRFD	SRLAFTHKAR	E.MHPEFYKD	CX
CRF02_AG_S	DREVLVWRFD	SRLAFRHTAR	E.LHPEYYKD	C.
CRF03_AB_R	EKEVLMWKFD	SRLALTHRAR	E.LHPEFYKD	C.
CRF03_AB_R	EKEVLMWKFD	SRLALTHRAR	E.LHPEFYKD	C.
CRF04_cpx_	EREVLKWKFD	SRLAYKHVAR	E.LHPEFYKD	C.
CRF04_cpx_	EREVLKWKFD	SRLAFKHVAR	E.LHPEFYKD	C.
CRF04_cpx_	EREVLKWKFD	SLLAYRHVAR	E.LHPEFYKD	C.
CRF05_DF_B	DREVLQWKFD	SSLALRHIAR	E.RHPEFYQD	..
CRF05_DF_B	DGEVLRWKFD	SSLALKHIAR	E.RRPEFYQD	..
CRF06_cpx_	EREVLKWKFD	SSLARRHIAR	E.KHPEFYKD	C.
CRF06_cpx_	EGEVLWKFD	SSLARRHIAR	E.LHPDFYKD	C.
CRF06_cpx_	EREVLWKFD	SSLARRHTAR	E.MHPEFYKD	C.
CRF06_cpx_	EKEVLMWKFD	SSLARRHIAX	E.XHPEFXKD	C.
CRF11_cpx_	EREVLKWKFD	SSLARKHIAR	E.LHPDFYKD	..
CRF11_cpx_	DREVLRWKFD	SSLARRHIAR	E.LHPDFYKD	..
D_CD_84ZR0	EKEVLVWRFN	SRLAFEHKAK	E.KYPEYFKN	C.
D_CD_EL1	ERQVLKWRFN	SRLAFEHKAR	E.MHPEFYKN	..
D_CD_NDK	ERQVLMWRFN	SRLALEHKAR	E.LHPEFYKD	C.
D_UG_94UG1	EREVLVWRFN	SRLAFEHKAK	M.KHPEYYKD	C.
F1_BE_VI85	DREVLRWKFD	SSLALRHIAR	E.RHPEFYQD	..
F1_BR_93BR	DKEVLKWEFD	SRLALRHIAR	E.RHPEYYQD	..
F1_FI_FIN9	DREVLKWKFD	SRLALKHIAR	E.RHPEFYRD	..
F1_FR_MP41	DREVLWWEFD	SRLAFRHIAR	E.KHPEFYQN	..
F2_CM_MP25	DKEVLKWKFD	SRLALRHIAR	E.RHPEYYKD	..
F2KU_BE_VI	EREVLVWKFD	SRLALKHLAR	E.KHPEYYKD	C.
G_BE_DRCBL	DGEVLVWRFD	SSLARRHLAR	E.LHPEYYKD	C.
G_NG_92NG0	DREVLVWRFN	SSLARRHLAR	E.LHPEYYKD	C.
G_SE_SE616	DREVLVWRFD	SSLARRHIAR	E.LHPEYYKD	C.
H_BE_VI991	EREVLWKFD	SRLALRHRAR	E.LHPEFYKD	C.
H_BE_VI997	EGEVLWKFD	SRLAFTHVAR	E.KHPEFYKD	C.
H_CF_90CF0	EREVLWKFD	SRLALTHLAR	V.KHPEY.KD	C.
J_SE_SE702	EREVLKWKFD	SSLARRHIAR	E.LHPEFYKD	C.
J_SE_SE788	EREVLQWKFD	SSLARRHIAR	E.LHPEFYKD	C.
K_CD_EQTB1	HREVLKWKFD	SSLARKHVAR	E.MHPEYYKD	..
K_CM_MP535	HREILMWKFD	SSLARRHVAR	E.LHPDYYKD	..
N_CM_YBF30	HKEVLVWRFD	SSLARRHVAR	E.LHPEFYKN	C.
O_CM_ANT70	HKEILMWKFD	RSLGNTHVAR	ITHPELFQKD	..
O_CM_MVP51	HGEILKWKFD	RSLGLTHIAL	QKHPELFPSN	..
O_SN_MP129	HGQILKWKFD	RSLGSTHVAR	VTNPELFNKD	..
O_SN_MP130	HKEMLKWKFD	RSLGSTHVAL	ITHPELFLKD	..
U_CD_83C	EKEVLMWKFD	SSLARRHLAR	E.LHPEFYKD	C.

Table 14. HIV Pol Sequence Alignment

GCG Multiple Sequence File.

Written by Omega 1.1

Name: 00BW0762_1	<u>SEQ ID NO: 803</u>	Len: 1046	Check: 4376	Weight: 1.00
Name: 00BW0768_2	<u>SEQ ID NO: 804</u>	Len: 1046	Check: 8430	Weight: 1.00
Name: 00BW0874_2	<u>SEQ ID NO: 805</u>	Len: 1046	Check: 8925	Weight: 1.00
Name: 00BW1471_2	<u>SEQ ID NO: 806</u>	Len: 1046	Check: 1324	Weight: 1.00
Name: 00BW1616_2	<u>SEQ ID NO: 807</u>	Len: 1046	Check: 935	Weight: 1.00
Name: 00BW1686_8	<u>SEQ ID NO: 808</u>	Len: 1046	Check: 8131	Weight: 1.00
Name: 00BW1759_3	<u>SEQ ID NO: 809</u>	Len: 1046	Check: 579	Weight: 1.00
Name: 00BW1773_2	<u>SEQ ID NO: 810</u>	Len: 1046	Check: 1975	Weight: 1.00
Name: 00BW1783_5	<u>SEQ ID NO: 811</u>	Len: 1046	Check: 216	Weight: 1.00
Name: 00BW1795_6	<u>SEQ ID NO: 812</u>	Len: 1046	Check: 5932	Weight: 1.00
Name: 00BW1811_3	<u>SEQ ID NO: 813</u>	Len: 1046	Check: 6525	Weight: 1.00
Name: 00BW1859_5	<u>SEQ ID NO: 814</u>	Len: 1046	Check: 2879	Weight: 1.00
Name: 00BW1880_2	<u>SEQ ID NO: 815</u>	Len: 1046	Check: 7093	Weight: 1.00
Name: 00BW1921_1	<u>SEQ ID NO: 816</u>	Len: 1046	Check: 2524	Weight: 1.00
Name: 00BW2036_1	<u>SEQ ID NO: 817</u>	Len: 1046	Check: 8279	Weight: 1.00
Name: 00BW2063_6	<u>SEQ ID NO: 818</u>	Len: 1046	Check: 3935	Weight: 1.00
Name: 00BW2087_2	<u>SEQ ID NO: 819</u>	Len: 1046	Check: 7898	Weight: 1.00
Name: 00BW2127_2	<u>SEQ ID NO: 820</u>	Len: 1046	Check: 728	Weight: 1.00
Name: 00BW2128_3	<u>SEQ ID NO: 821</u>	Len: 1046	Check: 5356	Weight: 1.00
Name: 00BW2276_7	<u>SEQ ID NO: 822</u>	Len: 1046	Check: 9456	Weight: 1.00
Name: 00BW3819_3	<u>SEQ ID NO: 823</u>	Len: 1046	Check: 6369	Weight: 1.00
Name: 00BW3842_8	<u>SEQ ID NO: 824</u>	Len: 1046	Check: 4573	Weight: 1.00
Name: 00BW3871_3	<u>SEQ ID NO: 825</u>	Len: 1046	Check: 6948	Weight: 1.00
Name: 00BW3876_9	<u>SEQ ID NO: 826</u>	Len: 1046	Check: 6609	Weight: 1.00
Name: 00BW3886_8	<u>SEQ ID NO: 827</u>	Len: 1046	Check: 8244	Weight: 1.00
Name: 00BW3891_6	<u>SEQ ID NO: 828</u>	Len: 1046	Check: 5718	Weight: 1.00
Name: 00BW3970_2	<u>SEQ ID NO: 829</u>	Len: 1046	Check: 3940	Weight: 1.00
Name: 00BW5031_1	<u>SEQ ID NO: 830</u>	Len: 1046	Check: 2442	Weight: 1.00
Name: 96BW01B21	<u>SEQ ID NO: 831</u>	Len: 1046	Check: 2358	Weight: 1.00
Name: 96BW0407	<u>SEQ ID NO: 832</u>	Len: 1046	Check: 8537	Weight: 1.00
Name: 96BW0502	<u>SEQ ID NO: 833</u>	Len: 1046	Check: 3948	Weight: 1.00
Name: 96BW06_J4	<u>SEQ ID NO: 834</u>	Len: 1046	Check: 7173	Weight: 1.00
Name: 96BW11_06	<u>SEQ ID NO: 835</u>	Len: 1046	Check: 973	Weight: 1.00
Name: 96BW1210	<u>SEQ ID NO: 836</u>	Len: 1046	Check: 5817	Weight: 1.00
Name: 96BW15B03	<u>SEQ ID NO: 837</u>	Len: 1046	Check: 5157	Weight: 1.00
Name: 96BW16_26	<u>SEQ ID NO: 838</u>	Len: 1046	Check: 3303	Weight: 1.00
Name: 96BW17A09	<u>SEQ ID NO: 839</u>	Len: 1046	Check: 1256	Weight: 1.00
Name: 96BWM01_5	<u>SEQ ID NO: 840</u>	Len: 1046	Check: 5593	Weight: 1.00
Name: 96BWM03_2	<u>SEQ ID NO: 841</u>	Len: 1046	Check: 3661	Weight: 1.00
Name: 98BWMC12_2	<u>SEQ ID NO: 842</u>	Len: 1046	Check: 7159	Weight: 1.00
Name: 98BWMC13_4	<u>SEQ ID NO: 843</u>	Len: 1046	Check: 3254	Weight: 1.00
Name: 98BWMC14_a	<u>SEQ ID NO: 844</u>	Len: 1046	Check: 5638	Weight: 1.00
Name: 98BWM014_1	<u>SEQ ID NO: 845</u>	Len: 1046	Check: 7680	Weight: 1.00
Name: 98BWM018_d	<u>SEQ ID NO: 846</u>	Len: 1046	Check: 1619	Weight: 1.00
Name: 98BWM036_a	<u>SEQ ID NO: 847</u>	Len: 1046	Check: 8852	Weight: 1.00
Name: 98BWM037_d	<u>SEQ ID NO: 848</u>	Len: 1046	Check: 4750	Weight: 1.00
Name: 99BW3932_1	<u>SEQ ID NO: 849</u>	Len: 1046	Check: 5391	Weight: 1.00
Name: 99BW4642_4	<u>SEQ ID NO: 850</u>	Len: 1046	Check: 1514	Weight: 1.00
Name: 99BW4745_8	<u>SEQ ID NO: 851</u>	Len: 1046	Check: 52	Weight: 1.00
Name: 99BW4754_7	<u>SEQ ID NO: 852</u>	Len: 1046	Check: 4905	Weight: 1.00
Name: 99BWMC16_8	<u>SEQ ID NO: 853</u>	Len: 1046	Check: 1544	Weight: 1.00
Name: A2_CD_97CD	<u>SEQ ID NO: 854</u>	Len: 1046	Check: 9703	Weight: 1.00
Name: A2_CY_94CY	<u>SEQ ID NO: 855</u>	Len: 1046	Check: 3235	Weight: 1.00
Name: A2D_97KR	<u>SEQ ID NO: 856</u>	Len: 1046	Check: 3776	Weight: 1.00
Name: A2G_CD_97C	<u>SEQ ID NO: 857</u>	Len: 1046	Check: 2059	Weight: 1.00
Name: A_BY_97BL0	<u>SEQ ID NO: 858</u>	Len: 1046	Check: 2724	Weight: 1.00



Name: A_KE_Q23_A	SEQ ID NO: 859	Len: 1046	Check: 1835	Weight: 1.00
Name: A_SE_SE659	SEQ ID NO: 860	Len: 1046	Check: 647	Weight: 1.00
Name: A_SE_SE725	SEQ ID NO: 861	Len: 1046	Check: 263	Weight: 1.00
Name: A_SE_SE753	SEQ ID NO: 862	Len: 1046	Check: 2271	Weight: 1.00
Name: A_SE_SE853	SEQ ID NO: 863	Len: 1046	Check: 5036	Weight: 1.00
Name: A_SE_SE889	SEQ ID NO: 864	Len: 1046	Check: 8414	Weight: 1.00
Name: A_SE_UGSE8	SEQ ID NO: 865	Len: 1046	Check: 3268	Weight: 1.00
Name: A_UG_92UG0	SEQ ID NO: 866	Len: 1046	Check: 2007	Weight: 1.00
Name: A_UG_U455	SEQ ID NO: 867	Len: 1046	Check: 2277	Weight: 1.00
Name: AC_IN_2130	SEQ ID NO: 868	Len: 1046	Check: 5353	Weight: 1.00
Name: AC_RW_92RW	SEQ ID NO: 869	Len: 1046	Check: 4695	Weight: 1.00
Name: AC_SE_SE94	SEQ ID NO: 870	Len: 1046	Check: 4206	Weight: 1.00
Name: ACD_SE_SE8	SEQ ID NO: 871	Len: 1046	Check: 7281	Weight: 1.00
Name: ACG_BE_VI1	SEQ ID NO: 872	Len: 1046	Check: 1400	Weight: 1.00
Name: AD_SE_SE69	SEQ ID NO: 873	Len: 1046	Check: 4640	Weight: 1.00
Name: AD_SE_SE71	SEQ ID NO: 874	Len: 1046	Check: 1057	Weight: 1.00
Name: ADHK_NO_97	SEQ ID NO: 875	Len: 1046	Check: 3502	Weight: 1.00
Name: ADK_CD_MAL	SEQ ID NO: 876	Len: 1046	Check: 2578	Weight: 1.00
Name: AG_BE_VI11	SEQ ID NO: 877	Len: 1046	Check: 8416	Weight: 1.00
Name: AG_NG_92NG	SEQ ID NO: 878	Len: 1046	Check: 9397	Weight: 1.00
Name: AGHU_GA_VI	SEQ ID NO: 879	Len: 1046	Check: 9562	Weight: 1.00
Name: AGU_CD_Z32	SEQ ID NO: 880	Len: 1046	Check: 8398	Weight: 1.00
Name: AJ_BW_BW21	SEQ ID NO: 881	Len: 1046	Check: 3451	Weight: 1.00
Name: B_AU_VH_AF	SEQ ID NO: 882	Len: 1046	Check: 2033	Weight: 1.00
Name: B_CN_RL42	SEQ ID NO: 883	Len: 1046	Check: 1369	Weight: 1.00
Name: B_DE_D31_U	SEQ ID NO: 884	Len: 1046	Check: 4607	Weight: 1.00
Name: B_DE_HAN_U	SEQ ID NO: 885	Len: 1046	Check: 1771	Weight: 1.00
Name: B_FR_HXB2	SEQ ID NO: 886	Len: 1046	Check: 4569	Weight: 1.00
Name: B_GA_OYI	SEQ ID NO: 887	Len: 1046	Check: 3682	Weight: 1.00
Name: B_GB_CAM1	SEQ ID NO: 888	Len: 1046	Check: 3161	Weight: 1.00
Name: B_GB_GB8_A	SEQ ID NO: 889	Len: 1046	Check: 6253	Weight: 1.00
Name: B_GB_MANC	SEQ ID NO: 890	Len: 1046	Check: 7670	Weight: 1.00
Name: B_KR_WK_AF	SEQ ID NO: 891	Len: 1046	Check: 8737	Weight: 1.00
Name: B_NL_3202A	SEQ ID NO: 892	Len: 1046	Check: 2083	Weight: 1.00
Name: B_TW_TWCYS	SEQ ID NO: 893	Len: 1046	Check: 3056	Weight: 1.00
Name: B_US_BC_L0	SEQ ID NO: 894	Len: 1046	Check: 3160	Weight: 1.00
Name: B_US_DH123	SEQ ID NO: 895	Len: 1046	Check: 1102	Weight: 1.00
Name: B_US_JRCSE	SEQ ID NO: 896	Len: 1046	Check: 5571	Weight: 1.00
Name: B_US_MNCG	SEQ ID NO: 897	Len: 1046	Check: 3988	Weight: 1.00
Name: B_US_P896	SEQ ID NO: 898	Len: 1046	Check: 2465	Weight: 1.00
Name: B_US_RF_M1	SEQ ID NO: 899	Len: 1046	Check:	Weight: 1.00
Name: B_US_SF2_K	SEQ ID NO: 900	Len: 1046	Check: 1754	Weight: 1.00
Name: B_US_WEAU1	SEQ ID NO: 901	Len: 1046	Check: 2993	Weight: 1.00
Name: B_US_WR27	SEQ ID NO: 902	Len: 1046	Check: 4098	Weight: 1.00
Name: B_US_YU2_M	SEQ ID NO: 903	Len: 1046	Check: 5564	Weight: 1.00
Name: BF1_BR_93B	SEQ ID NO: 904	Len: 1046	Check: 4182	Weight: 1.00
Name: C_BR_92BR0	SEQ ID NO: 905	Len: 1046	Check: 5481	Weight: 1.00
Name: C_BW_96BW0	SEQ ID NO: 906	Len: 1046	Check: 6833	Weight: 1.00
Name: C_BW_96BW1	SEQ ID NO: 907	Len: 1046	Check: 2166	Weight: 1.00
Name: C_BW_96BW1	SEQ ID NO: 908	Len: 1046	Check: 5817	Weight: 1.00
Name: C_BW_96BW1	SEQ ID NO: 909	Len: 1046	Check: 5157	Weight: 1.00
Name: C_ET_ETH22	SEQ ID NO: 910	Len: 1046	Check: 3509	Weight: 1.00
Name: C_IN_93IN1	SEQ ID NO: 911	Len: 1046	Check: 5471	Weight: 1.00
Name: C_IN_93IN9	SEQ ID NO: 912	Len: 1046	Check: 4102	Weight: 1.00
Name: C_IN_93IN9	SEQ ID NO: 913	Len: 1046	Check: 3150	Weight: 1.00
Name: C_IN_94IN1	SEQ ID NO: 914	Len: 1046	Check: 5157	Weight: 1.00
Name: C_IN_95IN2	SEQ ID NO: 915	Len: 1046	Check: 4641	Weight: 1.00
Name: CRF01_AE_C	SEQ ID NO: 916	Len: 1046	Check: 87	Weight: 1.00
Name: CRF01_AE_C	SEQ ID NO: 917	Len: 1046	Check: 3758	Weight: 1.00
Name: CRF01_AE_C	SEQ ID NO: 918	Len: 1046	Check: 2775	Weight: 1.00

Name:	CRF01_AE_T	SEQ ID NO: 919	Len: 1046	Check: 1864	Weight: 1.00
Name:	CRF01_AE_T	SEQ ID NO: 920	Len: 1046	Check: 7414	Weight: 1.00
Name:	CRF01_AE_T	SEQ ID NO: 921	Len: 1046	Check: 7837	Weight: 1.00
Name:	CRF01_AE_T	SEQ ID NO: 922	Len: 1046	Check: 3529	Weight: 1.00
Name:	CRF01_AE_T	SEQ ID NO: 923	Len: 1046	Check: 7503	Weight: 1.00
Name:	CRF01_AE_T	SEQ ID NO: 924	Len: 1046	Check: 5730	Weight: 1.00
Name:	CRF02_AG_F	SEQ ID NO: 925	Len: 1046	Check: 9432	Weight: 1.00
Name:	CRF02_AG_F	SEQ ID NO: 926	Len: 1046	Check: 2064	Weight: 1.00
Name:	CRF02_AG_G	SEQ ID NO: 927	Len: 1046	Check: 9849	Weight: 1.00
Name:	CRF02_AG_N	SEQ ID NO: 928	Len: 1046	Check: 1793	Weight: 1.00
Name:	CRF02_AG_S	SEQ ID NO: 929	Len: 1046	Check: 4817	Weight: 1.00
Name:	CRF02_AG_S	SEQ ID NO: 930	Len: 1046	Check: 1764	Weight: 1.00
Name:	CRF03_AB_R	SEQ ID NO: 931	Len: 1046	Check: 1695	Weight: 1.00
Name:	CRF03_AB_R	SEQ ID NO: 932	Len: 1046	Check: 1425	Weight: 1.00
Name:	CRF04_cpx	SEQ ID NO: 933	Len: 1046	Check: 8496	Weight: 1.00
Name:	CRF04_cpx	SEQ ID NO: 934	Len: 1046	Check: 2074	Weight: 1.00
Name:	CRF04_cpx	SEQ ID NO: 935	Len: 1046	Check: 9245	Weight: 1.00
Name:	CRF05_DF_B	SEQ ID NO: 936	Len: 1046	Check: 62	Weight: 1.00
Name:	CRF05_DF_B	SEQ ID NO: 937	Len: 1046	Check: 3427	Weight: 1.00
Name:	CRF06_cpx	SEQ ID NO: 938	Len: 1046	Check: 142	Weight: 1.00
Name:	CRF06_cpx	SEQ ID NO: 939	Len: 1046	Check: 6688	Weight: 1.00
Name:	CRF06_cpx	SEQ ID NO: 940	Len: 1046	Check: 8524	Weight: 1.00
Name:	CRF06_cpx	SEQ ID NO: 941	Len: 1046	Check: 4725	Weight: 1.00
Name:	CRF11_cpx	SEQ ID NO: 942	Len: 1046	Check: 2194	Weight: 1.00
Name:	CRF11_cpx	SEQ ID NO: 943	Len: 1046	Check: 8466	Weight: 1.00
Name:	D_CD_84ZR0	SEQ ID NO: 944	Len: 1046	Check: 515	Weight: 1.00
Name:	D_CD_ELI_K	SEQ ID NO: 945	Len: 1046	Check: 2096	Weight: 1.00
Name:	D_CD_NDK_M	SEQ ID NO: 946	Len: 1046	Check: 3376	Weight: 1.00
Name:	D_UG_94UG1	SEQ ID NO: 947	Len: 1046	Check: 3505	Weight: 1.00
Name:	F1_BE_VI85	SEQ ID NO: 948	Len: 1046	Check: 3993	Weight: 1.00
Name:	F1_BR_93BR	SEQ ID NO: 949	Len: 1046	Check: 2251	Weight: 1.00
Name:	F1_FI_FIN9	SEQ ID NO: 950	Len: 1046	Check: 9772	Weight: 1.00
Name:	F1_FR_MP41	SEQ ID NO: 951	Len: 1046	Check: 1447	Weight: 1.00
Name:	F2_CM_MP25	SEQ ID NO: 952	Len: 1046	Check: 2842	Weight: 1.00
Name:	F2KU_BE_VI	SEQ ID NO: 953	Len: 1046	Check: 5026	Weight: 1.00
Name:	G_BE_DRCBL	SEQ ID NO: 954	Len: 1046	Check: 5377	Weight: 1.00
Name:	G_NG_92NG0	SEQ ID NO: 955	Len: 1046	Check: 6000	Weight: 1.00
Name:	G_SE_SE616	SEQ ID NO: 956	Len: 1046	Check: 7901	Weight: 1.00
Name:	H_BE_VI991	SEQ ID NO: 957	Len: 1046	Check: 9107	Weight: 1.00
Name:	H_BE_VI997	SEQ ID NO: 958	Len: 1046	Check: 5776	Weight: 1.00
Name:	H_CF_90CF0	SEQ ID NO: 959	Len: 1046	Check: 9201	Weight: 1.00
Name:	J_SE_SE702	SEQ ID NO: 960	Len: 1046	Check: 9700	Weight: 1.00
Name:	J_SE_SE788	SEQ ID NO: 961	Len: 1046	Check: 8817	Weight: 1.00
Name:	K_CD_EQTB1	SEQ ID NO: 962	Len: 1046	Check: 3723	Weight: 1.00
Name:	K_CM_MP535	SEQ ID NO: 963	Len: 1046	Check: 3729	Weight: 1.00
Name:	N_CM_YBF30	SEQ ID NO: 964	Len: 1046	Check: 3336	Weight: 1.00
Name:	O_CM_ANT70	SEQ ID NO: 965	Len: 1046	Check: 9461	Weight: 1.00
Name:	O_CM_MVP51	SEQ ID NO: 966	Len: 1046	Check: 2986	Weight: 1.00
Name:	O_SN_99SE	SEQ ID NO: 967	Len: 1046	Check: 377	Weight: 1.00
Name:	O_SN_99SE	SEQ ID NO: 968	Len: 1046	Check: 9312	Weight: 1.00
Name:	U_CD_83C	SEQ ID NO: 969	Len: 1046	Check: 1358	Weight: 1.00

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SEQ ID NO	1	50
636	00BW0762_1 MGGKWSKSS. IVGWPAVRER IR....RTDP .....	....AAEGVG
637	00BW0768_2 MGGKWSKSSI V.GWPEVRER IRR..TEP.. .....	....AAEGVG
638	00BW0874_2 MGGKWSKSS. LTGWPAVRER IR....RTEP .....	....AAEGVG
639	00BW1471_2 MGGKWSKSS. IVGWPAVKER IRR..TNPR. ....	.TERAAVGVG

640	00BW1616_2	MGNKWSKSS.	IVGWPAVRDR	MRR..AEP..	.....	....AAEGVG
641	00BW1686_8	MGGKWSKRS.	KADWPAVREK	LR....TTEP	.....	....AAEGVG
642	00BW1759_3	MGNKWSKS..	...WPAVRER	IRR..TRPAR	.....	GNEPAAEGVG
643	00BW1773_2	MGSKWSKSSI	V.GWPKVRET	IRR..TEP..	.....	....AAEGVG
644	00BW1783_5	MGNKWSKS..	...WPAIRER	IRR..TNPAA	.....	ERTRAAEGVG
645	00BW1795_6	MGGKWSKSS.	VVGWPAIRER	MRR.....	.....	.TEPAAEGVG
646	00BW1811_3	MGGKWSKSC.	KIGWPAVRER	MRR.....	.....	.TEPAVEGVG
647	00BW1859_5	MGGKWSKSG.	KVGWPEVRER	MRR..TRPAA	EGG.....	..DSAAEGVG
648	00BW1880_2	MGGKWSKSS.	LVGWPAVRER	IRT..TAP..	.....	.....
649	00BW1921_1	MGGKWSKSS.	IVGWPAVRER	MR....KTEP	.....	....AAEGVG
650	00BW2036_1	MGGKWSKSS.	IVGWPAVRER	IRR.....	.....	.TEPAAEGVG
651	00BW2063_6	MGGKWSKSSI	I.GWPAVRER	MRK..AEP..	.....	....AAEGVG
652	00BW2087_2	MGSKWSKSS.	IVGWPAVRER	IRR..T....	.....	RTEPAAEGVG
653	00BW2127_2	MGGKWSKSSI	I.GWPAIRER	IRR..TEP..	.....	....AAEGVG
654	00BW2128_3	MGSKWSKCSI	I.GWPAVRER	IRR..AEP..	.....	....AAVGVG
655	00BW2276_7	MGSKWSKC..	.SGWPDVRER	MRR..ATPAA	EAGRA...AP	AAEGAAPGVG
656	00BW3819_3	MGSKWSKCSI	V.GWPDVRER	MRR..ARPAV	RERRRQTEPA	AEGVAAEGVG
657	00BW3842_8	MGGKWSKGR.	IVGWPAVRER	MRR.....	.....	.TEPAAEGVG
658	00BW3871_3	MGSKWSKRS.	IVEWPAVRER	LR....KTEP	.....	....AAEGVG
659	00BW3876_9	MGGKWSKSS.	IVGWPAVRER	IRQ..TGAR.	.....	....AAEGV G
660	00BW3886_8	MGGKWSKSS.	IVGWSAVRER	MK....RTEP	.....	....AAEGVG
661	00BW3891_6	MGGKWSKSS.	IVGWPTVRER	MRR..TQP..	.....	....AAEGVG
662	00BW3970_2	MGSKWSKRS.	TAGWPAVRER	MRR..TQPAA	EG.....	.TQSAAEGVG
663	00BW5031_1	MGGKWSKSS.	LVGWPEVRDR	IRR..TDP..	.....	....AAEGVG
664	96BW01B21	MGGKWSKSSI	V.GWPAVRER	IRR..TEP..	.....	....AAEGVG
665	96BW0407	MGGKWSKSSI	V.GWPAVRER	MRR..AEP..	.....	....AAEGVG
666	96BW0502	MGGKWSK...	CSGWPAVRER	MRR..TRPAV	EGR.....	.TESAAEGVG
667	96BW06_J4	MGGKWSKSS.	IVGWPAVRER	IR....RTDP	.....	....PAEVR
668	96BW11_06	MGGKWSKSSI	I.GWPAIRER	IRR..TEPAA	ER.....V	..GAAAEGVG
669	96BW1210	MGNKWSKG..	...WPAVRDR	IRR..TEPAT	.....	..EPAAEGVG
670	96BW15B03	MGGKWSKSS.	IVGWPAVRER	IRR.....	.....	.TEPAAEGVG
671	96BW16_26	MGGKWSK...	...WPAVRER	MRR..TR...	.....	.....VG
672	96BW17A09	MGXKWSKRS.	IVGWPNVRER	IRR..TNPLT	ER.....	EAERAAGVG
673	96BWM01_5	MGSKWSKSSI	I.GWPAVRER	IRK..TEPRK	.....	.TEPAAEGVG
674	96BWM03_2	MGGKWSKSS.	IVGWPAVRER	MRR..TRPGA	AE.....	.....GVG
675	98BWMC12_2	MGSKWSKSS.	IIGWPAVRER	MR....RTEP	.....	....AAEGVG
676	98BWMC13_4	MGGKWSKSS.	IIGWPAVRER	MRR.....	.....	.TEPAAEGVG
677	98BWMC14_a	MGGKWSKSS.	LVGWPDVRER	IR....KPRP	KP.....	....AAEGVG
678	98BWM014_1	MGSKLSKSK.	IVGWPAIRER	LR.....	.....	RTEPAAEGVG
679	98BWM018_d	MGGKWSKSS.	IVGWPAVRER	IRQ..TDPRE	RI.....R	QTEPAAEGVG
680	98BWM036_a	MGGKWSKSSI	V.GWPAVRER	IRR..TEPRR	.....	.AEPAAEGVG
681	98BWM037_d	MGGKWSKSS.	IVGWPEVRER	LR....RTAP	.....	....AAEGVG
682	99BW3932_1	MGGKWSKRKI	V.QWPTVRER	LRR..TEP..	.....	....AEGVG
683	99BW4642_4	MGGKWSKSS.	IVGWPAVRER	IRR..TQPAA	EG.....	.....VG
684	99BW4745_8	MGSKLSKSC.	TAGWPTVRER	IRQ..AEP..	.....	....AAEGVG
685	99BW4754_7	MGGKWSKSS.	IVGWANVRER	MRR.....	.....	.TEPAAVGVG
686	99BWMC16_8	MGNKWSKS..	...WPAVRER	IRR..TEPAV	RV.....R	RTEPAAEGVG

687	A2_CD_97CD	MGGKWSKRT.	IVGWPEIRER	MRR..TPPAA	EG.....VR	PTPPAAEGVG
688	A2_CY_94CY	MGGKWSKRS.	IPGWPAIRER	MRRTPTAQR	TE.....	AVSPAAPGVG
689	A2D___97KR	MGGKWSKRS.	LPGWPAIRER	MRRTPPAAER	TP.....	PAA.AAEGVG
690	A2G_CD_97C	MGSKWSKSS.	IVGWPAVRAR	IR...QTPP.	.....	AAEGVG
691	A_BY_97BL0	XXGKWSKSS.	IXXWPQVXER	IRRAPAP...	.....	AARXVG
692	A_KE_Q23	MGGKWSKSS.	IVGWPEIRER	MRRAPP....	.....	AAPGVG
693	A_SE_SE659	MGGKWSKSS.	IVGWPEIRER	MRRAPS....	.....	AAAPGVG
694	A_SE_SE725	MGSKWSKSS.	IVGWREVRER	LRQTLAAARG	.....	VG
695	A_SE_SE753	MGGRWSKSR.	IVGWPEVRER	IRRAPP....	.....	AATGVG
696	A_SE_SE853	MGGKWSKRS.	KEGWSEVREK	IRQT.....	.....	PPAAKGVG
697	A_SE_SE889	MGGKWSKSS.	IVGWPKVRER	MARTPP....	.....	AAKGVG
698	A_SE_UGSE8	MGNKWSK...	..GWPEVRER	IRQARAPAHT	.....	PAPTAATGVG
699	A_UG_92UG0	MGNKWSKSC.	IVGWPEVRER	IRQTPTAARE	RTR.....	QAPTAAGVG
700	A_UG_U455	MGGKWSKKS.	RVEWPEVRKR	MRETPA....	.....	AAKGVG
701	AC_IN_2130	MGGKWPKSS.	VVGWPEVRER	IRRTPA....	.....	AAPGVG
702	AC_RW_92RW	MGSKWSKCSP	V.GWPAVRER	LRQ..TEP..	.....	AAEGVG
703	AC_SE_SE94	MGGKWSKSS.	IIGWPQIRER	IRRTPP....	.....	AATGVG
704	ACD_SE_SE8	MGGKWLKSSI	V.GWPAVRER	IRR..TEP..	.....	AAEGVG
705	ACG_BE_VI1	MGGKWSKRS.	KVEWPQVRER	MRQ..TPIAA	EA.....EG	...AAAEGVG
706	AD_SE_SE69	MGGKWSKSS.	IVGWPAVRER	IKR..T....	.....	DPAAEGVG
707	AD_SE_SE71	MGGKWSKSS.	IVGWPEVRER	MRRARAP...	.....	SAAPGVG
708	ADHK_NO_97	MGGKWSKSS.	IVGWPAIRER	MRR..AEP..	.....	AAEGVG
709	ADK_CD_MAL	MGGKWSKSS.	IVGWPKIRER	IRRTPTTETG	.....	...VGAVSQD
710	AG_BE_VI11	MGGKWSKSS.	PVGWSRVREK	MRR..TPPAA	EG.....	...AAAEGVG
711	AG_NG_92NG	IGGKWSKSS.	IVGWPAVRER	IR...QTP..	.....	PAEGVG
712	AGHU_GA_VI	MGGWWSRSS.	IVGWSTIRER	MRRAEP....	.....	AAAGVG
713	AGU_CD_Z32	MGNKWSKG..	...WPAVRER	IRQ..TPPAP	P.....	...AAEGVG
714	AJ_BW_BW21	MGSNWSKS.S	IIGWPQVRER	MKR....AP	A.....P	...AAEGVG
715	B_AU_VH	MGGKWSKRI.	RSEWPTVRER	IIQ..AEPAA	AG.....	.....VG
716	B_CN_RL42	MGGKWSKHS.	MFGWPSVRER	MKR..AEPAA	DG.....	.....VG
717	B_DE_D31	MGGKWSKSS.	VVGWPAIRER	MK.....	.....	RAEPAAEGVG
718	B_DE_HAN	MGGKWSK...	CSGWPTVRER	MKQAEP....	.....	..EPAADGVG
719	B_FR_HXB2	MGGKWSKSS.	VIGWPTVRER	MR.....	.....	RAEPAADRVG
720	B_GA_OYI	MGGKWSKCS.	MKGWPTIRER	MKR..AELQP	PE.....	...PAAEGVG
721	B_GB_CAM1	MGGKWSKRS.	LGGWSAVREK	MQR..AEP..	.....	RAEPAAEGVG
722	B_GB_GB8	MGGKLSKRS.	MFGWSRVDR	MQQ..AEP..	.....	AAEGVG
723	B_GB_MANC	MGGKWSKSR.	KIGWPTVRER	MKQ..VDPAE	EGR....KK	QAEPAAGVG
724	B_KR_WK	MGGKWSKRS.	VPGWNTIRKR	MRR..AEPAA	EG.....	.....VG
725	B_NL_3202A	MGGKWSKSS.	VVGWPAIRER	MK.....	.....	RAEPAADGVG
726	B_TW_TWCYS	MGGKWSKRS.	IPGWSNIRER	IRQ..AEPA.	.....	...AADGVG
727	B_US_BC	MGGKWSKRM.	EGGWHAVREK	MR.....	.....	RAEPAADGVG
728	B_US_DH123	MGGKLSKCG.	GVGWSTVRER	MRR..AEPAA	DR.....	..EP.AVGVG
729	B_US_JRCSF	MGGKWSKHS.	VPGWSTVRER	MRR..AEPAT	DR.....VR	QTEPAAGVG
730	B_US_MNCG	MGGKWSKR..	VTGWPTVRER	MRR..AEP..	.....	..AELAADGVG
731	B_US_P896	MGGKWSKRR.	AEGWQTIRER	MRRAEPA...	.....	..EPAADGVG
732	B_US_RF	MGGKWSKSK.	MGGWPAVRER	MQK..AEPAA	DG.....	.....VG
733	B_US_SF2	MGGKWSKRS.	MGGWSAIRER	MRR..AEP..	.....	RAEPAADGVG

734	B_US_WEAU1	MGGIWSKRS.	GSGWPAIRER	MKR..AEPAA	EG.....	.....VG
735	B_US_WR27	MGGKWSKRS.	VGGWPAIRER	MX.....	.....	RAEPAAEGVG
736	B_US_YU2	MGGKWSKRS.	MAGWPTVRER	MRR..AEPAA	ER.....MR	RAEPAADGVG
737	BF1_BR_93B	MGSKWSKSS.	IVGWPAIRER	LRQ..TP...	.....	...PAAEGVG
738	C_BR_92BR0	MGNKWSKCST	V.GRPAIRER	MRR...AP..	.....	...AAEGVG
739	C_BW_96BW0	MGGKWSKSSI	V.GWPAVRER	MRR..TEP..	.....	...AAEGVG
740	C_BW_96BW1	MGGKWSKRSK	I.EWPTIRDR	MRR..TEPAA	EG.....V	..GAAAEGVG
741	C_BW_96BW1	MGNKWSKG..	...WPAVRDR	IRR..TEPAT	.....	..EPAAEGVG
742	C_BW_96BW1	MGGKWSKSS.	IVGWPAVRER	IRR.....	.....	..TEPAAEGVG
743	C_ET_ETH22	MGGTMSKCSP	V.GWPAIRER	IRR..AAP..	.....	...AAEGVG
744	C_IN_93IN1	MGGKWSKCSI	V.GWPAIRER	MRR..AEP..	.....	...AAEGVG
745	C_IN_93IN9	MGGKWSKCSI	V.GWPDIRER	MRR..TQP..	.....	...AAEGVG
746	C_IN_93IN9	MGGKWSKCSI	V.GWPAVRER	MRR..TEP..	.....	...AAEGVG
747	C_IN_94IN1	MGGKWSKCSI	V.GWPEIRER	MRR..TQP..	.....	...AADGVG
748	C_IN_95IN2	MGGKWSKCSI	V.GWPDIRER	MRR..TEP..	.....	...AAEGVG
749	CRF01_AE_C	MGGKWSKN.R	IVGWQVRER	IRR..TPAAA	.....	.....EGVG
750	CRF01_AE_C	MGGKWSKSC.	IVGWQVRER	IRQ..TPVAE	E.....R	QTPAAAEGVG
751	CRF01_AE_C	MGNKWSKS..	...WPQIRER	IRQ..TPVAT	.....	.....EGVG
752	CRF01_AE_T	MGGKWSKS.S	IVGWQVREK	IKQ..TPPAA	.....	.....EGVG
753	CRF01_AE_T	MGGKWSKS.S	IVGWQVREK	IKQ..TPPAA	.....	.....EGVG
754	CRF01_AE_T	MGGKWSKS.S	IVGWQVRER	IKQ..TPPAA	.....	.....EGVG
755	CRF01_AE_T	MGAKWSKRG.	...WPQVRER	IRQ..TPPAA	.....	.....EGVG
756	CRF01_AE_T	MGSKWSKS.S	IVGWQVREK	IKQ..TPPAT	.....	.....EGVG
757	CRF01_AE_T	MGNKWSKS..	...WPRVRER	IKQ..TPPAA	.....	.....EGVG
758	CRF02_AG_F	MGGKWSKSS.	IVGWPKVRER	IR...QTPP.	.....	...AATGVG
759	CRF02_AG_F	MGGKWSKSS.	LVGWPKVRER	II...QTPP.	.....	...AATGVG
760	CRF02_AG_G	MGGKWSKSS.	IVGWQVRER	IR...QTPT.	.....	...AAKGVG
761	CRF02_AG_N	MGGKWSKSS.	IVGWPKVMKR	MR...QTPT.	.....	...AATGVG
762	CRF02_AG_S	MGGKWSKSS.	IVGWQIRDR	IR...QTPP.	.....	...AARGVG
763	CRF02_AG_S	MGGKWSKSS.	LVGWQVRER	IRRTOPTPS.	.....	...AAIGVG
764	CRF03_AB_R	MGGKWSKSS.	IVGWQVRER	IRRAPAP...	.....	...AARGVG
765	CRF03_AB_R	MGGKWSKSS.	IVGWQIRER	IRRAPAP...	.....	...AARGVG
766	CRF04_cpx_	MGGKWSKSS.	IVGWPEIRER	MRR..ARAEP	ERM...RA	QAEPAAAGVG
767	CRF04_cpx_	MGGKWSKSS.	LVGWPAIRER	MRR..ARAEP	.....AA	QAEPAAAGVG
768	CRF04_cpx_	MGNKWSKS..	...WPAVRER	MRR..ARAEP	.....A	RAEPAAVGVG
769	CRF05_DF_B	MGGKWSKSS.	VVGWPAIREK	MRR..TP...	.....	...PAAEGVG
770	CRF05_DF_B	MGGKWSKNR.	IVGWPAIRER	MRR..TPPAA	.....	..GAAAEGVG
771	CRF06_cpx_	MGNKWSK...	...GWSQVRER	MRR..TPPTE	R.....	...AAEGVG
772	CRF06_cpx_	MGSKWSKS.S	IVGWQVRER	IRQ..TPPTE	G.....	...AAKGVG
773	CRF06_cpx_	MGGKWSKS.S	LVGWQVRER	IRQ..TPPTE	G.....	...AAEGVG
774	CRF06_cpx_	MGGKWSKS.S	IVGWPKVRER	MRQ..TPPAA	E.....R	QTPPAAEGVG
775	CRF11_cpx_	MGGKWSKS.S	IVGWPEIRER	LRR.....	.....T	PPAAAADGVG
776	CRF11_cpx_	MGGNWSKS.S	IVGWPEIRER	LRR.....	.....T	PPTAAAEGVG
777	D_CD_84ZR0	MGGKWSKSS.	IVGWPAIRER	IRK..TDPRE	RR.....	RPEPAADGVG
778	D_CD_ELI	MGGKWSKSS.	IVGWPAIRER	IRR..T....	.....	..NPAADGVG
779	D_CD_NDK	MGGKWSKSS.	LVGWPAIRER	IRK..T....	.....	..DPAADGVG
780	D_UG_94UG1	MGGKWSKSS.	IVGWPAVRER	MRR..T....	.....	..EPAAEGVG

781	F1_BE_VI85	MGGKWSKSS.	IVGWPAVGER	MRQ..TP...	...TAAEGVG
782	F1_BR_93BR	MGGKWSKSS.	IVGWPAIRER	MRR..TPPT.	...PPAAEGVG
783	F1_FI_FIN9	MGGKWSKSS.	IVGWPAIRER	MRR..PP...	...PAAAEVG
784	F1_FR_MP41	MGGKWSKSS.	IVGWPAVRER	MRR..TP...	...PAAEGVG
785	F2_CM_MP25	MGGKWSKSS.	IVGWPAIRER	IRR..TP...	...VAAEGVG
786	F2KU_BE_VI	MGGKWSK...	..GWPSVRER	IRR..TPPAA	P.....AADGVG
787	G_BE_DRCBL	MGNKWSKRK.	VAGWPEVRER	LR...QHPA.	...AAEGVG
788	G_NG_92NG0	MGGKWSKSS.	IVGWPIRER	IR...QTPV.	...AAEGVG
789	G_SE_SE616	MGGKWSKSS.	IVGWPEVRER	IR...NTPT.	...AAEGVG
790	H_BE_VI991	MGGKWSKGC.	ISGWPAVRER	IRQ..TEP..	...AAEGVG
791	H_BE_VI997	MGGKWSKSS.	IVGWPAVRER	IRR..AQP..	...AADGVG
792	H_CF_90CF0	MGGKWSKSR.	MGGWSTIRER	MRR..AEP..	...VAEGVG
793	J_SE_SE702	MGNKWSKS..	...WPQVRDR	MRR..A..AP	A.....P...AADGVG
794	J_SE_SE788	MGNKWSKS..	...WPQVRER	MRR.....AP	A.....P...AADGVG
795	K_CD_EQTB1	MGGKWSKS.S	IVGWSTVRER	MR.....	...KTPPAADGVG
796	K_CM_MP535	MGGKWSKS.S	IVGWPAIRER	MRR..ARPAA	DR.....VGTQPAADGVG
797	N_CM_YBF30	MGKIWSKSS.	LVGWPEIRER	MRRQTQEP..	...AVEPAVGAG
798	O_CM_ANT70	MGNALRK GK.	FEGWAAVRER	MRRTRTF...	...P ESEPCAPGVG
799	O_CM_MVP51	MGNAWSKSK.	FAGWSEVRDR	MRRSSS....	...D PQQPCAPGVG
800	O_SN_MP129	MGNVLGKDI.	FKGWSAVRER	MRGTS.....	...P DPEPCAPGVG
801	O_SN_MP130	MGNVLGKDK.	FKGWSAVRER	MRKTS.....	...P EPEPCAPGVG
802	U_CD___83C	MGNKWSKQ..	...WPAIRER	MRR..ARPAA	E.....P...AADGVG

	51			100
00BW0762_1	LQVR.....	.....GDK.	....PHSEAG	AERQ.....GTLNFPQITL
00BW0768_2	LQVRG.....	.....DNN.	....PCSEAG	AERQ.....GTLNCPQITL
00BW0874_2	PQARAISPTS	REPQVRRDN.	....SRFEAG	VEREG.....TLNFPQITL
00BW1471_2	LQVR.....	.....GDN.	....PRSEAG	AERQG.....TLNLPQITL
00BW1616_2	LQVR.....	.....GNN.	....PLSEAG	GERQ.....GTLNFPQITL
00BW1686_8	LQVR.....	.....GDN.	....PRSEAG	AERQ.....GTLNLPQITL
00BW1759_3	LQVRG.....	.....NN.	....PRSEAG	AERQ.....GTLNFPQITL
00BW1773_2	LQVR.....	.....GDN.	....PRSEAG	AERQ.....GTLNFPQITL
00BW1783_5	LQVR.....	.....GDN.	....PCSEAG	DERQ.....GTFNFPQITL
00BW1795_6	LQVR.....	.....GDN.	....PLSEAG	AERQ.....GTLNFPQITL
00BW1811_3	LQVR.....	.....GDN.	....PRFEAG	EKRQG.....NLNFPQITL
00BW1859_5	LQVR.....	.....GDD.	....PRSEAG	AERQ.....GTLNFPQITL
00BW1880_2	LQVR.....	.....GDN.	....PRSEAG	AEGQ.....GTLNFPQITL
00BW1921_1	LQVR.....	.....GDN.	....PCSEAG	AERQG.....TLNFPQITL
00BW2036_1	LQVR.....	.....GDN.	....PRSEAG	AERQ.....GTLNFPQITL
00BW2063_6	L..R.....	.....GDN.	....PCSEAG	DERQ.....GTLNFPQITP
00BW2087_2	NSPTSREL..	...QVRGDN.	....PSIKAG	PERQ.....GALNFPQITL
00BW2127_2	LQVR.....	.....GDN.	....PRSEAG	AERQG.....SLNFPQITL
00BW2128_3	LQVR.....	.....GDN.	....TRSEAG	AKKQ.....GTLNFPQITL
00BW2276_7	LQVR.....	.....GDN.	....PRAEAG	AERQG.....TLNFPQITL
00BW3819_3	LQVR.....	.....GDN.	....PRSEAG	DERQG.....ALNFPQITL
00BW3842_8	LQVR.....	.....GDN.	....PRSEAG	AERQGT..LQGTNFPQITL
00BW3871_3	LQVR.....	.....GDN.	....PRSEAG	ADRQ.....GTLNFPQITL
00BW3876_9	LQVR.....	.....GDN.	....PHSEAG	AERQ.....GTLNFPQITL
00BW3886_8	LQVR.....	.....GDN.	....PRSEAG	AERQG.....SLNFPQITL
00BW3891_6	LQVR.....	.....GDN.	....PRSEAG	AERQG.....TLNFPQITL
00BW3970_2	LQVR.....	.....GDN.	....PRSETG	AEGQG.....TFNFPQITL
00BW5031_1	LQVR.....	.....GDN.	....PRSEAG	DEREG.....TLNFPQITL
96BW01B21	LQVR.....	.....GDN.	....PRSEAG	AEGQG.....ALNLPQITL
96BW0407	LQVR.....	.....GDN.	....PRSETR	VEGQG.....NFNFPQITL

96BW0502	LQVR.....	.....GDN.	....PRSEAG	AEGQGT..LQ	GTLNCPQITL
96BW06_J4	LQIR.....	.....GDN.	....PRFEAG	TKRQ.....	GTLNFPQITL
96BW11_06	LRG.....	.....NN.	....PCSEAG	DERQ.....	GTLNFPQITL
96BW1210	LQVR.....	.....GDN.	....PCSEAG	AEGQG.....	TTFSEFPQITL
96BW15B03	LQVR.....	.....GDN.	....PRSEAG	AERQ.....	GTLNFPQITL
96BW16_26	LQVW.....	.....GDN.	....PRSETG	AKGQ.....	GTFNFPQITL
96BW17A09	LQVR.....	.....GDN.	....PRSEAG	AERQG.....	.TLNFLQITL
96BWM01_5	L..R.....	.....GDN.	....PCSEAG	DERQGT..LQ	GALNFPQITL
96BWM03_2	LQAR.....	.....TNSP.	....TSREAG	VEGQG.....	.TLNFPQITL
98BWMC12_2	P.....	...QARGDN.	....TRFEAG	DEGQG.....	.TLNFPQITL
98BWMC13_4	P..R.....	.....GDN.	....PCSEAG	AERQ.....	GTLNLPQITL
98BWMC14_a	LQVR.....	.....GDN.	....PRSEAG	AEGQ.....	GTLNFPQITL
98BWM014_1	LQVREQTR..	...ANSSTS.	....RELQAG	AKRQ.....	GALNCPQITL
98BWM018_d	LQVR.....	.....GDN.	....PCSEAG	AERQGS....	.TLNFPQITL
98BWM036_a	LQVR.....	.....GDK.	....PRSEAG	AEGQG.....	.TLNFPQITL
98BWM037_d	LQVR.....	.....GDN.	....PRSEAG	GERQG.....	.TLKFPQITL
99BW3932_1	FQVR.....	.....GDN.	....PCSEAG	AERQG.....	.SLNFPQITL
99BW4642_4	LQIR.....	.....GDD.	....PRSEAG	AERQ.....	RTLNFPQITL
99BW4745_8	LQVR.....	.....GGN.	....PHSEAG	AERQG.....	.TLNFPQITL
99BW4754_7	LQVR.....	.....GDN.	....PHSEAR	VKGQ.....	GTPNFPQITL
99BWMC16_8	LQVR.....	.....GDK.	....SRSEAG	VEKQG.....	.NLNFPQITL
A2_CD_97CD	...GGR....	.....DN.	....LLAEAG	E..QG...AV	HPCNFPQITL
A2_CY_94CY	LENGGR....	.....DN.	....LLPEAG	TGDQG...TI	QSCNFPQITL
A2D___97KR	LWNGGG....	.....DN.	....PLAEAG	AEKQG...TT	HSCNFPQITL
A2G_CD_97C	PRVRR.....	.....GDS.	....LLPEAG	DEG...KGAV	YPCNFPQITL
A_BY_97BL0	LD.GGR....	.....DN.	....PLPETG	TERQG...TV	SSFNFPQITL
A_KE_Q23_A	LWDGGR....	.....DS.	....LPSEAG	AERQGT..G.	PTLSFPQITL
A_SE_SE659	PWDRRR....	.....DS.	....LPSETG	ADP.....	.TFSFPQITL
A_SE_SE725	FWDGGR....	.....DS.	....LPSEAG	AERQGT..E.	LTFSEFPQITL
A_SE_SE753	LWNEGR....	.....DS.	....LPSEAG	AEG..T..R.	PTFSFPQITL
A_SE_SE853	LWDGGS....	.....DN.	....LPSEAG	AERQGT..G.	PTLSFPQITL
A_SE_SE889	LWDGGR....	.....DN.	....LPSEAG	EERQGV..GG	TTLNFPQITF
A_SE_UGSE8	..DGGR....	.....DS.	....LPSEAG	AKQP.....	.TFSFPQITL
A_UG_92UG0	LWDEGR....	.....DS.	....LPSEAG	AERQGP..E.	PTFSFPQITL
A_UG_U455_	LWDGGK....	.....DD.	....LPCETG	AERQ....GT	DSFSFPQITL
AC_IN_2130	LQIR.....	.....GDN.	....PRTEAG	AKRQG.....	.TLNFPQITL
AC_RW_92RW	LWNGG....	.....RDS.	....LSSETG	AERQG.....	.TFNFPQITL
AC_SE_SE94	LRDGGGR....	.....D..	....NSEAG	TDRQGT..G.	PAFSFPQITL
ACD_SE_SE8	LRVWRR....	.....DN.	....PLPEAG	AERQ....GT	VSFSLPQITL
ACG_BE_VI1	LWEGGR....	.....DR.	....LLPEAG	TEGQG...TI	SSFNFPQITL
AD_SE_SE69	LRVWRG....	.....DS..	....TFSETG	AER....QGA	VSFSEFPQITL
AD_SE_SE71	LWDGGR....	.....DS.	....LPSEAG	AEKQG...TG	STLNFPQITL
ADHK_NO_97	LWDRGR....	.....DN..	....LLSEAG	TEGQG...TA	PSLSFPQITL
ADK_CD_MAL	LRVWGG....	.....DK..	....TLSETG	AERQ....GI	VSFSEFPQITL
AG_BE_VI11	LGDGGR....	.....DN.	....PLSEAG	TEGHG...TI	SSLNFPQITL
AG_NG_92NG	LRVRR....	.....GDS.	....PFPEAG	AEG...KGIT	SIN.LPQITL
AGHU_GA_VI	LRVRR....	.....GDS.	....PLPEAG	AKG....KGA	VSFNLPQITL
AGU_CD_Z32	LRDER....	.....GDN.	....LLSEAG	TEGQG...TI	PSFSFPQITL
AJ_BW_BW21	LRVWR....	.....GDS.	....PLPEAG	GEGQ....GT	VSFNFPQITL
B_AU_VH_AF	LQVWGR....	.....DNN.	....SLSEAG	ADR....QGT	VSFSEFPQITL
B_CN_RL42	LQVWGR....	.....DNN.	....SISEAG	ADR....QGT	ISFSFPQITL
B_DE_D31_U	LQVWGR....	.....DSN.	....SLSEAG	ADR....QGT	VSFSEFPQITL
B_DE_HAN_U	LQVWG....	.....SNS.	....SLSEAG	ADR....QGT	VSLSLPQITL
B_FR_HXB2_	LQVWGR....	.....DNN.	....SPSEAG	ADR....QGT	VSFNFPQVTL
B_GA_OYI_	LRVWGR....	.....DNN.	....SPSEAG	ADR....QGT	VSFNLPQITL
B_GB_CAM1_	LQVWGR....	.....ENN.	....SLSEAG	ADR....QGT	VSFSEFPQITL
B_GB_GB8_A	LQVRGR....	.....DNN.	....SLTETG	ADK....QGT	VSFSEFPQITL
B_GB_MANC_	LQVWGR....	.....DNN.	....SCSEAG	TDR....QGT	VSLSEFPQTTL
B_KR_WK_AF	LQVWGR....	.....DNN.	....SLSEAG	ANR....QGT	VSFSEFPQITL
B_NL_3202A	LQVWGR....	.....DNN.	....SLSEAG	AEG....QGT	VSLSLPQITL

B_TW_TWCYS	LQVWGT....	.....DNN.	....SLSEAG	ADR....QGP	VSFSFPQITL
B_US_BC_L0	LQVWGG....	.....DNN.	....SPSEAG	AGR....QGN	VSLSFPPQITL
B_US_DH123	LQVWGG....	.....DSN.	....SLSEAG	AEG.....T	ISLSLPQITL
B_US_JRCSF	LQVWGR....	.....DSN.	....SLSEAG	AEAGADRQGI	VSNFNPQITL
B_US_MNCG	LQVWGR....	.....DNN.	....SLSEAG	EEAGDDRQGP	VSFSFPQITL
B_US_P896	LQVWGG....	.....DNN.	....SLSEAG	ADR....QGT	VSLSFPPQITL
B_US_RF_M1	LQVWGR....	.....DN.	....SLSEAG	EDR....QGT	VSFSFPQITL
B_US_SF2_K	LQVWGG....	.....ENN.	....SLSEAG	ADR....QGT	VSNFNPQITL
B_US_WEAU1	LQVQGR....	.....DNN.	....SLSEAG	ANR....QGA	VSNFNPQITL
B_US_WR27	LQVWXR....	.....DNN.	....SLSEAG	TDR....QGT	VSFSFPQITL
B_US_YU2_M	RQVWRR....	.....DNN.	....SLSEAG	ADR....QGT	VSFSFPQITL
BF1_BR_93B	LQVWGR....	.....GNN.	....SLSETG	ADR....QGD	VSFGFPQITL
C_BR_92BR0	LQVWGR....	.....DNN.	....SLSEAG	DDRQG....	TALNFPQITL
C_BW_96BW0	LQVR.....	.....GDN.	....PRSETR	AEGQG....	.TLNFPQITL
C_BW_96BW1	LRG.....	.....NN.	....PCSEAG	DERQ....	GTLNFPQITL
C_BW_96BW1	LQVR.....	.....GDN.	....PCSEAG	AEGQG....	TTFSFPQITL
C_BW_96BW1	LQVR.....	.....GDN.	....PRSEAG	AERQ....	GTLNFPQITL
C_ET_ETH22	LQVR.....	.....GSN.	....TFSEAG	AERQG....	.SLNFPQITL
C_IN_93IN1	LQVR.....	.....GDN.	....PSSKAG	AERQG....	.TLNFPQITL
C_IN_93IN9	LQVR.....	.....GDT.	....PSSKAG	AERQG....	.TLNFPQITL
C_IN_93IN9	LQVR.....	.....GDN.	....PRSEAG	AKRQG....	.TLNFPQITL
C_IN_94IN1	LQVR.....	.....GDT.	....PSSKAG	AEREG....	.TLNFPQITL
C_IN_95IN2	LQVR.....	.....GDN.	....PSSEAG	AERQG....	.TFNFPQITL
CRF01_AE_C	LGDGGR....	.....DN.	....LLPEAG	AERQG...TP	FSFSFPQITF
CRF01_AE_C	LGDGGR....	.....DN.	....LLPEAG	AERQE...TA	SSFSFPQITL
CRF01_AE_C	LRDGGR....	.....DN.	....LLLEAG	AERQG...TS	SSLSFPQITL
CRF01_AE_T	LGDGGR....	.....DN.	....LLTEAG	AERQG...TS	SSFSFPQITL
CRF01_AE_T	MGDGGR....	.....DN.	....LLTEAG	AERQ...GS	SSFSFPQITL
CRF01_AE_T	LGDGG....	.....	.....G	AERQG...TS	SSFSFPQITL
CRF01_AE_T	LGDGGR....	.....DN.	....LLAETG	AERQG...TP	SSFNFPQITL
CRF01_AE_T	LGDGGR....	.....DNG	GRDNLLTEAG	AERQG...TS	SSFSFPQITL
CRF01_AE_T	LGDGGR....	.....DN.	....LLPEAG	AERQG...TP	SSFSFPQITL
CRF02_AG_F	LGDGGR....	.....DN.	....LPSEAG	SEPG...TI	SSLSFPQITL
CRF02_AG_F	LWDGGR....	.....DN.	....LPSEAG	TEGPG...TI	SPSSFPQITL
CRF02_AG_G	LWDKGR....	.....NN.	....LLSAAG	TEGQG...TI	SSFNFPQITL
CRF02_AG_N	LWDGGR....	.....DT.	....SLSTAG	TEGQG...AI	SSFNFPQITL
CRF02_AG_S	PWDRGR....	.....DN.	....LLSEAG	TGGQG...TI	SSLSFPQITL
CRF02_AG_S	LWDGGR....	.....DN.	....LLPEAG	TGGQG...TI	PSFNFPQITL
CRF03_AB_R	LWDGGR....	.....DN.	....PLPETG	TEGQG...TA	SSFNFPQITL
CRF03_AB_R	LWDGGR....	.....DN.	....PLPETG	TERQG...TA	SSFNLPQITL
CRF04_cpx	LREERG....	.....DN.	....LLSEAG	TEGQ...GT	ISFNFPQITL
CRF04_cpx	LRDERG....	.....DN.	....LLSEAG	TEGQ...GT	ISFNFPQITL
CRF04_cpx	LRDERG....	.....DN.	....LLSEAG	TEGQ...GT	ISHNFPQITL
CRF05_DF_B	LQVWGG....	.....DS.	....LLSEAG	AEG...RGTV	PSLSFPQITL
CRF05_DF_B	LRVWRG....	.....DN.	....PLAEAG	AEG...RGEV	PSLSFPQITF
CRF06_cpx	LRFR....	.....GDS.	....PLPETG	VEGEGGKGAI	SLS.LPQITL
CRF06_cpx	LRVRR....	.....GDS.	....PLPGAE	AEG...KGAI	SLN.FPQITL
CRF06_cpx	LRVRR....	.....GDS.	....PLPEAG	TEGKG.KGAI	SLS.FPQITL
CRF06_cpx	LRVRG....	.....GNS.	....PLPEAG	AEG...EGAI	SLS.FPQITL
CRF11_cpx	LRVRR....	.....GDS.	....PLPETG	AEGEGE..GA	ISFNLPQITL
CRF11_cpx	LRVRG....	.....GDN.	....PLPETG	AQGE...GT	ISYNFPQITL
D_CD_84ZR0	LRVWGG....	.....DN.	....PLPETG	TEG...QRQGT	VLSFPQITL
D_CD_ELI_K	LRVWGR....	.....DN.	....PLSKTG	AE...RQGT	VSNFNPQITL
D_CD_NDK_M	LRVWGG....	.....DN.	....PLSETG	AE...RQGT	VSFSFPQITL
D_UG_94UG1	LRIRGG....	.....DN.	....TSSETG	AER...QGT	VSNFNPQITL
F1_BE_VI85	LRVQRG....	.....DN.	....PLSEAG	AERR...GTV	PSLSFPQITL
F1_BR_93BR	LQVRGG....	.....DN.	....PISEAG	AERR...GTV	PSLSFPQITL
F1_FI_FIN9	PRDQRR....	.....GN.	....SLSEAG	AERR...GTV	PSLSFPQITL
F1_FR_MP41	LRVQRG....	.....NN.	....PLSEAG	AEGRGT.GTV	SSLSLPQITF
F2_CM_MP25	LRVRGG....	.....DS.	....SLPEAG	AERQG...TG	SSLDFFQITL



F2KU_BE_VI	LRVWGG.....	.....DK..	....PLSEAG	DERQG...TG	ASFNLPQITL
G_BE_DRCBL	LRVRG.....	.....GDS.	....PLPEAG	AEG...KGTI	S.SIFPQITL
G_NG_92NG0	LRIRR.....	.....GDS.	....PLPEAG	AKG...EGAI	SLN.FPQITL
G_SE_SE616	PRVRR.....	.....GDS.	....PLPEAG	DEG...KGAI	S...LPQITL
H_BE_VI991	LRVRR.....	.....GDH.	....PLSEAG	AE.....RTG	TSFNFPQITL
H_BE_VI997	LRVRG.....	.....GDD.	....LLPEAG	AE.....GQG	TSLCFPQITL
H_CF_90CF0	LRVRR.....	.....GDD.	....PLSEAG	AAE.....GQG	TSLSFPQITL
J_SE_SE702	PRVRR.....	.....GD..	....PLPETG	AEGQ....GT	VSSNFPQITL
J_SE_SE788	PRARR.....	.....GD..	....PLPETG	AEGQ....GT	VSSNFPQITL
K_CD_EQTB1	LWVRGE.....	.....DN..	....PLSETG	NERSG...TG	SSFNFPQITL
K_CM_MP535	LRVRGG.....	.....DN..	....PLSEAG	DQRQG...TE	PSFNFPQITL
N_CM_YBF30	LWVSG.....	.....GEEH	TGEGDAGEPG	EDRE...LSV	PTFNFPQITL
O_CM_ANT70	GSEGTG.....	.....ESG.	.....TERG	PER.....A	LSVCLPQIPL
O_CM_MVP51	GSEGTR.....	.....ESE.	.....SEGG	SGR.....A	VPICLPQIPL
O_SN_99SE_	GNEGTR.....	.....ESG.	.....TEGG	PER.....T	LSVCLPQIPL
O_SN_99SE_	GNEGTR.....	.....KSG.	.....TEGG	PER.....T	LSVCLPQIPL
U_CD___83C	LRVRR.....	.....GDN.	....PLAEAG	AEGQG..VPL	PSFNFPQITL

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150

00BW0762_1	WQRPLVSIKV	GGQIKEALLD	TGADDTVLED	INLPGKWPK	MIGGIGGFIK
00BW0768_2	WQRPLVSIRV	GGQIKEALLD	TGADDTVLEE	ISLPGKWPK	MIGGIGGFIK
00BW0874_2	WQRPLVSIKI	EGQIREALLD	TGADDTVLEE	ITLSGRWKPK	MIGGIGGFIK
00BW1471_2	WQRPLVSIKV	GGQIKEALLD	TGADDTVLED	INLPGKWPK	MIGGIGGFIK
00BW1616_2	WQRPLVSIKV	GGQIKEALLD	TGADDTVLEE	INLPGKWPK	MIGGIGGFIK
00BW1686_8	WQRPLVTIKV	GGQVKEALLD	TGADDTVLEE	ISLPGKWPK	MIGGIGGFIK
00BW1759_3	WQRPLVSIKV	GGQVKEALLD	TGADDTVLEE	LALPGRWKPK	MIGGIGGFIK
00BW1773_2	WQRPLVSIKV	GGQIKEALLD	TGADDTVLEE	INLPGKWPK	MIGGIGGFIK
00BW1783_5	WQRPLVTIKV	GGQIKEALLD	TGADDTVLED	INLPGKWPK	MIGGIGGFIK
00BW1795_6	WQRPLVSIKV	GGQIKEALLD	TGADDTVLED	INLPGKWPK	MIGGIGGFIK
00BW1811_3	WQRPLVTIKV	GGQTKAALLD	TGADDTVLEE	MNLPGKWPK	MIGGIGGFIK
00BW1859_5	WQRPLVSIKV	GGQIKEALLD	TGADDTVLEE	ISLPGKWPK	MIGGIGGFIK
00BW1880_2	WQRPLVSIKV	GGQIKEALLD	TGADDTVLEE	INLPGKWPK	MIGGIGGFIK
00BW1921_1	WQRPLVSIKV	GGQIKEALLD	TGADDTVLEE	INLPGKWPK	MIGGIGGFIK
00BW2036_1	WQRPLVSIKV	GGQIKEALLD	TGADDTVLEE	MSLPGKWPK	MIGGIGGFIK
00BW2063_6	WQRPLVSIKV	GGQIKEALLD	TGADDTVLED	INLLGKWPK	MIGGIGGFIK
00BW2087_2	WQRPLVSIKI	EGQIKEALLD	TGADDTVLEE	MNLPGRWKPK	MIGGIGGFIK
00BW2127_2	WQRPLVSIKV	GGQIKEALLD	TGADDTVLEE	INLPGKWPK	MIGGIGGFIK
00BW2128_3	WQRPLVSIKI	GDQVKEALLD	TGADDTVLEE	IKLPGKWPK	MIGGIGGFIK
00BW2276_7	WQRPLVSIKV	GGQIREALLD	TGADDTVLEE	INLPGKWPK	MIGGIGGFIK
00BW3819_3	WQRPLVSIKV	GGQIKEALLD	TGADDTVLED	INLSGKWPK	MIGGIGGFIK
00BW3842_8	WQRPLVTIKV	GGQIKEALLD	TGADDTVLEE	MNMPGKWPK	MIGGIGGFIK
00BW3871_3	WQRPLVTIKV	GGQVKEALLD	TGADDTVLEE	INLPGKWPK	MIGGIGGFIK
00BW3876_9	WQRPLVSIKV	GGQIKEALLD	TGADDTVLEE	ISLPGKWPK	MIGGIGGFIK
00BW3886_8	WQRPLVSIKV	GGQIKEALLD	IGADDTVLEE	LSLPGKWPK	MIGGIGGFIK
00BW3891_6	WQRPLVTIKV	GGQIKEALLD	TGADDTVLEE	ISLPGKWPK	MIGGIGGFIK
00BW3970_2	WQRPLVSIKV	GGQIKEALLD	TGADDTVLEE	INLPGKWPK	MIGGIGGFIK
00BW5031_1	WQRPLVSIKV	GGQIKEALLD	TGADDTVLED	INLPGKWPK	MIGGIGGFIK
96BW01B21	WQRPLVTIRV	GGQIKEALLD	TGADDTVLEE	INLPGKWPK	MIGGIGGFIK
96BW0407	WQRPLVSIKV	GGQIREALLD	TGADDTVLED	INLPGKWPK	MIGGIGGFIK
96BW0502	WQRPLVSIKV	GGQIKEALLD	TGADNTVLEE	INLPGKWPK	MIGGIGGFIK
96BW06_J4	WQRPLVSIKV	GGQIKEALLD	TGADDTVLEE	MSLSGKWPK	MIGGIGGFIK
96BW11_06	WQRPLVSIKV	GGQIKEALLD	TGADDTVLEE	INLPGKWRPK	MIGGIGGFIK
96BW1210	WQRPLVSIKV	GGQIKEALLD	TGADDTVLED	INLPGKWPK	MIGGIGGFIK
96BW15B03	WQRPLVSIKV	GGQIKEALLD	TGADDTVLEE	MSLPGKWPK	MMGGIGGFIK
96BW16_26	WQRPLVSIKV	GGQVKEALLD	TGADDTVLEE	INLPGKWPK	MIGGIGGFIK
96BW17A09	WQRPLVSIKV	GGQIREALLD	TGADDAVLED	INLPGKWPK	MIGGIGGFIK
96BWM01_5	WQRPLVSIKV	GGQIKEALLD	TGADDTVLEE	VNLPGKWPK	MIGGIGGFIK
96BWM03_2	WQRPLVSIKV	GGQIKEALLD	TGADDTVLEE	INLPGKWPK	MIGGIGGFIK
98BWMC12_2	WQRPLVSIKI	GGQIREALLD	TGADDTVLEE	LSLPGRWKPK	MIGGIGGFIK
98BWMC13_4	WQRPLVSIKV	GGQVKEALLD	TGADDTVLED	IELPGKWRPK	MIGGIGGFIK

98BWMC14_a	WQRPLVSIKV	GGQTKEALLD	TGADDTVLEE	INLPGKWPK	MIGGIGGFIK
98BWM014_1	WQRPLVSIKI	GGQIKEALLD	TGADDTVLEE	MSLPGRWKPK	MIGGIGGFIK
98BWM018_d	WQRPLVSIKV	GGQIKEALLD	TGADDTVLED	INLPGKWPK	MIGGIGGFIK
98BWM036_a	WQRPLVSIKV	GGQTKEALLD	TGADDTVLEE	INLPGKWPK	MIGGIGGFIK
98BWM037_d	WQRPLVSIKV	GGQIREALLD	TGADDTVLED	INLPGKWPK	MIGGIGGFIK
99BW3932_1	WQRPLVPIKV	GGQIKEALLD	TGADDTVLEE	INLPGKWPK	MIGGIGGLIK
99BW4642_4	WQRPLVSIKV	GGQIKEALLD	TGADDTVLED	ISLPGKWPK	MIGGIGGFIK
99BW4745_8	WQRPLVSIKV	GGQIKEALLD	TGADDTVLEE	INLPGKWPK	MIGGIGGFIK
99BW4754_7	WQRPLVSIKV	GGQIKEALLD	TGADDTVLED	INLPGKWPK	MIGGIGGFIK
99BWMC16_8	WRRPLVTIKV	GGQIKEALLH	PGADDTVLEE	INLPRKWPK	MIGGIGGFIK
A2_CD_97CD	WQRPLVTVKI	EGQLREALLD	TGADDTVLED	INLPWKWKPK	MIGGIGGFIK
A2_CY_94CY	WQRPLVTVKI	EGQLKEALLD	TGADDTVLEE	INLPGKWPK	MIGGIGGFIK
A2D_97KR	WQRPLVTVKI	EGQLREALLD	TGADDTVLED	INLPGKWPK	MIGGIGGFIK
A2G_CD_97C	WQRPLVTVKI	GGQLIEALLD	TGADDTVLED	INLPGRWKPK	MIGGIGGFIK
A_BY_97BL0	WQRPLVTVRI	GGQLKEALLD	TGADXTVLED	INLPGKWPK	MIXGIXGFIK
A_KE_Q23_A	WQRPLVTVRI	GGQLKEALLD	TGADDTVLED	INLPGKWPK	MIGGIGGFIK
A_SE_SE659	WQRPLVTVKV	GGQLREALLD	TGADDTVLED	INLPGKWPK	MIGGIGGFIK
A_SE_SE725	WQRPLVTVKI	GGQLREALLD	TGADDTVLED	INLPGKWPK	MIGGIGGFIK
A_SE_SE753	WQRPLVTVKI	EGQLKEALLD	TGADDTVLED	INLPGKWPK	MIGGIGGFIK
A_SE_SE853	WQRPLVTVKV	GGQLKEALLD	TGADDTVLED	INLPGKWRPK	MIGGIGGFIK
A_SE_SE889	WQRPLVTVRI	GGMQKEALLD	TGADDTVLED	INLPGKWPK	MIGGIGGFIK
A_SE_UGSE8	WQRPIVTVRI	GGQLKEALLD	TGADDTVLED	INLPGKWPK	MIGGIGGFIK
A_UG_92UG0	WQRPLVTVKI	GGQLKALLD	TGADDTVLED	INLPGKWPK	MIGGIGGFIK
AC_U455_	WQRPLVTVKI	GGQLIEALLD	TGADDTVLED	INLPGKWPK	IIGGIGGFIK
AC_IN_2130	WQRPLVSIRV	GGQTKEALLD	TGADDTVLEE	INLPGKWPK	MIGGIGGFIK
AC_RW_92RW	WQRPLVTVKI	GGQLREALLD	TGADDTVLEE	INLPGKWPK	MIGGIGGFIK
AC_SE_SE94	WQRPLVTVRI	GGQLKEALLD	TGADDTVLED	INLPGKWPK	MIGGIGGFIK
ACD_SE_SE8	WQRPLVKVKI	GGQLKEALLD	TGADDTVLED	INLPGKWPK	MIGGIGGFIK
ACG_BE_VI1	WQRPLVTVRL	GGQLIEALLD	TGADDTVLEQ	INLPGKWPK	MIGGIGGFIK
AD_SE_SE69	WQRPLVTVKI	GGQLREALLD	TGADDTVLEE	INLPGKWPK	MIGGIGGFIK
AD_SE_SE71	WQRPLVTVKI	GGQLKEALLD	TGADDTVLED	INLPGKWPK	MIGGIGGFIK
ADHK_NO_97	WQRPVTVKV	GGQLKEALLD	TGADDTVLED	MNLPGKWPK	MIGGIGGFIK
ADK_CD_MAL	WQRPVTVRV	GGQLKEALLD	TGADDTVLEE	INLPGKWPK	MIGGIGGFIK
AG_BE_VI11	WQRPLVTVRI	GGQLIEALLD	TGADDTVLAE	ISLPGKWPK	MIGGIGGFIK
AG_NG_92NG	WQRPLVTVRI	GGQLIEALLD	TGADDTVLEQ	INLPGKWPK	MIGGIGGFIK
AGHU_GA_VI	WQRPLVTVKI	GGQLIEALLD	TGADDTVLEE	INLLGKWPK	MIGGIGGFIK
AGU_CD_Z32	WQRPIVTVKI	GGQPIEALLD	TGADDTVLEE	IKLPGKWPK	MIGGIGGFIK
AJ_BW_BW21	WQRPLVTIRV	AGQVKEALLD	TGADDTVLEE	MELPGKWPK	MIGGIGGFIK
B_AU_VH_AF	WQRPIVTIKI	GGQLKEALLD	TGADDTVLEE	MCLPGRWKPK	MIGGIGGFIK
B_CN_RL42_	WQRPLVTIKV	GGQLKEALLD	TGADDTVLED	MNLPGRWKPK	MIGGIGGFIK
B_DE_D31_U	WQRPLVTIKI	GGQLKEALLD	TGADDTVLEE	MSLPGRWKPK	MIGGIGGFIK
B_DE_HAN_U	WQRPLVTIKI	GGQLKEALLD	TGADDTVLEE	MSLPGRWKPK	MIGGIGGFIK
B_FR_HXB2_	WQRPLVTIKI	GGQLKEALLD	TGADDTVLEE	MSLPGRWKPK	MIGGIGGFIK
B_GA_OYI_	WQRPIVTIKI	GGQLKEALLD	TGADDTVLEE	MNLPGRWKPK	MIGGIGGFIK
B_GB_CAM1_	WQRPLVTIKI	GGQLKEALLD	TGADDTVLEE	MNLPGRWKPK	MIGGIGGFIK
B_GB_GB8_A	WQRPIVTIKI	GGQLKEALLD	TGADDTVLED	MNLPGRWKPK	MIGGIGGFIK
B_GB_MANC_	WQRPLVTIKI	GGQLKEALLD	TGADDTVLEE	MNLPGRWKPK	MIGGIGGFIK
B_KR_WK_AF	WQRPLVAIKI	GGQLKEALLD	TGADDTVLEE	MSLPGRWKPK	MIGGIGGFIK
B_NL_3202A	WQRPLVTIKI	GGQLKEALLD	TGADDTVLEE	MNLPGRWKPK	MIGGIGGFIK
B_TW_TWCYS	WQRPLVTIRI	GGQLKEALLD	TGADDTVLEE	MNLPGKWPK	MIGGIGGFIK
B_US_BC_L0	WQRPLVTIKI	GGQLKEALLD	TGADDTVLEE	MNLPGRWKPK	MIGGIGGFIK
B_US_DH123	WQRPLVKIKI	GGQLKEALLD	TGADDTVLEE	INLPGKWPK	MIGGIGGFIK
B_US_JRCSE	WQRPLVTIKI	GGQLKEALLD	TGADDTVLED	MDLPGRWKPK	MIGGIGGFIK
B_US_MNCG_	WQRPIVTIKI	GGQLKEALLD	TGADDTVLEGE	MNLPRRWKPK	MIGGIGGFIK
B_US_P896_	WQRPLVTIKV	GGQLKEALLD	TGADDTVLED	MSLPGRWKPK	MIGGIGGFIK
B_US_RF_M1	WQRPIVTVKI	GGQLKEALLD	TGADDTVLEE	MNLPGKWPK	MIGGIGGFIK
B_US_SF2_K	WQRPLVTIRI	GGQLKEALLD	TGADDTVLEE	MNLPGKWPK	MIGGIGGFIK
B_US_WEAU1	WQRPLVTIKI	EGQLKEALLD	TGADDTVLED	MNLPGKWPK	MIGGIGGFIK
B_US_WR27_	CQRPLVAIKI	GGQIKEALLD	TGADDTVLEE	MSLPGRWKPK	MVGIGGFIK
B_US_YU2_M	WQRPLVTIKI	GGQLKEALLD	TGADDTVLEE	MNLPGRWKPK	MIGGIGGFIK

BF1_BR_93B	WQRPLVTVKI	GGQLKEALLD	TGADDTVLEE	INLPGRWKPK	MIGGIGGFIK
C_BR_92BR0	WQRPLVNIKV	GGQLKEALLD	TGADDTVLEE	IKLPGNWKPK	MIGGIGGFIK
C_BW_96BW0	WQRPLVSIKV	GGQIREALLD	TGADDTVLED	INLPGKWPK	MIGGIGGFIK
C_BW_96BW1	WQRPLVSIKV	GGQIKEALLD	TGADDTVLEE	INLPGKWRPK	MIGGIGGFIK
C_BW_96BW1	WQRPLVSIKV	GGQIKEALLD	TGADDTVLED	INLPGKWPK	MIGGIGGFIK
C_BW_96BW1	WQRPLVSIKV	GGQIKEALLD	TGADDTVLEE	MSLPGKWPK	MMGGIGGFIK
C_ET_ETH22	WQRPLVTIKI	GGQLKEALLD	TGADDTVLEE	INLPGKWPK	MIGGIGGFIK
C_IN_93IN1	WQRPLVSIRV	GGQIKEALLD	TGADDTVLEE	VNLPKWPK	MIGGIGGFIK
C_IN_93IN9	WQRPLVSIRV	GGQIKETLLD	TGADDTVLEE	VNLPKWPK	MIGGIGGFIK
C_IN_93IN9	WQRPLVSIKV	GGQIREALLD	TGADDTVLEE	VNLPKWPK	MIGGIGGFIK
C_IN_94IN1	WQRPLVSIRV	GGQTREALLD	TGADDTVLEE	VNLPKWPK	MIGGIGGFIK
C_IN_95IN2	WQRPLVSIRV	GGQIKEALLD	TGADDTVLEE	VSLPGKWRPK	MIGGIGGFIK
CRF01_AE_C	WQRPLVTVKI	EGQLKEALLD	TGADDTVLED	INLPGRWKPK	MIGGIGGFIK
CRF01_AE_C	WQRPLVTVKV	GGQLKEALLD	TGADDTVLED	INLPGKWPK	MIGGIGGFIK
CRF01_AE_C	WQRPIVTVKI	GGQLKEALLD	TGADDTVLED	INLPGKWPK	MIGGIGGFIK
CRF01_AE_T	WQRPLVTVKI	GGQLKEALLD	TGADDTVLED	INLPGKWPK	MIGGIGGFIK
CRF01_AE_T	WQRPLVTVKI	GGQLKEALLD	TGADDTVLED	INLPGKWPK	MIGGIGGFIK
CRF01_AE_T	WQRPLVTIKI	GGQLKEALLD	TGADDTVLED	INLPGKWPK	MIGGIGGFIK
CRF01_AE_T	WQRPLVTVKI	GGELKEALLD	TGADDTVLED	INLPGKWPK	MIGGIGGFIK
CRF01_AE_T	WQRPLVTVKI	GGQLKEALLD	TGADDTVLED	INLPGKWPK	MIGGIGGFIK
CRF01_AE_T	WQRPLVTVKI	GGQLKEALLD	TGADDTVLED	INLPGKWPK	MIGGIGGFIK
CRF02_AG_F	WQRPLVTVKI	GGQLIEALLD	TGADDTVLEE	INLPGKWPK	MIGGIGGFIK
CRF02_AG_F	WQRPLVTVRI	GGQLIEALLD	TGADDTVLEE	INLPGKWPK	MIGGIGGFIK
CRF02_AG_G	WQRPLVTVRI	GGQLIEALLD	TGADDTVLED	INLPGKWPK	MIGGIGGFIK
CRF02_AG_N	WQRPLVTVRI	EGQLIEALLD	TGADDTVLED	INLPGKWPK	MIGGIGGFIK
CRF02_AG_S	WQRPLVTVKI	GGQLIEALLD	TGADDTVLEE	INLPGKWPK	MIGGIGGFIK
CRF02_AG_S	WQRPLFTVRI	EGQLIKALLD	TGANDTVLEK	INLPGKWPK	MIGGIGGFIK
CRF03_AB_R	WRRPLVTVRI	GGQLKEALLD	TGADDTVLED	INLPGKWPK	MIGGIGGFIK
CRF03_AB_R	WQRPLVTVRI	GGQLKEALLD	TGADDTVLED	INLPGKWPK	MIGGIGGFIK
CRF04_cpx_	WQRPLVTIKL	GGQIREALLD	TGADDTVLEE	INLPGKWPK	MIGGIGGFIK
CRF04_cpx_	WQPPLVTIKI	GGQIREALLD	TGADDTVLED	INLPGKWPK	MIGGIGGFIK
CRF04_cpx_	WQRPLVTIKI	GGQLREALLD	TGADDTVLEE	INLPGRWKPK	MIGGIGGFIK
CRF05_DF_B	WQRPVVTIRI	GGQLKEALLD	TGADDTVLED	INLPGKWPK	MIGGIGGFIK
CRF05_DF_B	WQRPVVTIKI	EGQLKEALLD	TGADDTVLEE	MNLPKWPK	MIGGIGGFIK
CRF06_cpx_	WQRPLVTVRI	GGQLIEALLD	TGADDTVLED	INLPGKWPK	MIGGIGGFIK
CRF06_cpx_	WQRPLVTVRI	GGQLIEALLD	TGADDTVLED	INLPGKWPK	MIGGIGGFIK
CRF06_cpx_	WQRPLVTGI	EGQLIEALLD	TGADDTVLED	INLPGKWPK	MIGGIGGFIK
CRF06_cpx_	WQRPLVTVKV	GEQLIEALLD	TGADDTVLEE	INLPGRWKPK	MIGGIGGFIK
CRF11_cpx_	WQRPIVKIKV	AGQLKEALLD	TGADDTVLEE	INLPGRWKPK	MIGGIGGFIK
CRF11_cpx_	WQRPVVPVKV	AGQLKEALLD	TGADDTVLEE	MSLPGRWKPK	MIGGIGGFIK
D_CD_84ZR0	WQRPVVTIKI	GGQLKEALLD	TGADDTVLED	INLPGKWPK	MIGGIGGFIK
D_CD_ELI_K	WQRPLVAIKI	GGQLKEALLD	TGADDTVLEE	MNLPKWPK	MIGGIGGFIK
D_CD_NDK_M	WQRPLVTIKI	GGQLKEALLD	TGADDTVLEE	INLPGKWPK	MIGGIGGFIK
D_UG_94UG1	WQRPVVTIKI	GGQLKEALLD	TGADDTVLEE	INLPGKWPK	MIGGIGGFIK
F1_BE_VI85	WQRPLVTIKI	GGQIKEALLD	TGADDTVLED	INLPGKWPK	MIGGIGGFIK
F1_BR_93BR	WQRPLVTIRV	GGQLKEALLD	TGADDTVLED	VNLPKWPK	MIGGIGGFIK
F1_FI_FIN9	WQRPLVTIKI	GGQLKEALLD	TGADDTVLED	INLPGKWPK	MIGGIGGFIK
F1_FR_MP41	WQRPLVTIRV	GGQLREALLD	TGADDTVLED	IDLPKWPK	IIGGIGGFIK
F2_CM_MP25	WQRPVVTIKV	GGQLREALLD	TGADDTVLED	INLPGKWPK	MIGGIGGFIK
F2KU_BE_VI	WQRPIVTIKI	GGQLREALLD	TGADDTVLED	INLPGKWPK	MIGGIGGFIK
G_BE_DRCBL	WQRPIVKVRI	GGQLIEALLD	TGADDTVLEE	IDLPKWPK	MIGGIGGFIK
G_NG_92NG0	WQRPLVTVKI	GGQLIEALLD	TGADDTVLEG	INLPGKWPK	MIGGIGGFIK
G_SE_SE616	WQRPLVTVKI	GGQLIEALLD	TGADDTVLEE	INLPGRWKPK	MIGGIGGFIK
H_BE_VI991	WQRPIVTVKI	EGQLKEALLD	TGADDTVLED	INLPGKWPK	MIGGIGGFIK
H_BE_VI997	WQRPLVTVKI	EGQLREALLD	TGADDTVLEE	INLLGRWKPK	MIGGIGGFIK
H_CF_90CF0	WQRPLVTVKI	EGQLREALLD	TGADDTVLEE	INLPGKWPK	MIGGIGGFIK
J_SE_SE702	WQRPLVTIRI	GGQLREALLD	TGADDTVLEE	IDLPKWPK	MIGGIGGFIK
J_SE_SE788	WQRPLVTIRI	GGQLREALLD	TGADDTVLED	IDLPKWPK	MIGGIGGFIK
K_CD_EQTB1	WQRPVVTVKV	GGQLREALLD	TGADDTVLEE	INLPGKWPK	MIGGIGGFIK
K_CM_MP535	WQRPIVTIKV	GGQLREALLD	TGADDTVLEE	INLPGKWPK	MIGGIGGFIK

N_CM_YBF30	WQRPVITVKI	GKEVREALLD	TGADDTVIEE	LQLEGKWKPK	MIGGIGGFIK
O_CM_ANT70	WDRPIVTARV	GGHLCEVLDD	TGADDTVLENN	IQLEGKWKPK	MIGGIGGFIK
O_CM_MVP51	WDRPIVTAKV	GGHLCEALLD	TGADDTVLENN	IQLEGRWTPK	MIGGIGGFIK
O_SN_99SE_	WDRPVVTARV	GGHLCEVLDD	TGADDTVLTN	IQLEGKWTPK	MIGGIGGFIK
O_SN_99SE_	WDRPIVPARV	GGHLCEVLDD	TGADDTVLENN	IQLEGKWTPK	MIGGIGGFIK
U_CD___83C	WQRPLVTVKI	GGQLKEALLD	TGADDTVVEE	MTLPGKWKPK	MIGGIGGFIK

	151		200
00BW0762_1	VRQYDQILIE	ICGKKAIGTV	LVGPTPVNII
00BW0768_2	VRQYDQILIE	ICGKKAIGTV	LVGPTPVNII
00BW0874_2	VRQYDQILIE	ICGKKAIGTV	LVGPTPVNII
00BW1471_2	VRQYDQIVIE	ICGKKAIGSV	LVGPTPVNII
00BW1616_2	VRQYDQIPIE	ICGKKAIGTV	LVGPTPVNII
00BW1686_8	VRQYDQISIE	ICGKKAIGTV	LVGPTPVNII
00BW1759_3	VRQYDQIPIE	ICGKKAIGTV	LVGPTPVNII
00BW1773_2	VRQYDQISIE	ICGKKAIGAV	LVGPTPVNII
00BW1783_5	VRQYDQILIE	ICGKKAIGSV	LVGPTPVNII
00BW1795_6	VRQYDHIPIE	ICGKKAIGTV	LVGPTPVNII
00BW1811_3	VRQYDEILIE	ICGKKAIGTV	LVGPTPVNII
00BW1859_5	VRQYDQILIE	ICGKKAIGTV	LVGPTPVNII
00BW1880_2	VRQYDQILIE	ICGKRAMGTV	LVGPTPVNII
00BW1921_1	VRQYDQITIE	ICGKKAIGAV	LVGPTPVNII
00BW2036_1	VRQYDQIPIE	ICGKKAIGTV	LIGPTPVNII
00BW2063_6	VRQYDQIPIE	ICGKKAIGTV	LVGPTPVNII
00BW2087_2	VRQYDQILIE	ICGKKAIGTV	LIGPTPVNII
00BW2127_2	VRQYDQVIE	ICGKKTIGTV	LVGPTPVNIV
00BW2128_3	VRQYDEIPIE	ICGKKAIGTV	LVGPTPVNII
00BW2276_7	VRQYDQILIE	ICGKKAIGTV	LIGPTPVNII
00BW3819_3	VRQYEQVPIE	ICGKKAIGTV	LVGPTPVNII
00BW3842_8	VRQYDQIVIE	ICGKKAIGTV	LIGPTPVNII
00BW3871_3	VRQYEQIPIE	ICGKKAIGTV	LVGPTPVNII
00BW3876_9	VRQYDQILVE	ICGKKAIGTV	SVGPTPVNII
00BW3886_8	VRQYDQIPIE	ICGKKAIGTV	LVGPTPVNII
00BW3891_6	VRQYDQIAIE	ICGKKAIGTV	LVGPTPVNII
00BW3970_2	VRQYDQILIE	ICGKKAIGTV	LVGPTPVNII
00BW5031_1	VRQYDQIMIE	ICGQKAIGTV	LVGPTPVNII
96BW01B21	VRQYDQILIE	ICGKKAIGTV	LVGPTPVNII
96BW0407	VRQYEQILIE	ICGKKTIGTV	LVGPTPVDII
96BW0502	VRQYDQIVIE	ICGKKAIGTV	LVGPTPVNII
96BW06_J4	VRQYDQIPIE	ICGKKAIGTV	LIGPTPVNII
96BW11_06	VRQYDQIPIE	ICGKKAIGTV	LVGPTPVNII
96BW1210	VRQYDQIVIE	ICGKKAIGSV	LVGPTPVNII
96BW15B03	VRQYDQILIE	ICGKKAIGTV	LIGPTPVNII
96BW16_26	VRQYDQITIE	ICGKKAIGTV	LVGPTPVNII
96BW17A09	VRQYDQIVIE	ICGKKAIGTV	LVGPTPVNII
96BWM01_5	VRQYDQIPIE	ICGKKAIGTV	LVGPTPVNII
96BWM03_2	VRQYDQIPIE	ICGKKAIGTV	LVGPTPVNII
98BWMC12_2	VRQYDQIPIE	ICGKKAIGTV	LVGPTPVNII
98BWMC13_4	VRQYDRIPIE	ICGKKAIGTV	LVGPTPVNII
98BWMC14_a	VRQYDQIPIE	ICGKKAIGTV	LVGPTPVNII
98BWM014_1	VGQYDQIPIE	ICGKKAIGTV	LIGPTPVNII
98BWM018_d	VKQYEQILIE	ICGKKAIGTV	LVGPTPVNII
98BWM036_a	VRQYDQILIE	ICGKKAIGTV	LVGPTPINII
98BWM037_d	VRQYDQILIE	ICGKKAIGTV	LVGPTPVNII
99BW3932_1	VRQYDQVIE	ICEKKTIGTV	LVGPTPVNII
99BW4642_4	VRQYDQIPIE	ICGKKAIGTV	LVGPTPVNII
99BW4745_8	VRQYDQILIE	ICGKKAIGTV	LVGPTPVNII
99BW4754_7	VRQYDQIHIE	ICGKKAIGTV	LVGPTPVNII
99BWMC16_8	VRQYDQILIE	ICGKKAIGTV	LVGPTPVNII
A2_CD_97CD	VRQYDQIVIE	ICGKKAIGTV	LVGPTPVNII

A2_CY_94CY	VRQYDQIAIE	ICGKRAIGTV	LVGPTPVNII	GRNMLVQLGC	TLNFPISPIE
A2D_97KR	VRQYDQITIE	ICEKRAIGTV	LVGPTPVNII	GRNMLVQLGC	TLNFPISPIE
A2G_CD_97C	VRQYDQILIE	ISGKKAIGTV	LVGPTPINII	GRNMLIQIGC	TLNFPISPIE
A_BY_97BL0	VRQYDQILVE	ICXKKAIXTV	LVGPTPXNII	XRNMLTQLGC	TLNFPISPIE
A_KE_Q23_A	VKQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
A_SE_SE659	VKQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
A_SE_SE725	VKQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
A_SE_SE753	VKQYDQVLIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
A_SE_SE853	VKQYDQISIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
A_SE_SE889	VKQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
A_SE_UGSE8	VRQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
A_UG_92UG0	VKQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTLIGC	TLNFPISPIS
A_UG_U455	VRQYDQILIE	ICGKKTIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
AC_IN_2130	VRQYDQISIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
AC_RW_92RW	VKQYDQILIE	ICGKKAIGTV	LVGPTSVNII	GRNMLTQIGC	TLNFPISPIE
AC_SE_SE94	VKQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
ACD_SE_SE8	VRQYDQILVE	ICGHKAIGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
ACG_BE_VI1	VRQYDQIMIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
AD_SE_SE69	VRQYDQILIE	ICGYKAIGTV	LVGPTPVNII	GRNLLTQIGC	ALNFPISPIE
AD_SE_SE71	VKQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
ADHK_NO_97	VRQYDXILIE	ICGKKAIGTV	LAGPTPVNII	GRNMLTQIGC	TLNFPISPIE
ADK_CD_MAL	VRQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
AG_BE_VI11	VRQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
AG_NG_92NG	VKQYDQILIE	IEGKKAIGTV	LVGPTPINII	GRNMLTQIGC	TLNFPISPIE
AGHU_GA_VI	VRQYDQVPIE	ICGKKAIGTV	LVGPTPINII	GRNMLTQIGC	TLNFPISPIE
AGU_CD_Z32	VRQYDQILIE	IGEKRAIGTV	LVGPTPINII	GRNILTQIGC	TLNFPISPIE
AJ_BW_BW21	VRQYNDIHIE	VEGKKAVGTV	LIGTPINII	GRNMLTQLGC	TLNFPISPIT
B_AU_VH_AF	VRQYDQVLVE	ICGHKAIGTV	LVGPTPVNII	GRNLLTQLGC	TLNFPISPIE
B_CN_RL42	VRQYDQIPIE	ICGHKAIGTV	LVGPTPVNII	GRNLLTQLGC	TLNFPISPIK
B_DE_D31_U	VRQYDQILIE	ICGHKAIGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
B_DE_HAN_U	VRQYDQILVE	ICGHKAIGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
B_FR_HXB2	VRQYDQILIE	ICGHKAIGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
B_GA_OYI	VRQYDQILIE	ICGHKAIGTV	LVGPTPVNII	GRNLLTQLGC	TLNFPISPIE
B_GB_CAM1	VRQYDQIPIE	ICGHKAIGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
B_GB_GB8_A	VKQYDQILVE	ICGHKAIGTV	LVGPTPVNII	GRNLLTQLGC	TLNFPISPIE
B_GB_MANC	VRQYDQILIE	ICGHKAIGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
B_KR_WK_AF	VRQYDQVAIE	ICGHKAIGTV	LIGTPVNII	GRNLLTQIGC	TLNFPISPIE
B_NL_3202A	VRQYDQIPIE	ICGHKAIGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
B_TW_TWCYS	VRQYDQIPIE	ICGHKAIGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPID
B_US_BC_L0	VRQYDQIPIE	ICGHKAIGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
B_US_DH123	VRQYDQVLIE	ICGHKAIGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
B_US_JRCSF	VRQYDQIPID	ICGHKAVGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
B_US_MNCG	VRQYDQITIG	ICGHKAIGTV	LVGPTPVNII	GRNLLTQLGC	TLNFPISPIE
B_US_P896	VRQYEQIDIE	ICGHKAKGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
B_US_RF_M1	VRQYDQILIE	ICGHKAIGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
B_US_SF2_K	VRQYDQIPVE	ICGHKAIGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
B_US_WEAU1	VRQYDQVPIE	ICGHKAIGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
B_US_WR27	VRQYDQIPIE	ICGHKAIGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
B_US_YU2_M	VRQYDQIPIE	ICGHKAIGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
BF1_BR_93B	VRQYDQIPIE	ICGRKATGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
C_BR_92BR0	VRQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
C_BW_96BW0	VRQYEQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
C_BW_96BW1	VRQYDQIPIE	ICGKKAIGTV	LVGPTPVNII	GRNLLTQLGC	TLNFPISPIE
C_BW_96BW1	VRQYDQIVIE	ICGKKAIGSV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIK
C_BW_96BW1	VRQYDQILIE	ICGKKAIGTV	LIGTPVNII	GRNMLTQLGC	TLNFPISPIE
C_ET_ETH22	VRQYDQIIIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGR	TLNFPISPIE
C_IN_93IN1	VRQYDQIPIE	ICGKKAIGTV	LVGPTPINII	GRNMLTQLGC	TLNFPISPIE
C_IN_93IN9	VRQYDQIPIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
C_IN_93IN9	VRQYDQIPIE	ICGKKAIGTV	LVGPTPVNII	GRNLLTQLGC	TLNFPISPIE
C_IN_94IN1	VRQYDQIPIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE

C_IN_95IN2	VRQYEEIPIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
CRF01_AE_C	VRQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPID
CRF01_AE_C	VRQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPID
CRF01_AE_C	VRQYDQIIIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPID
CRF01_AE_T	VRQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPID
CRF01_AE_T	VRQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPIS.PD
CRF01_AE_T	VRQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPID
CRF01_AE_T	VRQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPID
CRF01_AE_T	VRQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPID
CRF01_AE_T	VRQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPID
CRF01_AE_T	VRQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPID
CRF02_AG_F	VRQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
CRF02_AG_F	VRQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
CRF02_AG_G	VRQYDQIPIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
CRF02_AG_N	VRQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
CRF02_AG_S	VRQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
CRF02_AG_S	LRQYDQILIE	ICGKKAMGSV	LVGPTPVNII	GKNILTQIGC	TLNFPISPIE
CRF03_AB_R	VRQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
CRF03_AB_R	VRQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
CRF04_cpx_	VRQYDQIPIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
CRF04_cpx_	VKQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
CRF04_cpx_	VRQYDQITIE	ICGKKATGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
CRF05_DF_B	VRQYDQILVE	ICGQKAIGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
CRF05_DF_B	VRQYDQILIE	ICGHKAVGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
CRF06_cpx_	VKQYDQILIE	ICGKKAIGTV	LVGPTPINII	GRNMLTQIGC	TLNFPISPIE
CRF06_cpx_	VRQYDQILIE	ICGKRAMGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
CRF06_cpx_	VRQYDQILIE	ICGKKAMGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
CRF06_cpx_	VRQYDQIPIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
CRF11_cpx_	VKQYEEIIIE	IEGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPID
CRF11_cpx_	VKQYEDITIE	IEGKKAIGTV	LIGPTPVNII	GRNMLTQIGC	TLNFPISPVD
D_CD_84ZR0	VRQYDHILIE	ICGHKAIGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
D_CD_ELI_K	VRQYDQIPIE	ICGQKAIGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
D_CD_NDK_M	VRQYDQILIE	ICGYKAMGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
D_UG_94UG1	VRQYDQIPIE	ICGHKAIGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
F1_BE_VI85	VKQYDNILIE	ICGHKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPVSPIE
F1_BR_93BR	VKQYDSILIE	ICGHRAIGTV	LVGPTPVNII	GRNMLTQIGC	TLHFPIEPIE
F1_FI_FIN9	VKQYDHILIE	ICGHKAIGTV	LVGPTPVNIV	GRNMLTQIGC	TLNFPISPIE
F1_FR_MP41	VKQYDQITID	ICGHKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
F2_CM_MP25	VRQYDQVSIE	ICGQKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
F2KU_BE_VI	VRQYDQVME	ICGQKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
G_BE_DRCBL	VRQYDQILIE	ISGKKAIGTV	LVGPTPINII	GRNMLTQIGC	TLNFPISPIE
G_NG_92NG0	VRQYDQILIE	ISGKKAIGTV	LVGPTPINII	GRNMLTQIGC	TLNFPISPIE
G_SE_SE616	VRQYDQVPIE	ISGKKAIGTV	LVGPTPINII	GRNMLTQIGC	TLNFPISPIE
H_BE_VI991	VRQYEQVAIE	IFGKKAIGTV	LVGPTPVNII	GRNILTQMG	TLNLPISPIE
H_BE_VI997	VRQYDQVAIE	ICGKKAIGTV	LVGPTPVNII	GRNILTQIGC	TLNFPISPIE
H_CF_90CF0	VRQYEQVAIE	ICGKKAIGTV	LVGPTPVNII	GRNILTQIGC	TLNFPISPIE
J_SE_SE702	VRQYNEVPPIE	IEGKKAIGTV	LIGPTPVNII	GRNMLTQLGC	TLNFPISPIE
J_SE_SE788	VRQYNEVPPIE	IEGKKAIGTV	LIGPTPVNII	GRNMLTQLGC	TLNFPISPIE
K_CD_EQTB1	VRQYDQVCME	ICGQKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
K_CM_MP535	VRQYDQVLIE	ICGQKAIGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
N_CM_YBF30	VRQYDNITVD	IQGRKAVGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
O_CM_ANT70	VKEYDNVTVE	IEGREVQGT	LVGPTPVNII	GRNILTGLGC	TLNFPISPIA
O_CM_MVP51	VKEYNNVTV	VQGKEVQGT	LVGPTPVNII	GRNILTGLGC	TLNFPISPIA
O_SN_99SE_	VKEYNQVPVE	IEGREVLGTV	LVGPTPVNII	GRNILTGLGC	TLNFPISPIA
O_SN_99SE_	VKEYNQVPVE	IEGREVLGTV	LVGPTPVNII	GRNILTGLGC	TLNFPISPIA
U_CD_83C	VRQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE

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00BW0762_1	TVPVKLKPGM	DGPKVRQWPL	TEEKIKALTA	ICDEMEKEGK	ITKIGPENPY
00BW0768_2	TVPVKLKPGM	NGPKVKQWPL	TEEKIKALTA	ICEEMEREK	ITKIGPENPY
00BW0874_2	TVPVKLKPGM	DGPKVKQWPL	TEEKIQALTA	ICEEMEKEGK	ITKIGPENPY

250

00BW1471_2	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALKA	ICEEMEKEGK	ITKIGPKNPY
00BW1616_2	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
00BW1686_8	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
00BW1759_3	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
00BW1773_2	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
00BW1783_5	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
00BW1795_6	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEDMEKEGK	ITKIGPENPY
00BW1811_3	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
00BW1859_5	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
00BW1880_2	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
00BW1921_1	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALKE	ICTEMEKEGK	ITKIGPENPY
00BW2036_1	TVPVRLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
00BW2063_6	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTG	ICEEMEKEGK	ITKIGPENPY
00BW2087_2	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
00BW2127_2	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	IEKIGPENPY
00BW2128_3	TVPLKLKPGM	DGPKVNQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
00BW2276_7	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALME	ICAEMEKEGK	ITKIGPDNPY
00BW3819_3	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICKEMEKEGK	IEKIGPENPY
00BW3842_8	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICEDMEREGK	ISKIGPENPY
00BW3871_3	TVPVKLKPGM	DGPKVKQRPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
00BW3876_9	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
00BW3886_8	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
00BW3891_6	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
00BW3970_2	TVPVKLKPGM	DGPKVKQWPL	TKEKIEALTA	ICEEMEKEGK	ITKIGPENPY
00BW5031_1	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
96BW01B21	TVPVKLKPGM	DGPKVKQWPL	AEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
96BW0407	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEDMEKEGK	ITKIGPENPY
96BW0502	TVPVKLKPGM	DGPKVKQWTL	TEEKIKALTE	ICEEMEKEGK	ITKIGPENPY
96BW06_J4	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICAEMEKEGK	ITKIGPENPY
96BW11_06	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
96BW1210	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICEEMEKEGK	VTKIGPENPY
96BW15B03	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
96BW16_26	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
96BW17A09	TIPVKLKPGM	DGPKVKQWPL	TEEKIKALKA	ICEEMEKEGK	ITKIGPENPY
96BWM01_5	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
96BWM03_2	TVPVKLKPGM	DGPKVKQWPL	TAEKIKALTE	ICEEMEKEGK	ITKIGPENPY
98BWMC12_2	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
98BWMC13_4	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
98BWMC14_a	TIPVKLKPGM	DGPKVKQWPL	TEEKIRALTA	ICDEMEKEGK	ITKIGPENPY
98BWM014_1	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICEEMEKEGK	ITKIGPENPY
98BWM018_d	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
98BWM036_a	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPH
98BWM037_d	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
99BW3932_1	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICKEMEKEGK	IEKIGPENPY
99BW4642_4	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
99BW4745_8	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICEEMEKEGK	ITKIGPENPY
99BW4754_7	TVPXKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ISKIGPENPY
99BWMC16_8	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEEEGK	IEKIGPENPY
A2_CD_97CD	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICKEMEKEGK	ISKIGPENPY
A2_CY_94CY	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICKEMEKEGK	ISKIGPENPY
A2D_97KR	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICKEMEKEGK	ISKIGPENPY
A2G_CD_97C	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICKEMEKEGK	ISKIGPENPY
A_BY_97BL0	TVPVTLKPGM	DGPKVKQWPL	TEEKIKALXD	ICKEXEKEGK	ISKIXPENPY
A_KE_Q23_A	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICTEMEKEGK	ISKIGPENPY
A_SE_SE659	TVPVKLKPGM	DGPRVKQWPL	TEEKIKALTE	ICTEMEKEGK	ISKIGPENPY
A_SE_SE725	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICTEMEKEGK	ISKIGPENPY
A_SE_SE753	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICTEMEKEGK	ISKIGPENPY
A_SE_SE853	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICTEMEKEGK	ISKIGPENPY
A_SE_SE889	TVPVTLKPGM	DGPRIKQWPL	TEEKIKALTE	ICREMEKEGK	ISKIGPENPY
A_SE_UGSE8	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICTEMEKEGK	ISKIGPENPY

A_UG_92UG0	TVPVKLKPGM	DGPRIKQWPL	TEEKIKALTE	ICADMEREGR	ISKIGPENPY
A_UG_U455_	TVPVKLKPEM	DGPKVKQWPL	TEEKIKALTE	ICNEMEKEGK	ISKIGPENPY
AC_IN_2130	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICDEMEKEGK	ISKIGPENPY
AC_RW_92RW	TVPVALKPGM	DGPKVKQWPL	TEEKIKALRE	ICTEMEKEGK	ISKIGPENPY
AC_SE_SE94	TVPVTLKPGM	DGPKVKQWPL	TEEKIKALTE	ICTDMEKEGK	LSRIGPENPY
ACD_SE_SE8	TVPVKLKPGM	DGPRVKQWPL	TEEKIKALIE	ICTEMEKEGK	ISRIGPENPY
ACG_BE_VI1	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTD	ICKEMEKEGK	ISKIGPENPY
AD_SE_SE69	TVPVQLKPGM	DGPKVKQWPL	TEEKIKALTE	ICTEMEKEGK	IARIGPENPY
AD_SE_SE71	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICTEMEKEGK	ISKIGPENPY
ADHK_NO_97	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICLEMEKEGK	ISKIGPENPY
ADK_CD_MAL	TVPVKLKPGM	DGPRVKQWPL	TEEKIKALTE	ICKDMEKEGK	ILKIGPENPY
AG_BE_VI11	TVPVKLKPGM	DGPRVKQWPL	TEEKIKALTE	ICTEMEKEGK	ISKIGPENPY
AG_NG_92NG	TVPVKLKPGI	DGPKVKQWPL	TEEKIKALTE	ICTDMEKEGK	ISKIGPENPY
AGHU_GA_VI	TVPVKLKPGI	DGPKVKQWPL	TEEKIKALTE	ICNEMEKEGK	ISRIGPENPY
AGU_CD_Z32	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICTEMEKEGK	ISKIGPENPY
AJ_BW_BW21	TVPVNLKPGM	DGPRVRQWPL	TEEKIKALTE	IFTEMEKEGK	ISKIGPENPY
B_AU_VH_AF	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALVE	ICTEMEKEGK	ISKIGPENPY
B_CN_RL42_	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALVE	ICTEMEKEGK	ISKIGPENPY
B_DE_D31_U	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALVE	ICTEMEKEGK	ISKIGPENPY
B_DE_HAN_U	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALIE	ICTEMEKEGK	ISKIGPENPY
B_FR_HXB2_	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALVE	ICTEMEKEGK	ISKIGPENPY
B_GA_OYI_	TVPVKLKPGM	DGPKVKQWPL	TEEKIKVLIE	ICTEMEKEGK	ISKVGPENPY
B_GB_CAM1_	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALVE	ICTEMEKEGK	ISKIGPENPY
B_GB_GB8_A	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALVE	ICTEMEKEGK	ISKIGPENPY
B_GB_MANC_	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALVE	ICTEMEKEGK	ISKIGPENPY
B_KR_WK_AF	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALVE	ICTEMEKEGK	ISKIGPENPY
B_NL_3202A	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALVE	ICTEMEKEGK	ISKIGPENPY
B_TW_TWCYS	TVPVKLKPGM	DGPKVKQWPL	TEEKIKVLIE	ICTEMEKEGK	ISKIGPENPY
B_US_BC_LO	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALVE	ICTEMEKEGK	ISKIGPENPY
B_US_DH123	TVPVKLKPGM	DGPRVKQWPL	SEEKIKALTE	ICTEMEKEGK	ISKIGPENPY
B_US_JRCSF	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALVE	ICTEMEKEGK	ISKIGPENPY
B_US_MNCG_	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALIE	ICTEMEKEGK	ISKIGPENPY
B_US_R896_	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALVE	ICTEMEKEGK	ISKIGPENPY
B_US_RF_M1	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALVE	ICTEMEKEGK	ISKIGPENPY
B_US_SF2_K	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALVE	ICTEMEKEGK	ISKIGPENPY
B_US_WEAU1	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALVE	ICTEMEKEGK	ISKIGPENPY
B_US_WR27_	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALVE	ICTEMEKEGK	VTKIGPENPY
B_US_YU2_M	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALVE	ICTEMEKEGK	ISKIGPENPY
BF1_BR_93B	TVPVKLKPGM	DGPRVKQWPL	TEEKIKALTE	ICTEMEKEGK	ISKIGPENPY
C_BR_92BR0	TVPVKLKPGM	DGPKVKQWLL	TEEKIKALTA	ICDEMEREKG	ITKIGPENPY
C_BW_96BW0	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
C_BW_96BW1	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
C_BW_96BW1	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICEEMEKEGK	VTKIGPENPY
C_BW_96BW1	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
C_ET_ETH22	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ISRIGPENPY
C_IN_93IN1	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICDEMEKEGK	ITKIGPENPY
C_IN_93IN9	TVPVKLKPGM	DGPKVKQWPL	TKEKIEALTA	ICDEMEKEGK	ITKIGPENPY
C_IN_93IN9	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICDEMEREKG	ITKIGPENPY
C_IN_94IN1	TVPVKLKPGM	DGPKVKQWPL	TKEKIEALTI	ICNEMEKEGK	ITKIGPENPY
C_IN_95IN2	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICDEMEKEGK	ITKIGPENPY
CRF01_AE_C	TVPVTLKPGM	DGPKVKQWPT	..EEKIALTE	ICKEMEEEGK	ISKIGPENPY
CRF01_AE_C	TVPVTLKPGM	DGPKVKQWPL	TEEKIKALTE	ICKEMEEEGK	ISKIGPENPY
CRF01_AE_C	TVPVTLKPGM	DGPKVKQWPL	TEEKIKALTE	ICKEMEEEGK	ISKIGPENPY
CRF01_AE_T	TVPVTLKPGM	DGPKVKQWPL	TEEKIKALTE	ICKEMEEEGK	ISKIGPENPY
CRF01_AE_T	TVPVTLKPGM	DGPKVKQWPL	TEEKIKALTE	TCKEMEEEGK	ISKIGPENPY
CRF01_AE_T	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICKEMEEEGK	ISKIGPENPY
CRF01_AE_T	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICKEMEEEGK	ISKIGPENPY
CRF01_AE_T	TVPVTLKPGM	DGPKVKQWPL	TEEKIKALTE	ICKEMEEEGK	ISKIGPENPY
CRF01_AE_T	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICKEMEEEGK	ISKIGPENPY
CRF02_AG_F	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICTEMEKEGK	ISKIGPENPY



CRF02_AG_F	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTD	ICAEMEKEGK	ISKIGPENPY
CRF02_AG_G	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTD	ICMEMEKEGK	ISKIGPENPY
CRF02_AG_N	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTD	ICTEMEKEGK	ISKIGPENPY
CRF02_AG_S	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTD	ICTEMEKEGK	ISRIGPENPY
CRF02_AG_S	TVPLKLKPGM	DGPKVKQWPL	TEEKIKALTD	ICAEMEKEGK	ISKIGPENPY
CRF03_AB_R	TVPVTLKPGM	DGPKVKQWPL	TEEKIKALTD	ICKEMEKEGK	ISKIGPENPY
CRF03_AB_R	TVPVTLKPGM	DGPKVKQWPL	TEEKIKALID	ICKEMEKEGK	ISKIGPENPY
CRF04_cpx_	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICTDMEKEGK	ISKIGPENPY
CRF04_cpx_	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICTEMEKEGK	ISKIGPENPY
CRF04_cpx_	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALRE	ICTEMEKEGK	ISKVGPENPY
CRF05_DF_B	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICTDMEKEGK	ISRIGPENPY
CRF05_DF_B	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICTDMEKEGK	ISRIGPENPY
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CRF06_cpx_	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICTEMEKEGK	ISRIGPENPY
CRF06_cpx_	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICTEMEKEGK	ISKIGPENPY
CRF06_cpx_	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICTEMEKEGK	ISKIGPENPY
CRF11_cpx_	TVPVQLKAGM	DGPKVKQWPL	TEEKIKALTE	ICTEMEKEGK	ISKIGPENPY
CRF11_cpx_	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICTEMEKEGK	ISKIGPENPY
D_CD_84ZR0	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICTDMEKEGK	ISRIGPENPY
D_CD_ELI_K	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICTDMEKEGK	ISRIGPENPY
D_CD_NDK_M	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICTEMEKEGK	ISRIGPENPY
D_UG_94UG1	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALIE	ICSELEKEGK	ISKIGPENPY
F1_BE_VI85	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICLEMEKEGK	ISKIGPENPY
F1_BR_93BR	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICMEMEKEGK	ISKIGPENPY
F1_FI_FIN9	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICTDMEKEGK	ISRIGPENPY
F1_FR_MP41	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICTDMEKEGK	ISKIGPENPY
F2_CM_MP25	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICTEMEKEGK	ISKIGPENPY
F2KU_BE_VI	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICLEMEKEGK	ISKIGPENPY
G_BE_DRCBL	TVPVKLKPGM	DGPRVKQWPL	TEEKIKALTE	ICNEMEKEGK	ISKIGPENPY
G_NG_92NG0	TVPVKLKPGM	DGPRVKQWPL	TEEKIKALTE	ICKDMEKEGK	ISKIGPENPY
G_SE_SE616	TVPVKLKPGM	DGPRVKQWPL	TEEKIKALTE	ICKEMEEEGK	ISKIGPENPY
H_BE_VI991	TVPVTLKPGM	DGPKVKQWPL	TEEKIKALTE	ICLEMEKEGK	ISKIGPENPY
H_BE_VI997	TVPVKLKPGM	DGPRVKQWPL	TEEKIKALTE	ICMEMEKEGK	ISKIGPENPY
H_CF_90CF0	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICTEMEKEGK	ISRIGPENPY
J_SE_SE702	TVPVKLKPGM	DGPKIKQWPL	TEEKIKALTQ	ICAELEEEGK	ISRIGPENPY
J_SE_SE788	TVPVKLKPGM	DGPKIKQWPL	TEEKIKALTQ	ICAEEMEEGK	ISRVGPENPY
K_CD_EQTB1	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALVE	ICTEMEKEGK	ISKIGPENPY
K_CM_MP535	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICTEMEKEGK	ISKIGPENPY
N_CM_YBF30	TVPVKLKPGM	DGPKVKQWPL	TEEKIEALRE	ICTEMEKEGK	ISRIGPENPY
O_CM_ANT70	PVPVKLKPGM	DGPKVKQWPL	SKEKIEALTA	ICQEMEKEGK	ISRIGPENPY
O_CM_MVP51	PVPVKLKPGM	DGPKVKQWPL	SREKIEALTA	ICQEMEKEGK	ISRIGPENPY
O_SN_99SE	PVPVKLKPGM	DGPKIKQWPL	SKEKIEALTA	ICQEMEKEGK	ISRIGPENPY
O_SN_99SE	PVPVKLKPGM	DGPKIKQWPL	SKEKIEALTA	ICQEMEKEGK	ISRIGPENPY
U_CD_83C	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICLEMEKEGK	ISKIGPENPY

00BW0762_1	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW0768_2	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW0874_2	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW1471_2	NTPIFAIKKK	DSTKWRKLVD	FKELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW1616_2	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW1686_8	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW1759_3	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW1773_2	NTPVFAIKKK	DSTKWRKLVD	FGELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW1783_5	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSL
00BW1795_6	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW1811_3	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW1859_5	NTPVFAIKKK	DSTKWKKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW1880_2	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW1921_1	NTPIFAIKKK	DSTKWRKLVD	FGELNKRTQD	FWEVQLGIPH	PAGLKKKKSV

00BW2036_1	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW2063_6	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW2087_2	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW2127_2	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW2128_3	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWKVQLGIPH	PAGLKKKKSV
00BW2276_7	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW3819_3	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKQKKSV
00BW3842_8	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW3871_3	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW3876_9	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW3886_8	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW3891_6	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW3970_2	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW5031_1	NTPVSAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PVGLKKKKSV
96BW01B21	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
96BW0407	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
96BW0502	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
96BW06_J4	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
96BW11_06	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
96BW1210	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
96BW15B03	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
96BW16_26	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
96BW17A09	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGSKKKKSV
96BWM01_5	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
96BWM03_2	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
98BWMC12_2	NTSVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
98BWMC13_4	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
98BWMC14_a	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
98BWM014_1	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
98BWM018_d	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
98BWM036_a	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
98BWM037_d	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
99BW3932_1	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGXKKKKSV
99BW4642_4	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
99BW4745_8	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
99BW4754_7	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
99BWMC16_8	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
A2_CD_97CD	NTPVFAIKKK	DSDKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
A2_CY_94CY	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKAV
A2D_97KR	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKMKKSV
A2G_CD_97C	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
A_BY_97BL0	NTPVFAIKKK	DSTKWRKLVD	FXELNKRTQD	FXEVQLGIPH	PAGLKKKKSV
A_KE_Q23_A	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
A_SE_SE659	NTPIFAIKKK	NSTRWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKNSV
A_SE_SE725	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
A_SE_SE753	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
A_SE_SE853	NTPIFAIKKK	DSNRWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
A_SE_SE889	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FW.....IPH	PAGKKKK.SV
A_SE_UGSE8	NTPIFAIKKK	NSDRWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
A_UG_92UG0	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
A_UG_U455_	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	TAGLKKKKSV
AC_IN_2130	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
AC_RW_92RW	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
AC_SE_SE94	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
ACD_SE_SE8	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
ACG_BE_VI1	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKRSV
AD_SE_SE69	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
AD_SE_SE71	NTPIFAIKKK	NSTRWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
ADHK_NO_97	NTPVFAIKKK	DSTKWXXXXD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
ADK_CD_MAL	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV

AG_BE_VI11	NTPIFAIKKK	GSNRWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKRKS
AG_NG_92NG	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKRSV
AGHU_GA_VI	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FCEVQLGIPH	PAGLKKKRSV
AGU_CD_Z32	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVRLGIPH	PARLKKKRSV
AJ_BW_BW21	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
B_AU_VH_AF	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
B_CN_RL42	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEAQLGIPH	PAGLKKKKSV
B_DE_D31_U	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
B_DE_HAN_U	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
B_FR_HXB2	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
B_GA_OYI	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
B_GB_CAM1	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
B_GB_GB8_A	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PSGLKKKKSV
B_GB_MANC	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
B_KR_WK_AF	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
B_NL_3202A	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSG
B_TW_TWCYS	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
B_US_BC_L0	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
B_US_DH123	NTPIFAIKKK	NSTRWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
B_US_JRCSF	NTPVFAIKKK	DSTKWRKLVD	FRELNRRTQD	FWEVQLGIPH	PAGLKKKKSV
B_US_MNCG	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
B_US_P896	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
B_US_RF_M1	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
B_US_SF2_K	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
B_US_WEAU1	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PSGLKKKKSV
B_US_WR27	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
B_US_YU2_M	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
BF1_BR_93B	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
C_BR_92BR0	NTPVFAIKKK	DSTKWRKLVD	FRELNKRT.D	FWEVQLGIPH	PAGLKKKKSV
C_BW_96BW0	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
C_BW_96BW1	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
C_BW_96BW1	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
C_BW_96BW1	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
C_ET_ETH22	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
C_IN_93IN1	NTPIFAIKKK	DSIKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
C_IN_93IN9	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEIQLGIPH	PAGLKKKKSV
C_IN_93IN9	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
C_IN_94IN1	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
C_IN_95IN2	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
CRF01_AE_C	NTPVFAIKEK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGVPH	PAGLKKKKSV
CRF01_AE_C	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
CRF01_AE_C	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
CRF01_AE_T	NTPVFAIKKK	DSTKWRKLVD	FRELNKGTQD	FWEVQLGIPH	PAGLKKKKSV
CRF01_AE_T	NTPVFAIKKK	D.STKRKLVG	FRELNKRTQD	FWEVQLGIPR	PAGLKKKKSV
CRF01_AE_T	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
CRF01_AE_T	NTPIFAIKKK	NSTRWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
CRF01_AE_T	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
CRF01_AE_T	NTPVFAIKKK	DSTRWRKLVD	FRELNKRTQD	FWEVQLGIPR	PAGLKKKKSV
CRF02_AG_F	NTPVFGIKKR	DSTKWRKLVD	FRELNKRTQD	SWEVQLGIPH	PAGLKKKKSV
CRF02_AG_F	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQG	FWEVQLRIPH	PAGLKKKKSV
CRF02_AG_G	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
CRF02_AG_N	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
CRF02_AG_S	NTPIFAIKKK	NSTRWRKLVD	FRELNKRTQD	FWEIQLGIPH	PAGLKKKKSV
CRF02_AG_S	NTPVFAIKRK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
CRF03_AB_R	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
CRF03_AB_R	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGLPH	PAGLKKKKSV
CRF04_cpx	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
CRF04_cpx	NTPIFAIKKK	NSTRWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
CRF04_cpx	NTPIFAIKKK	NSNRWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
CRF05_DF_B	NTPIFAIKKK	DSTRWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSI

CRF05_DF_B	NTPIFAIKKK	DSTRWRKLVN	FRELNKKTQD	FWEVQLGIPH	PAGLKKKKSV
CRF06_cpx_	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
CRF06_cpx_	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
CRF06_cpx_	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
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CRF11_cpx_	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
CRF11_cpx_	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEIQLGIPH	PAGLKKKKSV
D_CD_84ZR0	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSI
D_CD_ELI_K	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
D_CD_NDK_M	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
D_UG_94UG1	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
F1_BE_VI85	NTPVFAIKKK	DSSKWRKLVD	FKELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
F1_BR_93BR	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
F1_FI_FIN9	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
F1_FR_MP41	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
F2_CM_MP25	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKRSV
F2KU_BE_VI	NTPIFAIKKK	NSNRWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
G_BE_DRCBL	NTPIFAIKKK	DSTRWRKLVD	FRELNKRTQD	FWEVPLGIPH	PGGLKQKRSV
G_NG_92NG0	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKRSV
G_SE_SE616	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
H_BE_VI991	NTPIFAIKKK	NSTRWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
H_BE_VI997	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
H_CF_90CF0	STPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
J_SE_SE702	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
J_SE_SE788	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
K_CD_EQTB1	NTPVFAIKKK	DSTKWKLVN	FRELNKRTPD	FWEVQLGIPH	PAGLKKKKSV
K_CM_MP535	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
N_CM_YBF30	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKQKKSV
O_CM_ANT70	NTPIFAIKKK	DGTKWRKLVD	FRELNKRTQE	FWEVQLGIPH	PGGLKQKQSV
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O_SN_99SE_	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PGGLKQKQSV
U_CD___83C	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV

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00BW0762_1	TVLDVGDAYF	SVPLDENFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
00BW0768_2	TVLDVGDAYF	SVPLDENFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
00BW0874_2	TVLDVGDAYF	SVPLDEGFRK	YTAFTIPSIN	NETPGIRYQY	NVLSQGWKGS
00BW1471_2	TVLDVGDAYF	SVPLDRDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
00BW1616_2	TVLDVGDAYF	SVPLDEDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
00BW1686_8	TVLDVGDAYF	SVPLDESFRK	YTAFTIPSRN	NETPGIRYQY	NVLPQGWKGS
00BW1759_3	TVLDVGDAYF	SVPLDESFRK	YTAFTIPSIN	NETPGVRYQY	NVLPQGWKGS
00BW1773_2	TVLDVGDAYF	SVPLDEDFRK	YTAFTIPSIN	NEAPGIRYQY	NVLPQGWKGS
00BW1783_5	TVLDVGDAYF	SVPLHENFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
00BW1795_6	TVLDVGDAYF	SIPLDEGFRK	YTAFTIPSIN	NATPGIRYQY	NVLPQGWKGS
00BW1811_3	TVLDVGDAYF	SVPLDEGFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
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00BW2127_2	TVLDVGDAYF	SVPLDESFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
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00BW3819_3	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
00BW3842_8	TVLDVGDAYF	SVPLDEDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
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00BW3876_9	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
00BW3886_8	TVLDVGDAYF	SVPLDESFRK	YTAFTIPSTN	NETPGIRYQY	NVLPQGWKGS

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00BW3891_6	TVLDVGDAYF	SVPLDEGFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
00BW3970_2	TVLDVGDAYF	SVPLDEGFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
00BW5031_1	TVLDVGDAYF	SVPLDENFRK	YTAFTIPSVN	NETPGIRYQY	NVLPQGWKGS
96BW01B21	TVLDVGDAYF	SVPLDEGFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
96BW0407	AVLDVGDAYF	SVPLDESFRK	YTAFTIPSIN	NSTPGIRYQY	NVLPQGWNGS
96BW0502	TVLDMGDAYF	SVPLDEGFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
96BW06_J4	TVLDVGDAYF	SVPLDEGFRK	YTAFTIPSIN	NETPGITYQY	NVLPQGWKGS
96BW11_06	TVLDVGDAYF	SVPLDESFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
96BW1210	TVLDVGDAYF	SVPLDESFRK	YTAFTIPSRN	NETPGIRYQY	NVLPQGWKGS
96BW15B03	TVLDVGDAYF	SVPLDEDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
96BW16_26	TVLDVGDAYF	SVPLDESFRK	YTAFTIPSIN	NATPGIRYQY	NVLPQGWKGS
96BW17A09	TVLDVGDAYF	SVPLDEDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
96BWM01_5	TVLDVGDAYF	SVPLDEGFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
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98BWMC12_2	TVLDVGDAYF	SVPLDEGFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
98BWMC13_4	TVLDVGDAYF	SVPLDEGFRK	YTAFTIPSVN	NETPGIRYQY	NVLPQGWKGS
98BWMC14_a	TVLDVGDAYF	SVPLDEDFRK	YTAFTIPSVN	NETPGIRYQY	NVLPQGWKGS
98BWM014_1	TVLDVGDAYF	SVPLDESFRK	YTAFTIPSTN	NETPGIRYQY	NVLPQGWKGS
98BWM018_d	TVLDVGDAYF	SVPLDENFRK	YTAFTIPSIN	NATPGIRHQY	NVLPQGWKGS
98BWM036_a	TVLDVGDAYF	SVPLDEDFRK	YTAFTIPSVN	NETPGIRYQY	NVLPQGWKGS
98BWM037_d	TVLDVGDAYF	SVPLDENFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
99BW3932_1	TVLDVGDAYF	SVPLDEDFRK	YTAFTIPSIN	NATPGIRYQY	NVLPQGWKGS
99BW4642_4	TVLDVGDAYF	SVPLDEGFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
99BW4745_8	TVLDVGDAYF	SVPLDEDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
99BW4754_7	TVLDVGDAYF	SIPLDENFRK	YTAFTIPSTN	NATPGVRYQY	NVLPQGWKGS
99BWMC16_8	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
A2_CD_97CD	TVLDVGDAYF	SVPLHEDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
A2_CY_94CY	TVLDVGDAYF	SVPLHEDFRK	YTAFTIPSTN	NETPGVRYQY	NVLPQGWKGS
A2D_97KR	TVLDVRDAYF	SVPLHEDFRK	YTAFTIPSTN	NETPGVRYQY	NVLPQGWKGS
A2G_CD_97C	TVLDVGDAYF	SVPLDEGFRK	YTAFTIPSIN	NETPGVRYQY	NVLPQGWKGS
A_BY_97BL0	TVLDVGDAYF	SVPLDESFRK	XXAFTIPSVN	NETPXIRYQY	NVLPQGWKGS
A_KE_Q23_A	TVLDVGDAYF	SVPLHEEFRK	YTAFTIPSTN	NETPGVRYQY	NVLPQGWKGS
A_SE_SE659	TVLDVGDAYF	SVPLHEDFRK	YTAFTIPSTN	NATPGIRYQX	NVLPQGWKGS
A_SE_SE725	TVLDVGDAYF	SVPLDESFRK	YTAFTIPSTN	NETPGVRYQY	NVLPQGWKGS
A_SE_SE753	TVLDDLDAYF	SVPLHEGFRK	YTAFTIPSTN	NATPGIRYQY	NVLPQGWKGS
A_SE_SE853	TVLDVGDAYF	SVPLDESFRK	YTAFTIPSTN	NETPGIRYQY	NVLPQGWKGS
A_SE_SE889	TVLDVGDAYF	SVPLDKNFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
A_SE_UGSE8	TVLDVGDAYF	SVPLDESFRK	YTAFTIPSTN	NETPGIRYQY	NVLPQGWKGS
A_UG_92UG0	TVLDVGDAYF	SVPLDESFRK	YTAFTIPSTN	NETPGIRYQY	NVLPQGWKGS
A_UG_U455_	TVLDVGDAYF	SVPLDESFRK	YTAFTIPSIN	NETPGVRYQY	NVLPQGWKGS
AC_IN_2130	TVLDVGDAYF	SVPLYEEFRK	YTAFTIPSTN	NETPGIRYQY	NVLPQGWKGS
AC_RW_92RW	TVLDVGDAYF	SVPLDESFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
AC_SE_SE94	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSTN	NETPGIRYQY	NVLPQGWKGS
ACD_SE_SE8	TILDVGDAYF	SVPLDESFRK	YTAFTIPSTN	NETPGIRYQY	NVLPQGWKGS
ACG_BE_VI1	TVLDVGDAYF	SVPLDKEFRK	YTAFTIPSVN	NETPGIRYQY	NVLPQGWKGS
AD_SE_SE69	TVLDVGDAYF	SVPLYEDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
AD_SE_SE71	TVLDVGDAYF	SVPLHEEFRK	YTAFTIPSTN	NETPGIRYQY	NVLPQGWKGS
ADHK_NO_97	TVLDVGDAYF	SVPLAEDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
ADK_CD_MAL	TVLDVGDAYF	SVPLDEDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
AG_BE_VI11	TVLDVGDAYF	SVPLDESFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
AG_NG_92NG	TVLDVGDAYF	SIPLDENFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
AGHU_GA_VI	TVLDVGDAYF	SVPLYEGFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
AGU_CD_Z32	TVLDVGDAYF	SVPLHEDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
AJ_BW_BW21	TVLDVGDAYF	SVPLDENFRK	YTAFTIPSVN	NETPGIRYQY	NVLPQGWKGS
B_AU_VH_AF	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
B_CN_RL42_	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSVN	NETPGIRYQY	NVLPQGWKGS
B_DE_D31_U	TVLDVGDAYF	SVPLDEDFRK	YTAFTIPSIN	NETPGVRYQY	NVLPQGWKGS
B_DE_HAN_U	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
B_FR_HXB2_	TVLDVGDAYF	SVPLDEDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
B_GA_OYI_	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS

B_GB_CAM1_	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSTN	NETPGIRYQY	NVLPQGWKGS
B_GB_GB8_A	TVLDVGDAYF	SVPLDKEFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
B_GB_MANC_	TVLDVGDAYF	SVPLYEDFRK	YTVFTIPSIN	NEAPGVRYQY	NVLPQGWKGS
B_KR_WK_AF	TVLDVGDAYF	SVPLDEDFRK	YTAFTIPSTN	NETPGIRYQY	NVLPQGWKGS
B_NL_3202A	TALDVGDAYF	SVPLDKDFRK	YTAFTIPSVN	NETPGIRYQY	NVLPQGWKGS
B_TW_TWCYS	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
B_US_BC_L0	TVLDVGDRYF	SVPLDKDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
B_US_DH123	TVLDVGDAYF	SIPLDEDFRK	YTAFTIPSVN	NAAPGIRYQY	NVLPQGWKGS
B_US_JRCSF	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
B_US_MNCG_	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
B_US_P896_	TVLDVGDAYF	SVPLDEDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
B_US_RF_M1	TVLDVGDAYF	SVPLDKEFRK	YTAFTIPSIN	NETPRIRYQY	NVLPQGWKGS
B_US_SF2_K	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
B_US_WEAU1	TVLDVGDAYF	SVPLDEDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
B_US_WR27_	TVLDVGDAXF	SVXLDXEXRK	YTAFTIPSHX	NETPGIRYQY	NVLPQGWKGS
B_US_YU2_M	TVLDVGDAYF	SVPLHEDFRK	YTAFTIPSIN	NETPGTRYQY	NVLPQGWKGS
BF1_BR_93B	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSTN	NETPGLRYQY	NVLPQGWKGS
C_BR_92BR0	TVLDVGDAYF	SVPLDEGFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
C_BW_96BW0	TVLDVGDAYF	SVPLDESFRK	YTAFTIPSIN	NSTPGIRYQY	NVLPQGWKGS
C_BW_96BW1	TVLDVGDAYF	SVPLDESFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
C_BW_96BW1	TVLDVGDAYF	SVPLDESFRK	YTAFTIPSRN	NETPGIRYQY	NVLPQGWKGS
C_BW_96BW1	TVLDVGDAYF	SVPLDEDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
C_ET_ETH22	TVLDVGDAYF	SVPLDEGFRK	YTAFTIPSTN	NETPGIRYQY	NVLPQGWKGS
C_IN_93IN1	TVLDVGDAYF	SVPLYEDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
C_IN_93IN9	TVLDVGDAYF	SVPLYEDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
C_IN_93IN9	TVLDVGDAYF	SVPLYEDFRK	YTAFTIPSRN	NETPGIRYQY	NVLPQGWKGS
C_IN_94IN1	TVLDVGDAYF	SVPLYEDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
C_IN_95IN2	TVLDVGDAYF	SVPLYEDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
CRF01_AE_C	TVLDVGDAYF	SVPLYEGFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
CRF01_AE_C	TVLDVGDAYF	SVPLDEGFRK	YTAFTIPSIN	NETPGVRYQY	NVLPQGWKGS
CRF01_AE_C	TVLDVGDAYF	SVPLHE.SRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
CRF01_AE_T	TVLDVGDAYF	SVPLDESFRK	YTAFTIPSIN	DETPGIRYQY	NVLPQGWKGS
CRF01_AE_T	TVLDVGDAYF	SVPLDESFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
CRF01_AE_T	TVLDVGDAYF	SVPLDESFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
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CRF01_AE_T	TVLDVGDAYF	SVPLDESFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
CRF01_AE_T	TVLDVGDAYF	SVPLDESFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
CRF02_AG_F	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSTN	NETPGIRYQY	NVLPQGWKGS
CRF02_AG_F	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSVN	NETPGIRYQY	NVLPQGWKGS
CRF02_AG_G	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
CRF02_AG_N	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSVN	NETPGIRYQY	NVLPQGWKGS
CRF02_AG_S	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
CRF02_AG_S	TVLDVGDAYF	SVPLDEDFRK	YTAFTIPSVN	NETPGIRYQY	NVLPQGWKGS
CRF03_AB_R	TVLDVGDAYF	SVPLDQDFRK	YTAFTIPSTN	NETPGIRYQY	NVLPQGWKGS
CRF03_AB_R	TVLDVGDAYF	SVPLDQDFRK	YTAFTIPSTN	NETPGIRYQY	NVLPQGWKGS
CRF04_cpx_	TVLDVGDAYF	SVPLDPEFRK	YTAFTIPSTN	NETPGIRYQY	NVLPQGWKGS
CRF04_cpx_	TVLDVGDAYF	SVPLDPAFRK	YTAFTIPSTN	NETPGVRYQY	NVLPQGWKGS
CRF04_cpx_	TVLDVGDAYF	SVPLDPEFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
CRF05_DF_B	TVLDVGDAYF	SVPLDKEFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
CRF05_DF_B	TVLDVGDAYF	SVPLHEDFRK	YTAFTIPSIN	NETPGFRYQY	NVLPQGWKGS
CRF06_cpx_	TVLDVGDAYF	SIPLDEKFRK	YTAFTIPSTN	NETPGIRYQY	NVLPQGWKGS
CRF06_cpx_	TVLDVGDAYF	SIPLDKDFRK	YTAFTIPSTN	NETPGIRYQY	NVLPQGWKGS
CRF06_cpx_	TVLDVGDAYF	SVPLGENFRK	YTAFTIPSLN	NETPGIRYQY	NVLPQGWKGS
CRF06_cpx_	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
CRF11_cpx_	TVLDVGDAYF	SVPLDENFRK	YTAFTIPSIN	NETPGVRYQY	NVLPQGWKGS
CRF11_cpx_	TVLDVGDAYF	SVLLDESFRK	YTAFTIPSLN	NETPGIRYQY	NVLPQGWKGS
D_CD_84ZR0	TVLDVGDAYF	SIPLCEDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
D_CD_ELI_K	TVLDVGDAYF	SVPLDEDFRK	YTAFTISSIN	NETPGIRYQY	NVLPQGWKGS
D_CD_NDK_M	TVLDVGDAYF	SVPLDEDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
D_UG_94UG1	TVLDVGDAYF	SVPLHEDFRK	YTAFTIPSTN	NETPGIRYQY	NVLPQGWKGS

F1_BE_VI85	TVLDVGDAYF	SVPLDKDFKK	YTAFTIPSVN	NETPGIRYQY	NVLPQGWKGS
F1_BR_93BR	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSTN	NETPGVRYQY	NVLPQGWKGS
F1_FI_FIN9	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSVN	NETPGIRYQY	NVLPQGWKGS
F1_FR_MP41	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSLN	NETPGIRYQY	NVLPQGWKGS
F2_CM_MP25	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
F2_KU_BE_VI	TVLDVGDAYF	SVPLDPEFRK	YTAFTIPSVN	NETPGVRYQY	NVLPQGWKGS
G_BE_DRCBL	TVLDVGDAYF	SVPLDENFRK	YTAFTIPSTN	NETPGIRYQY	...PQGWKGS
G_NG_92NG0	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
G_SE_SE616	TVLDVGDAYF	SVPLDEDFRK	YTAFTIPSIN	NETPGVRYQY	NVLPQGWKGS
H_BE_VI991	SVLDVGGAYF	SVPLHEDFRK	YTAFTIPSTN	NETPGIRYQY	NVLPQGWKGS
H_BE_VI997	SVLDVGDAYF	SVPLDKDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
H_CF_90CF0	SVLDVGDAYF	SVPLDKDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
J_SE_SE702	TVLDVGDAYF	SVPLYEDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
J_SE_SE788	TVLDVGDAYF	SVPLYEDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
K_CD_EQTB1	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
K_CM_MP535	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSIN	NETPGVRYQY	NVLPQGWKGS
N_CM_YBF30	TVLDVGDAYF	SCPLDKDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
O_CM_ANT70	TVLDVGDAYF	SCPLDPDFRK	YTAFTIPSVN	NETPGIRYQY	NVLPQGWKGS
O_CM_MVP51	TVLDVGDAYF	SCPLDPDFRK	YTAFTIPSVN	NETPGVRYQY	NVLPQGWKGS
O_SN_99SE_	TVLDVGDAYF	SCPLDPDFRK	YTAFTIPSVN	NETPGIRYQY	NVLPQGWKGS
O_SN_99SE_	TVLDVGDAYF	SCPLDPDFRK	YTAFTIPSVN	NETPGIRYQY	NVLPQGWKGS
U_CD___83C	TVLDVGDAYF	SVPLDENFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS

	351			400	
00BW0762_1	PAIFQSSMTR	ILEPFRTQNP	EIVIQYMDD	LYVGSdleig	QHRVKIEELR
00BW0768_2	PAIFQDSMTK	ILEPFRAQNP	EIVIQYMDD	LYVGSNLEIG	QHRAKIEELK
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00BW1471_2	PAIFQSSMTK	ILEPFRAQNP	EIVIQYMDN	LYVRSdleig	QHRAKIEELR
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00BW1686_8	PAIFQSTMTK	ILEPFRAQNP	EIVIQYMDD	LYVGSdleig	QHRAKIEELR
00BW1759_3	PAIFQSSMTK	ILEPFRAQNP	EIVIQYMDD	LYVGSdleig	QHRAKIEELR
00BW1773_2	PSIFQSSMTK	ILEPFRTQNP	EIVIQYMDD	LYVGSdleig	QHRAKIEGLR
00BW1783_5	PAIFQSSMTK	ILGPFRTQNP	DIVIQYMDD	LYVGSdleig	KHRAKIEELR
00BW1795_6	PAIFQSSMTR	ILEPFRTQNP	EIVIQYMDD	LYVGSdleig	QHRAKIEKLR
00BW1811_3	PAIFQSSMTK	ILEPFRAQNP	EIVIQYMDD	LYVGSdleig	QHRAKIEELR
00BW1859_5	PAIFQSSMTR	ILEPFRTQNP	EIVIQYMDD	LYVESdleig	QHRAKIEELK
00BW1880_2	PAIFQSSMTK	ILEPFRAQNP	EIVIQYMDD	LYVGSdlkig	QHRAKIEELR
00BW1921_1	PAIFQSSMTK	ILEPFRAQNP	DIVIQYMDD	LYVGSdleig	QHRAKIEELR
00BW2036_1	PAIFQSSMTK	ILEPFRAKNP	ELVIQYMDD	LYVGSdleig	QHRARIEELR
00BW2063_6	PAIFQSSMTK	ILEPFRAKNP	DIVIQYMDD	LYVGSdlDIG	QRREKIEDLR
00BW2087_2	PAIFQCSMTK	ILEPFRAQNP	EIVIQYMDD	LYVGSdleig	QHRAKIEELR
00BW2127_2	PAIFQSSMTK	ILEPFRAQNP	EIVIQYMDD	LYVGSdleig	QHRAKIEELR
00BW2128_3	PSIFQSSMTK	ILKPFRAQNP	EIVIQYMDD	LYVGSdleig	QHRAKIQELR
00BW2276_7	PAIFQSSMTR	ILEPFRAQNP	DIVIQYMDD	LYVGSdleig	QHRAKIEELR
00BW3819_3	PAIFQCSMTK	ILEPFRAKNP	EIVIQYMDD	LYVGSdleig	QHRAKIEELR
00BW3842_8	PAIFQSSMTK	ILEPFRAKNP	DIVIQYMDD	LYVGSdleig	QHRAKIEELR
00BW3871_3	PAIFQSSMTR	ILEPFRTQNP	EIVIQYMDD	LYVGSdleig	QHRAKIEELR
00BW3876_9	PAVFQSSMTK	ILEPFRVQNP	EIVVQYMDD	LYVGSdleig	QHRAKIEELR
00BW3886_8	PAIFQCSMTK	ILEPFRAQNP	EIVIQYMDD	LYVGSdleig	QHRAKIEELR
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96BW01B21	PAIFQSSMTK	ILEPFRALNP	EIVIQYMDD	LYVGSdleig	QHRAKIEELR
96BW0407	PAIFQSSMTK	ILEPFRTKNP	DILIQYMDD	LYVGSdlQIG	QHRAKLEELT
96BW0502	PAIFQSSMTK	ILEPFRLQNP	EIVIQYMDD	LYVGSdleig	QRRAQIEELR
96BW06_J4	PAIFQSSMTR	ILEPFRTQNP	EIVIQYMDD	LYVGSdleig	QHRAKIEELR
96BW11_06	PSIFQSSMTK	ILEPFRAKNP	ELVIQYMDD	LYVGSdleig	QHRAKIEELR
96BW1210	PAIFQSSMTK	ILEPFRAQNP	EIVIQYMDD	LYVGSdleig	QHTAKIEELR
96BW15B03	PSIFQSSMTK	ILEPFRAQNP	EIVIQYMDD	LYVGSdleig	QHRAKIEELR
96BW16_26	PAIFQSSMTK	ILEPFRAQNP	GIVIQYMDD	LYVGSdleig	QHRAKIEELR

96BW17A09	PAIFQSSMTK	ILEPFRAQNP	EIVYQYMD	LYVGXDLEIG	QHRAKIEELR
96BWM01_5	PAIFQSSMTK	ILELFRAKNP	EIVYQYMD	LYVGSDEIG	QHRAKIEELR
96BWM03_2	PAIFQASMIK	ILEPFRAQNP	EMVYQYMD	LYVGSDEIG	QHRAKIEELR
98BWM012_2	PAIFQSSMTK	ILEPFRAQNP	EIVYQYMD	LYVGSDEIG	QHRAKIEELR
98BWM013_4	PAIFQCSMTK	ILEPFRAQNP	EIVYQYMD	LYVGSDEIG	QHRAKIEELR
98BWM014_a	PAIFQSSMTK	ILEPFRAQNP	DIVYQYMD	LYVGSDEIG	QHRAKIEELR
98BWM014_1	PAIFQCSMTK	ILEPFRAQNP	EIVYQYMD	LYVGSDEIG	QHRAKIEELR
98BWM018_d	PAIFQSSMTK	ILEPFRTQNP	DIVYQYMD	LYVGSDEIG	QHRAKIEELR
98BWM036_a	PAIFQCSMTK	ILEPFRAQNP	EIVYQYMD	LYVGSDEIG	QHRAKIEELR
98BWM037_d	PAIFQCSMTK	ILEPFRAQNP	EIVYQYMD	LYVGSDEIG	QHRAKIEELR
99BW3932_1	PAIFQSSMTK	ILKPFREQNP	EMVYQYMD	LYVGSDEIG	QHTAKIEELR
99BW4642_4	PAIFQSSMTK	ILEPFRIQNP	EIVYQYMD	LYVGSDEIG	QHRAKIEELR
99BW4745_8	PAIFQSSMTK	ILEPFRAQNP	EIVYQYMD	LYVGSDEIG	QHRAKIEELR
99BW4754_7	PAIFQSSMTK	ILEPFRAQNP	DIVYQYMD	LYVGSDEIG	QHRAKIEELR
99BWM016_8	PAIFQSSMTK	ILEPFRTQNP	DIVYQYMD	LYVGSDEIG	QHRAKIEELR
A2_CD_97CD	PAIFQSSMTK	ILDPFRARNP	EMVYQYMD	LYVGSDEIG	QHRAKIEELR
A2_CY_94CY	PAIFQSSMTK	ILEPFRSKNP	ELIYQYMD	LYVGSDEIG	QHRVKEELR
A2D_97KR	PAIFQSSMTK	ILEPFRKQNP	EIVYRYMD	LYVGSDEIG	QHRTKIEELR
A2G_CD_97C	PAIFQSSMTK	ILEPFRADNP	EIVYQYMD	LYVGSDEIG	QHRAKIEELR
A_BY_97BL0	PSIFQSSMTK	ILEPFRKQNP	EIVYQYMD	LYVGSDEIG	QHRTKIEELR
A_KE_Q23_A	PAIFQSSMTK	ILEPFRSKNP	EIVYQYMD	LYVGSDEIG	QHRAKIEELR
A_SE_SE659	PAIFQSSMTK	ILEPFRSKNP	DIVYQYMD	LYVGSDEIG	QHRAKIEELR
A_SE_SE725	PAIFQSSMTK	ILEPFRKQNP	EIVYQYMD	LYVGSDEIG	QHRTKIEELR
A_SE_SE753	PAIFQSSMTK	ILEPFRERNP	EIVYQYMD	LYVGSDEIG	QHRTKIEELR
A_SE_SE853	PSIFQSSMTK	ILEPFRSKNP	EIVYQYMD	LYVGSDEIG	QHRTKIEELR
A_SE_SE889	PAIFQSSMIK	ILEPFRVQNP	EIVYQYMD	LYVGSDEIG	QHRKVEELR
A_SE_UGSE8	PAIFQSSMTK	ILEPFRSKNP	EIVYQYMD	LYVGSDEIG	QHRTKIEELR
A_UG_92UG0	PAIFQASMTK	ILEPFRSKNP	DIVYQYMD	LYVGSDEIG	QHRTKIEELR
A_UG_U455_	PSIFQSSMTK	ILEPFRSQHP	DIVYQYMD	LYVGSDEIG	QHRAKIEELR
AC_IN_2130	PAIFQASMTK	ILEPFRAQNP	EIVYQYMD	LYVGSDEIG	QHRAKIEELR
AC_RW_92RW	PAIFQNSMTK	ILEPFRAQNP	EIVYQYMD	LYVGSDEIG	QHRAKIEELR
AC_SE_SE94	PAIFQSSMTK	ILEPFRSQNP	EIVYQYMD	LYVGSDEIG	QHRTKIEELR
ACD_SE_SE8	PAIFQSSMTK	ILEPFRSKNP	DIVYQYMD	LYVGSDEIG	QHRTKIEELR
ACG_BE_VI1	PAIFQASMTK	ILDPFRERNP	EIVYQYMD	LYVGSDEIG	QHRAKIEELR
AD_SE_SE69	PAIFQSSMTK	ILEPFRKQNP	EMVYQYMD	LYVGSDEIG	QHRKIEELR
AD_SE_SE71	PAIFQSSMTK	ILEPFRSKNP	ELIYQYMD	LYVGSDEIG	QHRKIEELR
ADHK_NO_97	PAIFQCSMTK	ILEPFRAQNP	EIVYQYMD	LYVGSDEIG	QHRTKIEELR
ADK_CD_MAL	PAIFQSSMTK	ILEPFRKQNP	EIVYQYMD	LYVGSDEIG	QHRTKIEELR
AG_BE_VI11	PAIFQASMTK	ILEPFRTENP	KIVYQYMD	LYVGSDEIG	QHRKIDELR
AG_NG_92NG	PAIFQSSMTK	ILEPFRTENP	EIVYQYMD	LYVGSDEIG	QHRKIEELR
AGHU_GA_VI	PAIFQSSMTK	ILEPFRKQNP	EMVYQYMD	LYVGSDEIG	QHRKIEELR
AGU_CD_Z32	PAIFQSSMTK	ILEPFRKQNP	EIVYQYMD	LYVGSDEIG	QHRKIEELR
AJ_BW_BW21	PAIFQYMTK	ILEPFRANNP	EIVYQYMD	LYVGSDEIG	QHRTKIEELR
B_AU_VH_AF	PAIFQSSMTK	ILEPFRKQNP	DIVYQYMD	LYVGSDEIG	QHRTKIEELR
B_CN_RL42_	PAIFQCSMTK	ILEPFRKQNP	DIVYQYMD	LYVGSDEIG	QHRKIEELR
B_DE_D31_U	PAIFQSSMTK	ILEPFRKQNP	DIVYQYMD	LYVGSDEIG	QHRTKIEELR
B_DE_HAN_U	PAIFQSSMTK	ILEPFRKQNP	DIVYQYMD	LYVGSDEIG	QHRTKIEELR
B_FR_HXB2_	PAIFQSSMTK	ILEPFRKQNP	DIVYQYMD	LYVGSDEIG	QHRTKIEELR
B_GA_OYI_	PAIFQSSMTK	ILEPFRKQNP	DIVYQYMD	LYVGSDEIG	QHRTKIEELR
B_GB_CAM1_	PAIFQSSMTK	ILEPFRKQNP	DIVYQYMD	LYVGSDEIG	QHRTKIEELR
B_GB_GB8_A	PAIFQSSMTK	ILEPFRKQNP	EIVYQYMD	LYVGSDEIG	QHRKIEELR
B_GB_MANC_	PAIFQSSMTK	ILEPFRKQNP	DIVYQYMD	LYVGSDEIG	QHRKIEELR
B_KR_WK_AF	PAIFQSSMTK	ILEPFRKQNP	DIVYQYMD	LYVGSDEIG	QHRKIEELR
B_NL_3202A	PAIFQCSMTK	ILEPFRKQNP	DIVYQYMD	LYVGSDEIG	QHRTKIEELR
B_TW_TWCYS	PAIFQSSMTK	ILEPFRKQNP	DIVYQYMD	LYVGSDEIG	QHRKVEELR
B_US_BC_L0	PAIFQSSMTK	ILEPFRKQNP	DIVYQYMD	LYVGSDEIG	QHRTKIEELR
B_US_DH123	PAIFQSSMTK	ILEPFRKQNP	DIVYQYMD	LYVGSDEIG	QHRTKIEELR
B_US_JRCSF	PAIFQSSMTK	ILEPFRKQNP	DIVYQYMD	LYVGSDEIG	QHRTKIEELR
B_US_MNCG_	PAIFQSSMTK	ILEPFRKQNP	DIVYQYMD	LYVGSDEIG	QHRKIEELR
B_US_P896_	PAIFQSSMTK	ILEPFRKQNP	DIVYQYMD	LYVGSDEIG	QHRKIEDLR



B_US_RF_M1	PAIFQSSMTK	ILEPFFKQNP	EIVYQYMDD	LYVGSLEIG	QHRKIEELR
B_US_SF2_K	PAIFQSSMTK	ILEPFRKQNP	DIVYQYMDD	LYVGSLEIG	QHRTKIEELR
B_US_WEAU1	PAIFQSSMTK	ILEPFRKQNP	DIVYQYMDD	LYVGSLEIG	QHRTKIEELR
B_US_WR27_	PTIFPSSMTQ	ILEPFRKQNP	EIVYQYMDD	LYVGSNLEIG	QHRTKIEELR
B_US_YU2_M	PAIFQSSMTT	ILEPFRKQNP	DLVYQYMDD	LYVGSLEIG	QHRTKIEELR
BF1_BR_93B	PAIFQSSMTK	ILEPFRKQNP	DIVYQYMDD	LYVGSLEIG	QHRTKIEELR
C_BR_92BR0	PSIFQSSTTK	ILEPFRAQNP	EIIIYQYMDD	LYVGSLEIG	QHRAKIEELR
C_BW_96BW0	PAIFQSSMIK	ILEPFRTKNP	DIVYQYMDD	LYVGSLEIG	QHRAKIEELR
C_BW_96BW1	PSIFQSSMTK	ILEPFRAKNP	ELVYQYMDD	LYVGSLEIG	QHRARIEELR
C_BW_96BW1	PAIFQSSMTK	ILEPFRAQNP	EIVYQYMDD	LYVGSLEIG	QHTAKIEELR
C_BW_96BW1	PSIFQSSMTK	ILEPFRRNP	EIVYQYMDD	LYVGSLEIG	QHRAKIEELR
C_ET_ETH22	PPIFQSSMPQ	ILEPFRAQNP	EIVYQYMDD	LYVGSLEIG	QHRAPIEELR
C_IN_93IN1	PAIFQSSMIR	ILEPFRAQNP	EIVYQYMDD	LYVGSLEIG	QHRAKIEELR
C_IN_93IN9	PAIFQSSMTR	ILEPFRRNP	EIVYQYMDD	LYVGSLEIG	QHRAKIEELR
C_IN_93IN9	PAIFQASMTK	ILEPFRAQNP	EIVYQYMDD	LYVGSLEIG	QHRAKIEELR
C_IN_94IN1	PAIFQSSMTK	ILEPFRGRNP	EIDIYQYMDD	LYVGSLEIG	QHRAKIEELR
C_IN_95IN2	PAIFQNSMTR	ILEPFRAQNP	EIVYQYMDD	LYVGSLEIG	QHRAKIEELR
CRF01_AE_C	PAIFQSSMTK	ILEPYRAKNP	EIVYQYMDD	LYVGSLEIG	QHRTKIEELR
CRF01_AE_C	PAIFQSSMTK	ILEPFRRNP	EIVYQYMDD	LYVGSLEIG	QHRTKVEDLR
CRF01_AE_C	PAIFQCSMTK	ILEPFRAKNP	EIVYQYMDD	LYVGSLEIG	QHGTKIEELR
CRF01_AE_T	PAIFQSSMTK	ILEPFRIKNP	EMVYQYMDD	LYVGSLEIG	QHRTKIEELR
CRF01_AE_T	PAIFQSSMTK	ILEPFRIKNP	EMVYQYMDD	LYVGSLEIG	QHRKIEELR
CRF01_AE_T	PAIFQSSMTK	ILEPFRIKNP	EMVYQYMDD	LYVGSLEIG	QHRTKIEELR
CRF01_AE_T	PAIFQSSMTK	ILEPFRIKNP	EMVYQYMDD	LYVGSLEIG	QHRTKIEELR
CRF01_AE_T	PAIFQSSMTK	ILEPFRIKNP	EMVYQYKDD	LYVGSLEIG	QHRTKIEELR
CRF01_AE_T	PAIFQCSTTK	ILEPFRTKNP	EIVYQYMDD	LYVGSLEIG	QHRTKIEELR
CRF02_AG_F	PAIFQASMTN	ILEHYRIKNP	EIMIYQYMDD	LYVGSLEIE	QHRAKIEELR
CRF02_AG_F	PAIFQASMTK	ILEPFRIKNP	EIVYQYMDD	LYVGSLEIG	QHRAKIEELR
CRF02_AG_G	PAIFQSSMTK	ILEPYRIKNP	EIVYQYMDD	LYVGSLEIG	QHRAKIEELR
CRF02_AG_N	PAIFQASMTK	ILEPFRTKNP	EIVYQYMDD	LYVGSLEIG	QHRAKIEELR
CRF02_AG_S	PAIFQASMTK	ILEPFRTKNP	EIVYQYMDD	LYVGSLEIG	QHRAKIEELR
CRF02_AG_S	PAIFQASMTK	ILEPFRTKNP	ELVYQYMDD	LYVGSLEIG	QHRAKIEELR
CRF03_AB_R	PAIFQSSMTK	ILEPFRKQNP	EIVYQYMDD	LYVGSLEIG	QHRTEIEELR
CRF03_AB_R	PAIFQSSMTK	ILEPFRKQNP	EIVYQYMDD	LYVGSLEIG	QHRKIEELR
CRF04_cpx_	PAIFQCSMTK	ILEPFRFKNP	EIVYQYMDD	LYVGSLEIG	QHRAKIEELR
CRF04_cpx_	PAIFQYSMTK	ILEPFRTRNP	EIVYQYMDD	LYVGSLEIG	QHRTKIEELR
CRF04_cpx_	PAIFQCSMTK	ILEPFRTKNP	EMVYQYMDD	LYVGSLEIG	QHKAKIEELR
CRF05_DF_B	PAIFQCSMTK	ILEPFRKQNP	EVVYQYMDD	LYVGSLEIG	QHRAKIKELR
CRF05_DF_B	PAIFQCSMTK	ILEPFRKQNP	EMVYQYMDD	LYVGSLEIG	QHRTKIEELR
CRF06_cpx_	PAIFQSSMIK	ILEPFRIKNP	EIVYQYMDD	LYVGSLEIG	QHRAKIEELR
CRF06_cpx_	PAIFQCSMTK	ILDPFRIKNP	ELVYQYMDD	LYVGSLEIG	QHRAKIEELR
CRF06_cpx_	PAIFQSSMIK	ILEPFRTKNP	EIVYQYMDD	LYVGSLEIG	QHRAKIEELR
CRF06_cpx_	PAIFQSSMIK	ILEPFRQKNP	EIVYQYMDD	LYVGSLEIG	QHREKVEELR
CRF11_cpx_	PAIFQSSMTK	ILEPFRTQNP	EIVYQYMDD	LYVGSLEIG	QHREKVEELR
CRF11_cpx_	PAIFQSSMTK	ILEPFRTQNP	EVVYQYMDD	LYVGSLEIG	QHREKVEELR
D_CD_84ZR0	PAIFQSSMIK	ILEPFRKQNP	EVVYQYMDD	LYVGSLEIG	QHRAKIEKLR
D_CD_ELI_K	PAIFQSSMTK	ILEPFRKQNP	EMVYQYMDD	LYVGSLEIG	QHRTKIEKLR
D_CD_NDK_M	PAIFQSSMTK	ILEPFRKQNP	EIVYQYMDD	LYVGSLEIG	QHRTKIEELR
D_UG_94UG1	PAIFQSSMTK	ILEPFRKQNP	EMIYQYMDD	LYVGSLEIG	QHRKIEELR
F1_BE_VI85	PAIFQCSMTK	ILEPFRMKNP	DIVYQYMDD	LYVGSLEIG	QHRTKIEELR
F1_BR_93BR	PAIFQYSMTK	ILDPFRAKNP	DIVYQYMDD	LYVGSLEIG	QHRTKIEELR
F1_FI_FIN9	PAIFQCSMTK	ILEPFRTRNP	DIVYQYMDD	LYVGSLEIG	QHRTKIEELR
F1_FR_MP41	PAIFQSSMTK	ILEPFRAKNP	DIVYQYMDD	LYVGSLELG	QHRMKIEELR
F2_CM_MP25	PAIFQSSMIK	ILEPFRKENP	EIVYQYMDD	LYVGSLEIG	QHRAKIEELR
F2KU_BE_VI	PAIFQYSMTK	ILEPFRTKNP	EMVYQYMDD	LYVGSLEIG	QHRTKIEELR
G_BE_DRCBL	PAIFQSSMTK	ILEPFRTQNP	EIVYQYMDD	LYVGSLEIG	QHRAKIEELR
G_NG_92NG0	PAIFQSSMTK	ILEPSRTKNP	EMVYQYMDD	LYVGSLEIG	QHRAKIEELR
G_SE_SE616	PAIFQSSMTR	ILEPFRANNP	EMVYQYMDD	LYVGSLEIG	QHRAKIEELR
H_BE_VI991	PAIFQSSMTK	ILEPFRKQNP	EVIIYQYMDD	LYVGSLEIG	QHREKIEELR
H_BE_VI997	PAIFQSSMTK	ILEPFRKQNP	EIIIYQYMDD	LYVGSLEIG	QHRAKIEELR

H_CF_90CF0	PAIFQSSMTK	ILAPFREQNP	EMVIYQYMDD	LYVGSdleig	QHRakIEELR
J_SE_SE702	PAIFQCSMTK	ILKPFrERNP	EIViyQYMDD	LYVGSdleIE	QHRrKIKELR
J_SE_SE788	PAIFQCSMTK	ILKPFrERNP	EIViyQYMDD	LYVGSdleIE	QHRrKIKELR
K_CD_EQTB1	PAIFQCSMTK	ILEPFRRKNP	DMVlyQYMDD	LYVGSdleIG	QHRakIEELR
K_CM_MP535	PAIFQHSMTK	ILEPFRIKNP	EMVIYQYMDD	LYVGSdleIG	QPRtKIEELR
N_CM_YBF30	PAIFQSTMTK	ILEPFREKHP	EIIiyQYMDD	LYVGSdleLA	QHREAVEDLR
O_CM_ANT70	PAIFQSSMTK	ILDPFRRDNP	ELeICQYMDD	LYVGSdlPLT	EHRKRIELLR
O_CM_MVP51	PAIFQSSMTK	ILDPFRKSNP	EVEiyQYIDD	LYVGSdlPLA	EHRKRVELLR
O_SN_99SE_	PAIFQSSMTK	ILDPFRKDNP	ELeICQYMDD	LYVGSdlPLT	EHRKRVELLR
O_SN_99SE_	PAIFQSSMTK	ILDPFRKNNP	ELeICQYMDD	LYVGSdlPLT	EHRKRVELLR
U_CD___83C	PAIFQSSMTK	ILEPFrKENP	EIViyQYMDD	LYVGSdleIG	QHRakIEELR

401

450

00BW0762_1	RHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKEDWTVND
00BW0768_2	DHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKNSWTVND
00BW0874_2	AHLLKWGLTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
00BW1471_2	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
00BW1616_2	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
00BW1686_8	DHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQTIQL	PTKESWTVND
00BW1759_3	NHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
00BW1773_2	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIKL	PDKDSWTVND
00BW1783_5	NHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIVL	PEKDSWTVND
00BW1795_6	EHLLKWGLTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIVL	PEKDSWTVND
00BW1811_3	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKD.STVND
00BW1859_5	DHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
00BW1880_2	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKEDWTVND
00BW1921_1	EHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIIL	PEQESWTVND
00BW2036_1	KHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIKL	PEKESWTVNG
00BW2063_6	NHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKESWTVND
00BW2087_2	GHLLQWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
00BW2127_2	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKGTVQPIQL	PEKDSWTVND
00BW2128_3	DHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
00BW2276_7	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
00BW3819_3	GHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
00BW3842_8	AHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIKL	PEKESWTVND
00BW3871_3	DHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQKIQL	PTKDSWTVND
00BW3876_9	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIKL	PEKESWTVND
00BW3886_8	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
00BW3891_6	EHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWAVQPIQL	PEKDSWTVND
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00BW5031_1	KHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
96BW01B21	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPINL	PEKESWTVND
96BW0407	EHLLIWGLTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PDKDSWTVND
96BW0502	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PDKDSWTVND
96BW06_J4	NHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PTKDSWTVND
96BW11_06	KHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQSIKL	PEKESWTVND
96BW1210	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKESWTVND
96BW15B03	KHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIEL	PEKESWTVND
96BW16_26	THLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PDKDSWTVND
96BW17A09	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
96BWM01_5	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DQWTVQPIQL	PEKESWTVND
96BWM03_2	EHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	AEKDSWTVND
98BWMC12_2	IHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTIQPIQL	PEKDSWTVND
98BWMC13_4	RHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKESWTVND
98BWMC14_a	DHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PTKDSWTVND
98BWM014_1	GHLLQWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
98BWM018_d	EHLLKWGLTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIVL	PEKDSWTVND
98BWM036_a	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
98BWM037_d	QHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
99BW3932_1	DHLLGWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKESWTVND

99BW4642_4	GHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
99BW4745_8	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
99BW4754_7	EHLLRWGLTT	PDKKHQKEPP	FLWMGYEPHP	DKWTVQPILL	PEKESWTVND
99BWMC16_8	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIML	PTKDSWTVND
A2_CD_97CD	AHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIKL	PEKDSWTVND
A2_CY_94CY	AHLLKWGFYT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIKL	PEKDSWTVND
A2D_97KR	NHLLKWGFYT	PDKKHQKEPP	FLWMEYELHP	DKWTVQPIKL	PEKDSWTVND
A2G_CD_97C	EHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PDKESWTVND
A_BY_97BL0	AHLLSWGFTT	PDKKHQKEPP	FLWXXYEXHP	DKWTVQPIML	PDKDSWTVND
A_KE_Q23_A	AHLLSWGLIT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIEL	PEKDSWTVND
A_SE_SE659	SHLLSWGFTT	PDQKHQKEPP	FLWMGYELHP	DKWTVQPIVL	PEKESWTVND
A_SE_SE725	AHLLSWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIEL	PEKESWTVND
A_SE_SE753	EHLLSWGFTT	PDKKHQKEPP	FLWMGYEVHP	DKWTVQPIVL	PEKESWTVND
A_SE_SE853	AHLLSWGLTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPINL	PEKESWTVND
A_SE_SE889	AHLLSWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PNKENWTVND
A_SE_UGSE8	AHLLSWGFFT	PDQKHQKEPP	FLWMGYELHP	DKWTVQPIKL	PEKESWTVND
A_UG_92UG0	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIEL	PEKESWTVND
A_UG_U455_	AHLLSWGFIT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
AC_IN_2130	EHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
AC_RW_92RW	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
AC_SE_SE94	AHLLSWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PDKDSWTVND
ACD_SE_SE8	AHLLSWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQSIKL	PEKESWTVND
ACG_BE_VI1	EHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
AD_SE_SE69	GHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPITL	PEKESWTVND
AD_SE_SE71	EHLLKWGFYT	PDQKHQKEPP	FLWMGYELHP	DRWTVQPIKL	PEKESWTVND
ADHK_NO_97	EHLLRWGLTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PDKESWTVND
ADK_CD_MAL	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PDKESWTVND
AG_BE_VI11	EHLLRWGLTT	PDQKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
AG_NG_92NG	NHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PNKESWTVND
AGHU_GA_VI	AHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQTVKL	PEKDSWTVND
AGU_CD_Z32	EHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PDKESWTVND
AJ_BW_BW21	EHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PDKEAWTVND
B_AU_VH_AF	QHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIVL	PEKDSWTVND
B_CN_RL42_	QHLLRWGFTT	PDKKHQKEPP	FLWMGYELHL	DKWTVQPIML	PEKDSWTVND
B_DE_D31_U	QHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPITL	PEKDSWTVND
B_DE_HAN_U	QHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIVL	PEKDSWTVND
B_FR_HXB2_	QHLLRWGLTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIVL	PEKDSWTVND
B_GA_OYI_	QHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIML	PEKDSWTVND
B_GB_CAM1_	QHLLRWGLTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIML	PEKDSWTVND
B_GB_GB8_A	QHLLRWGFST	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIVL	PEKDSWTVND
B_GB_MANC_	QYLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPITL	PEKDSWTVND
B_KR_WK_AF	QHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIVL	PEKDSWTVND
B_NL_3202A	QHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIVL	PEKDSWTVND
B_TW_TWCYS	QHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIVL	PEKDSWTVND
B_US_BC_L0	QHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIVL	PEKDSWTVND
B_US_DH123	QHLLRWGLFT	PDQKHQKEPP	FLWMGYELHP	DKWTVQPIVL	PEKDSWTVND
B_US_JRCSF	QHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIVL	PEKDSWTVND
B_US_MNCG_	RHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIVL	PEKDSWTVND
B_US_P896_	QHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIVL	PEKDSWTVND
B_US_RF_M1	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIVL	PEKDSWTVND
B_US_SF2_K	QHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIML	PEKDSWTVND
B_US_WEAU1	QHLLRWGFTT	PDKKHQKDEPP	FLWMGYELHP	DKWTVQPIKL	PEKESWTVND
B_US_WR27_	QHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIEL	PEKDSWTVND
B_US_YU2_M	QHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIVL	PEKDSWTVND
BF1_BR_93B	QHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIVL	PEKDSWTVND
C_BR_92BR0	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
C_BW_96BW0	EHLLKWGLTT	PYKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PDKDSWTVHD
C_BW_96BW1	KHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQSIKL	PEKESWTVND
C_BW_96BW1	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKESWTVND
C_BW_96BW1	KHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIEL	PEKESWTVND

C_ET_ETH22	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
C_IN_93IN1	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
C_IN_93IN9	GHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
C_IN_93IN9	QHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
C_IN_94IN1	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
C_IN_95IN2	KHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
CRF01_AE_C	DHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DRWTVQPIEL	PEKDSWTVND
CRF01_AE_C	AHLLSWGFTT	PDKKHQKEPP	FLWMGYELHP	DRWTVQPIVL	PEKDSWTVND
CRF01_AE_C	AHLLSWGFTT	PDKKHQKESP	FLWMGYELHP	DRWTVQPIQL	PDKESWTVDD
CRF01_AE_T	AHLLSWGFTT	PDKKHQKEPP	FLWMGYELHP	DRWTVQPIEL	PEKDSWTVND
CRF01_AE_T	AHLLSWGFTT	PDKKHQKEPP	FLWMGYELHP	DRWTVQPIEL	PEKDSWTVND
CRF01_AE_T	AHLLSWGFTT	PDKKHQKEPP	FLWMGYELHP	DRWTVQPIEL	PEKDSWTVND
CRF01_AE_T	AHLLSWGFTT	PDQKHQKEPP	FLWMGYELHP	DRWTVQPIEL	PEKDSWTVND
CRF01_AE_T	AHLLSWGFTT	PDKKHQKEPP	FLWMGYELHP	DRWTVQPIEL	PEKDSWTVND
CRF01_AE_T	AHLLSWGFTT	PGKKHQKEPP	FLWMGYELHP	DRWTVQPIEL	PEKDSWTVND
CRF02_AG_F	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
CRF02_AG_F	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
CRF02_AG_G	EHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIML	PEKDSWTVND
CRF02_AG_N	GHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPVEL	PEKDSWTVND
CRF02_AG_S	EHLLRWGFTT	PDEKHQKEPP	FLWMGYELHP	DKWTVQPIVL	PEKDSWTVND
CRF02_AG_S	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
CRF03_AB_R	EHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIVL	PEKDSWTVND
CRF03_AB_R	DHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIVL	PEKDSWTVND
CRF04_cpx_	EHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQP	AEKDSWTVND
CRF04_cpx_	EHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
CRF04_cpx_	EHLLRWGFTT	PDQKHQKEPP	FLWMGYELHP	DKWTVQPIQL	VEKESWTVND
CRF05_DF_B	EHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PDKDSWTVND
CRF05_DF_B	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PNKDSWTVND
CRF06_cpx_	EHLLKWGLTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PDKESWTVND
CRF06_cpx_	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PNKESWSIND
CRF06_cpx_	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PDKDSWTVND
CRF06_cpx_	AHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PDKDSWTVND
CRF11_cpx_	KHLLRWGLTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PDKECWTVND
CRF11_cpx_	KHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PDKESWTVND
D_CD_84ZR0	EHLLRWGLTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQSITL	PEKESWTVND
D_CD_ELI_K	EHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQSIKL	PEKESWTVND
D_CD_NDK_M	EHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPINL	PEKESWTVND
D_UG_94UG1	GHLLKWGFTT	PDKKYQKEPP	FLWMGYELHP	DKWTVQPIHL	PEKESWTVND
F1_BE_VI85	EHLLRWGFTT	PDKKHQKEPP	FLWMGHELHP	DKWTVQPIQL	PNKDSWTVND
F1_BR_93BR	EHLLKWGLTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PDKDSWTVND
F1_FI_FIN9	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PDKDSWTVDD
F1_FR_MP41	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
F2_CM_MP25	EHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQAIQL	PDKSSWTVND
F2KU_BE_VI	EHLLRWGFTT	PDEKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PDKEDWTVND
G_BE_DRCBL	EHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PNKENWTVND
G_NG_92NG0	EHLLKWGLTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKEDWTVND
G_SE_SE616	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PDKESWTVND
H_BE_VI991	AHLLRWGFTT	PDQKHQKEPP	FLWMGYELHP	DKWTVQPVKL	PEKDSWTVND
H_BE_VI997	AHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPVKL	PEKDSWTVND
H_CF_90CF0	AHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQTVKL	PEKDSWTVND
J_SE_SE702	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKEDWTVND
J_SE_SE788	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKEDWTVND
K_CD_EQTB1	EHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PDKDSWTVND
K_CM_MP535	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PDKDSWTVND
N_CM_YBF30	DHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIKL	PEKDVWTVND
O_CM_ANT70	EHLYQWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQSIQL	PNKDVWTVND
O_CM_MVP51	EHLYQWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PDKEVWTVND
O_SN_99SE_	EHLYQWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PNKEEWTVND
O_SN_99SE_	EHLYQWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PNKEEWTVND
U_CD_83C	AHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PNKDDWTVND

451

500

00BW0762_1	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGA	KALTDIVPLT	EEAELELAEN
00BW0768_2	IQKLVGKLNW	ASQIYPGIKV	RQLCRLLRGA	KVLTDIVPLT	EEAELELAEN
00BW0874_2	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGT	KALTDIVPLT	EEAELELAEN
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00BW1616_2	IQKLVGKLNW	ASQIYPGVKV	KQLCKLLRGT	KALTDIVPLT	EEAELELAEN
00BW1686_8	IQKLVGKLNW	ASQIYSGIKV	KQLCKLLRGT	KALTDIVPLT	EEAELELAEN
00BW1759_3	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGA	KALTDIVPLT	EEAELELAEN
00BW1773_2	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGA	KALTDIVPLT	EEAELELAEN
00BW1783_5	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGA	KALTDIVPLT	EEAELELAEN
00BW1795_6	IQKLVGKLNW	ASQIYPGIKV	TQLCKLLRGA	KALTDIVPLT	DEAELELAEN
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00BW2128_3	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGT	KALTDIIPLT	EEAELELAEN
00BW2276_7	IQKLVGKLNW	VSQIYPGIKV	RQLCKLLRGA	KALTDIVPLT	EEAELELAEN
00BW3819_3	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGA	KALTDIVPLT	EEAELELAEN
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96BW01B21	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGA	KALTDIVPLT	EEAELELAEN
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96BW0502	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGA	KALTDVPLT	EEAELELAEN
96BW06_J4	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGT	KALTDVPLN	EEAELELAEN
96BW11_06	IQKLVGKLNW	ASQIYPGVKV	RQLCKLLRGA	KALTDIVPLT	EEAELELAEN
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96BW16_26	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGA	KALTDIIPLT	EEAELELAEN
96BW17A09	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGA	KALTDIVPLT	EEAELELAEN
96BWM01_5	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGA	KALTDIVPLT	DEAELELAEN
96BWM03_2	VQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGA	KALTDIVPLT	EEAELELAEN
98BWMC12_2	IQRLVGKLNW	ASQIYSGIKV	RQLCKLLRGA	KALTDIVPLT	EEAELELAEN
98BWMC13_4	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGA	KALTDIVPLT	EEAELELAEN
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98BWM018_d	IQKLVGKLNW	ASQIYPGIKV	RQLCKLIRGT	KKLTDIVPLT	EEAELELAEN
98BWM036_a	IQKLVGKLNW	ASQIYPGIKV	KNLCKLLRGA	KALTDIVPLT	EEAELELAEN
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99BWMC16_8	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGA	KALTDIVPLT	EEAELELAEN
A2_CD_97CD	IQKLVGKLNW	ASQIYAGIKV	RQLCKLLRGT	KALTDIVPLT	REAELELEEN
A2_CY_94CY	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGA	KALTDIVTLT	KEAELELEEN
A2D_97KR	IQKLVGKLNW	ASQIYAEIKV	KQLCKLLRGA	KALTDIVPLT	KEAELELEEN
A2G_CD_97C	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGT	KALTEIVSLT	AEAELELAEN
A_BY_97BL0	IQKLXGKLNW	ASQIYPEIKV	RQLCKLLXGA	KALTDIVTLT	EEAELELAEN
A_KE_Q23_A	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGA	KALTDVVTLT	EEAELELAEN
A_SE_SE659	IQKLVGKLNW	ASQIYPGIKV	KQLCRLLRGA	KALTDIVELT	EEAELELAEN

A_SE_SE725	IQKLVGKLNW	ASQIYAGIKV	KQLCRLLRGA	KALTDIVTLT	EEAELELAEN
A_SE_SE753	IQKLVGKLNW	ASQIYAGIKV	RQLCKLLRGA	KALTDIVTLT	EEAELELAEN
A_SE_SE853	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGA	KALTDIVTLT	EEAELELAEN
A_SE_SE889	IQKLVGKLNW	ASQIYVGIKV	KQLCKLLRGA	KALTDIVTLT	EEAELELAEN
A_SE_UGSE8	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGA	KALTDIVTLT	EEAELELAEN
A_UG_92UG0	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGT	KALTDIVTLT	EEAELELAEN
A_UG_U455	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGA	KALTDIVTLT	EEAELELAEN
AC_IN_2130	IQKLVGKLNW	ASQIYPGIKV	RQLCRLLRGA	KALTDIVPLT	EEAELELAEN
AC_RW_92RW	IQKLVGKLNW	ASQIYPGVKV	RQLCKLLRGT	KALTDIVPLT	EEAELELAEN
AC_SE_SE94	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGT	KSLTDVVTLT	EEAELELAEN
ACD_SE_SE8	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGA	KALTDVVTLT	EEAELELAEN
ACG_BE_VI1	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGA	KALTDIVPLT	EEAELELAEN
AD_SE_SE69	IQKLVGKLNW	ASQIYPGIKV	RQLCKCIRGA	KALTEVVPLT	EEAELELAEN
AD_SE_SE71	IQKLVGKLNW	ASQIYAGIKV	KQLCKCLRGA	KALTEIVPLT	EEAELELAEN
ADHK_NO_97	IQKLVGKLNW	ASQIYPGIKV	RQLCRLLRGT	KALTDIVPLT	AEAELELAEN
ADK_CD_MAL	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGA	KALTDIVPLT	AEAELELAEN
AG_BE_VI11	IQKLVGKLNW	ASQIYAGIRV	KQLCKLLRGA	KALTDIVTLT	EEAELELAEN
AG_NG_92NG	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGA	KALTDIVPLT	EEAELELAEN
AGHU_GA_VI	IQKLVGKLNW	ASQIYSGIKV	KQLCKLLRGA	KALTDIVPLT	EEAELELAEN
AGU_CD_Z32	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGT	KALTDIVPLT	AEAELELAEN
AJ_BW_BW21	IQKLVGKLNW	ASQIYPGIQV	RHLCRLLRGA	KALTDIVPLT	AEAELELAEN
B_AU_VH_AF	IQKLVGKLNW	ASQIYSGIKV	RQLCKLLRGT	KALTEVIPLT	EEAELELAEN
B_CN_RL42	IQKLVGKLNW	ASQIYAGIKV	KELCKLLRGT	KALTEVIPLT	EEAELELAEN
B_DE_D31_U	IQKLVGKLNW	ASQIYAGIKV	RQLCKLLRGA	KALTEVIPLT	KEAELELAEN
B_DE_HAN_U	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGP	KALTEVIPLT	KEAELELAEN
B_FR_HXB2	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGT	KALTEVIPLT	EEAELELAEN
B_GA_OYI	IQKLVGKLNW	ASQIYAGIKV	KNLCKLLRGT	KALTEVIPLT	EEAELELAEN
B_GB_CAM1	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGT	KALTEVVPLT	EEAELELAEN
B_GB_GB8_A	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGA	KALTEVITLT	EEAELELAEN
B_GB_MANC	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGA	KALTEVIPLT	KEAELELAEN
B_KR_WK_AF	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGT	KALTEVVPLT	EEAELELAEN
B_NL_3202A	IQKLVGKLNW	ASQIYAGIKV	RHLCCKLLRGT	KALTEVIPLT	EEAELELAEN
B_TW_TWCYS	IQKLVGKLNW	ASQIYAGIKV	RQLCKLLRGT	KALTEVVPLT	KEAELELAEN
B_US_BC_L0	IQKLVGKLNW	ASQIYSGIKV	KQLCKLLRGT	KALTEVVTLT	EEAELELAEN
B_US_DH123	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGA	KALTEVIPLT	EEAELELAEN
B_US_JRCSE	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGT	KALTEVIPLT	KEAELELAEN
B_US_MNCG	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGT	KALTEVIPLT	EEAELELAEN
B_US_P896	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGT	KALTEVVPLT	EEAELELAEN
B_US_RF_M1	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGT	KALTEVVQLT	KEAELELAEN
B_US_SF2_K	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGT	KALTEVIPLT	EEAELELAEN
B_US_WEAU1	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGT	KALTEIIPIT	EEAELELAEN
B_US_WR27	IQKLVGKLNW	XSQIYAGIKV	XQLCKLLRGT	KALTEVVPLT	EEAELELAGN
B_US_YU2_M	IQKLVGKLNW	ASQIYAGIKV	RQLCKLLRGT	KALTEVIPLT	EEAELELAEN
BF1_BR_93B	IQKLVGKLNW	ASQIYAGIKV	RQLCKLLRGT	KALTEVVPLT	AEAELELAEN
C_BR_92BR0	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGA	KALTDIVPLT	EEAELELAEN
C_BW_96BW0	IQKLVGKLNW	ASQIYPGIRV	KHLCKLLRGA	KALTDIVPLT	EEAELELAEN
C_BW_96BW1	IQKLVGKLNW	ASQIYPGVKV	RQLCKLLRGA	KALTDIVPPT	EEAELELAEN
C_BW_96BW1	IQKLVGKLNW	ASQIYPGIKV	RQLCKILRGV	KALTDIVTLT	EEAELELAEN
C_BW_96BW1	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGA	KALTDIVPLT	EEAELELAED
C_ET_ETH22	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGA	KALTDIVTLT	EEAELELAEN
C_IN_93IN1	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGA	KALTDIVPLT	EEAELELAEN
C_IN_93IN9	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGA	KALTDIVPLT	EEAELELAEN
C_IN_93IN9	IQKLVGKLNW	ASQIYPGIKV	KQLCRLLRGA	KVLTDIVPLT	EEAELELAEN
C_IN_94IN1	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGA	KALTDIVPLT	EEAELELAEN
C_IN_95IN2	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGT	KALTDIVPLT	EEAELELAEN
CRF01_AE_C	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGA	KALTEVVPLT	EEAELELAEN
CRF01_AE_C	IQKLVGKLNW	ASQIYAGIKV	RQLCKLLRGA	KALTDIVTLT	EEAELELAEN
CRF01_AE_C	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGA	KALTDIVPLT	EEAELELAEN
CRF01_AE_T	IQKLVGKLNW	ASQIYAGIKV	KQLCKPLRGT	KALTDIVPLT	EEAELELAEN
CRF01_AE_T	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGA	KALTDIVPLT	EEAELELAEN

CRF01_AE_T	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGT	KALTDIVPLT	EEAELELEEN
CRF01_AE_T	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGA	KALTDIVPLT	EEAELELAEN
CRF01_AE_T	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGA	KALTDIVPLT	EEAELELAEN
CRF01_AE_T	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGA	KALTDIVPLT	EEAELELAEN
CRF02_AG_F	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGA	KALTDIVPLT	EEAELELAEN
CRF02_AG_F	IQKLVGKLNW	ASQIFAGIKV	KQLCRLLRGA	KALTDIVPLT	EEAELELAEN
CRF02_AG_G	IQKLVGKLNW	ASQIYAGIKV	KELCKLLRGA	KALTDIVTLT	EEAELELAEN
CRF02_AG_N	IQKLVGKLNW	ASQIYAGIKI	KQLCRLLRGA	KALTDIVALT	EEAELELAEN
CRF02_AG_S	IQKLVGKVNW	QVRIYAGIKV	KQLCKLLRGA	KTLTDIVTLT	EEAELELAEN
CRF02_AG_S	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGT	KALTDIVPLT	EEAELELAEN
CRF03_AB_R	IQKLVGKLNW	ASQIYAGIKV	RQLCKLLRGA	KALTEVIPLT	AEAELELAEN
CRF03_AB_R	IQKLVGKLNW	ASQIYAGIKV	RQLCKLLRGA	KALTEIIPLT	AEAELELAEN
CRF04_cpx_	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGA	KALTDIVPLT	TEAELELAEN
CRF04_cpx_	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGT	KALTDIVPLT	TEAELELAEN
CRF04_cpx_	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGA	KALTDIVPLT	TEAELELAEN
CRF05_DF_B	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGT	KALTEVIPLT	EEAELELAEN
CRF05_DF_B	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGT	KALTEVVPLT	EEAELELAEN
CRF06_cpx_	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGA	KALTDIVPLT	AEAELELAEN
CRF06_cpx_	IQKLVGKLNW	ASQIYSGIKV	RQLCKLLRGA	KALTDIVPLT	AEAELELAEN
CRF06_cpx_	IQKLVGKLNW	ASQIYPGIKV	KHLCKLLRGA	KALTDIVPLT	AEAELELAEN
CRF06_cpx_	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGA	KALTDIVPLT	AEAELELAEN
CRF11_cpx_	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGT	KALTDIVPLT	AEAELELAEN
CRF11_cpx_	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGA	KALTDIVPLT	AEAELELAEN
D_CD_84ZR0	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGT	KALTEVIPLT	EEAELELAEN
D_CD_ELI_K	IQNLVERLNW	ASQIYPGIKV	RQLCKLLRGT	KALTEVIPLT	EEAELELAEN
D_CD_NDK_M	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGT	KALTEVVPLT	EEAELELAEN
D_UG_94UG1	IQKLVGKLNW	ASQIYPGIKV	RQLCKCLRGA	KALTEVIPLT	AEAELELAEN
F1_BE_VI85	IQKLVGKLNW	ASQIYPGIKV	RPLCKLLRGA	KALTDIVPLT	AEAELELAKN
F1_BR_93BR	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGA	KALTDIVPLT	TEAELELAEN
F1_FI_FIN9	IQKLVGKLNW	ASXIYPGIKV	RQLCKLLRGA	KALTDIVPLT	AEANLELAEN
F1_FR_MP41	IQKLVGKLNW	ASQIYPGIKI	KQLCKLLRGA	KALTDIVPLT	EEAELELAEN
F2_CM_MP25	IQKLVGKLNW	ASQIYPGIRV	KHLCKLLRGT	KALTDVVPLT	AEAELELAEN
F2KU_BE_VI	IQKLVGKLNW	ASQIYPGIKV	KQLCKLIRGA	KTLTDIVPLT	AEAELELAEN
G_BE_DRCBL	IQKLVGKLNW	ASQIYPGIKV	KQLCKLIRGA	KALTDIVSMT	AEAELELAEN
G_NG_92NG0	IQKLVGKLNW	ASQIYPGIKV	KHLCKLLRGA	KALTDIVPLT	AEAELELAEN
G_SE_SE616	IQKLVGKLNW	ASQIYPGIKV	THLCKLLRGA	KALTDIVSLT	AEAELELAEN
H_BE_VI991	IQKLVGKLNW	ASQIYPGIKV	KQLCXLLRGA	KALTEIVPLT	KEAELELAEN
H_BE_VI997	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGA	KALTDVVPLT	KEAELELAEN
H_CF_90CF0	IQKLVGKLNW	ASQIYPNIKV	KQLCKLLRGA	KALTDIIPLT	KEAELELAEN
J_SE_SE702	IQKLVGKLNW	ASQIYPGIKI	KELCKLIRGA	KALTDIVPLT	REAELELAEN
J_SE_SE788	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLKGA	KALTDIVPLT	REAELELAEN
K_CD_EQTB1	IQKLVGKLNW	ASQIFPGIKV	KQLCKLLRGV	KALTDIVPLT	AEAELELAEN
K_CM_MP535	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGV	KALTDIVPLT	AEAELELAEN
N_CM_YBF30	IQKLVGKLNW	ASQIYPGIRV	KQLCKLIRGT	KALTEVVNFT	EEAELELAEN
O_CM_ANT70	IQKLIGKLNW	ASQIYQGIRV	RELCKLIRGT	KSLTEVVPLS	REAELELEEN
O_CM_MVP51	IQKLVGKLNW	ASQIYQGIRV	KELCKLIRGT	KSLTEVVPLS	KEAELELEEN
O_SN_99SE_	IQKLVGKLNW	ASQIYQGIRV	KELCKLIRGA	KSLTEIVPLS	KEAELELEEN
O_SN_99SE_	IQKLVGKLNW	ASQIYQGIRV	KELCKLIRGT	KSLTEVVPLS	KEAELELEEN
U_CD___83C	IQKLVGKLNW	ASQIYPGIQV	RQLCKLLRGT	KALTDIVPMT	KEAELELAEN

501

00BW0762_1	R.EILKEPVH	GVYYDPSKDL	IADIQKQGND	QWTYQIYQEP	FKNLKTGKYA
00BW0768_2	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGQD	QWTYQIYQEP	FKNLKTGKYA
00BW0874_2	R.EILKEPVH	GVYYDPSKDL	VAEIQKQGQD	QWTYQIYQEP	FKNLKTGKYA
00BW1471_2	R.KILKEPVH	GVYYDPSKDL	IAEIQKQGHE	QWTYQIYQEP	FKNLKTGKYA
00BW1616_2	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGHD	QWTYQIYQEP	FKNLKTGKYA
00BW1686_8	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGHD	QWTYQIYQEP	FKNLKTGKYA
00BW1759_3	R.EILKEPVH	GVYYDPSKEL	IAELQKQGND	QWTYQIYQEP	FKNLKTGKYA
00BW1773_2	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGHD	QWTYQIYQEP	FKNLKTGKYA
00BW1783_5	R.EILKEPVH	GVYYDPSKDL	KAIEQKQGND	QWTYQIYQEP	FKNLKTGKYA

550

00BW1795_6	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGH	D	QWTYQIYQEP	FKNLKTGKYA
00BW1811_3	R.EILKEPVH	GAYYDPSKDL	IAEIQKQGH	D	QWTYQIYQEP	FKNLKTGKYA
00BW1859_5	R.EILKEPVH	EVYYDPSKDL	IAEIQKQGH	D	QWTYQIYQEP	FKNLKTGKYA
00BW1880_2	R.EILKEPVH	GVYYDPSKDL	IAEVQKQGD	D	QWTYQIYQEP	LKNLKTGKYA
00BW1921_1	R.EILKEPVH	GVYYDPSKEL	IAEIQKQGD	D	QWSYQIYQEP	FKNLKTGKYA
00BW2036_1	R.EILRGPVH	GVYYDPSKDL	VAEIQKQGH	D	QWTYQIFQEP	FKNLKTGKYA
00BW2063_6	R.EILREPVH	GVYYDPSKDL	VAEIQKQGN	D	QWTYQIYQEP	FKNLKTGKYA
00BW2087_2	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGH	D	QWTYQIYQEP	FKNLKTGKYA
00BW2127_2	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGN	D	QWTYQIYQEP	FKNLKTGKYA
00BW2128_3	R.EILKEPVH	GVYYDSSKEL	IAEIQKQGH	G	QWTYQIYQEP	FKNLKTGKYA
00BW2276_7	R.EILKEPVH	GVYYDPSDEL	IAEIQKQGH	D	QWTYQIYQEP	FKNLKTGKYA
00BW3819_3	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGH	D	QWTYQIYQEP	FKNLKTGKYA
00BW3842_8	R.EILREPVH	GVYYDPSKDL	VAEIQKQGH	D	QWTYQIYQEP	FKNLKTGKYA
00BW3871_3	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGN	D	QWTYQIYQEP	FKNLKTGKYA
00BW3876_9	RXEILKEPVH	GVYYDPSKDL	IAEIQKQGY	D	QWTYQIYQEP	YKNLKTGKYA
00BW3886_8	R.EILKGPVH	GVYYDPSKDL	IAEIQKQGG	D	QWTYQIYQEP	FKNLKTGKYA
00BW3891_6	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGN	G	.QTYQIYQEP	FKNLKTGKYA
00BW3970_2	R.EILREPVH	GVYYDPSKDL	IAEIQKQGN	D	QWTYQIYQEP	FKNLKTGKYA
00BW5031_1	R.EILREPVH	GVYYDPSKDL	IAEIQKQGD	D	QWTYQIYQEP	FKNLKTGKYA
96BW01B21	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGH	D	QWTYQIYQEP	FKNLKTGKYA
96BW0407	R.EILKEPVH	GVYYDPSDEL	IAEVQKQGH	Y	QWTYQIYQEP	FKNLKTGKYA
96BW0502	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGH	D	QWTYQIYQEP	FKNLKTGKYA
96BW06_J4	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGD	D	QWTYQIYQEP	FKNLKTGKYA
96BW11_06	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGD	D	QWTYQIYQEP	FKNLKTGKYA
96BW1210	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGH	D	QWTYQIYQEP	FKNLKTGKYA
96BW15B03	R.EILREPVH	GVYYDPSKDL	VAEIQKQGH	D	QWTYQIYQEP	FKNLKTGKYA
96BW16_26	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGH	D	QWTYQIYQEP	FKNLKTGKYA
96BW17A09	R.EILKEPVH	GAYYDPSKDL	IAEIQKQGN	G	QWTYQIYQEP	FKNLKTGKYA
96BWM01_5	R.EILREPVH	GVYYDPSKDL	IAEIQKQGH	D	QWTYQIYQEP	FKNLKTGKYA
96BWM03_2	R.EILKEPVH	GVYYDPSKEL	IAEIQKQGD	D	QWTYQIYQEP	HKNLKTGKYA
98BWMC12_2	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGY	D	QRTYQIYQEP	FKNLKTGKYA
98BWMC13_4	R.EILKEPVH	GVYYDPSKDL	VAEIQKQGL	D	QWTYQIYQEP	FKNLKTGKYA
98BWMC14_a	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGN	D	QWTYQIYQEP	FKNLKTGKYA
98BWM014_1	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGH	D	QWTYQIYQEP	FKNLKTGKYA
98BWM018_d	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGD	D	QWTYQIYQEP	FKNLKTGKYA
98BWM036_a	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGH	D	QWTYQIYQEP	FKNLKTGKYA
98BWM037_d	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGD	D	QWTYQIYQEP	FKNLKTGKYA
99BW3932_1	R.ELLKEPVH	GVYYDPSKDL	ITEIQKQGH	D	QWTYQIYQEP	FKNLKTGKYA
99BW4642_4	R.EILKEPVH	GVYYDPSKDL	IAEVQKQGC	E	QWTYQIYQEP	FKNLKTGKYA
99BW4745_8	R.EILKEPVH	GVYYDPSKDL	IAEVQKQGN	D	QWTYQIYQEP	FKNLKTGKYA
99BW4754_7	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGN	G	QWTYQIYQEP	FKNLKTGKYA
99BWMC16_8	R.EILKEPVH	GVYYDPSKEL	IAEIQKQGN	D	QWTYQIYQEP	FKNLKTGKYA
A2_CD_97CD	R.EILKDPVH	GVYYDPSKDL	IAEIQKQGG	D	QWSYQIYQEP	FKNLKTGKYA
A2_CY_94CY	R.EILKTPVH	GVYYDPSKDL	IAEIQKQGD	D	QWTYQIYQEP	FKNLKTGKYA
A2D_97KR	R.EILKDPVH	GVYYDPSKDL	IAEVQKQGP	D	QWTYQIYQEP	FKNLKTGKYA
A2G_CD_97C	R.EILKEPVH	GAYYEPSKEL	IAEVQKQGL	D	QWTYQIYQEP	YKNLKTGKYA
A_BY_97BL0	R.EILKXPVH	XVYYDPSKDL	VAEIQKQGD	D	QWTYQIYQEP	FKNLKTGKYA
A_KE_Q23_A	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGD	D	QWTYQIFQEP	FKNLKTGKYA
A_SE_SE659	R.EILKDPVH	GVYYDPSKDL	IAEIQKQGD	D	QWTYQIYQEP	FKNLKTGKYA
A_SE_SE725	R.EILKDPVH	GVYYDPSKDL	IAEIQKQGL	D	QWTYQIYQEP	FKNLKTGKYA
A_SE_SE753	R.EILKDPVH	GAYYDPSKDL	IVEIQKQGD	D	QWTYQIYQET	FKNLKTGKYA
A_SE_SE853	R.EILKAPVH	GVYYDPSKDL	IAEIQKQGD	D	QWTYQIYQEP	FKNLKTGKYA
A_SE_SE889	R.EILKDPVH	GVYYDPSKDL	IAEIQKQGD	D	QWTYQIYQEP	FKNLKTGKYA
A_SE_UGSE8	R.EILKDPVH	GVYYDPSKDL	IAEIQKQGD	D	QWTYQIYQEP	FKNLKTGKYA
A_UG_92UG0	R.EILKDPVH	GAYYDPSKDL	IAEIQKQGD	D	QWIYQIYQEP	FKNLKTGKYA
A_UG_U455_	R.EILKDPVH	GVYYDPSKDL	VAEIQKQGD	D	QWTYQIYQEP	FKNLKTGKYA
AC_IN_2130	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGD	D	QWTYQIYQEP	FKNLKTGKYA
AC_RW_92RW	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGH	D	QWTYQIYQEP	FKNLKTGKYA
AC_SE_SE94	R.EILRDPVH	GVYYDPSKDL	IAEIQKQGD	D	QWTYQIYQEP	FKNLKTGKYA
ACD_SE_SE8	R.EILKDPVH	GVYYDPSKDL	IAEIQKQGE	D	QWTYQIYQEP	FKNLKTGKYA



ACG_BE_VI1	R.EILKEPVH	GVYYDPAKDL	VAEIQKQGQD	QWTYQIYQEP	FKNLKTGKYA
AD_SE_SE69	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGQD	QWTYQIYQEQ	YKNLKTGKYA
AD_SE_SE71	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGQD	QWSYQIYQEQ	YKNLKTGKYA
ADHK_NO_97	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGRG	QWTYQIYQEP	YKNLKTGKYA
ADK_CD_MAL	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGQG	QWTYQIYQEQ	YKNLKTGKYA
AG_BE_VI11	R.EILKEPVH	GVYYDPGKEL	IAEIQKQGQD	QWTYQIYQEP	FKNLKTGKYA
AG_NG_92NG	R.EILKEPVH	GVYYDPSKEL	IAELQKQGCD	QWTYQIYQEP	YKNLKTGKYA
AGHU_GA_VI	R.EILKEPVH	GVYYDPSKDL	VAEVQKQGP	QWTYQIYQEP	FKILKTGKYA
AGU_CD_Z32	R.EILKEPVH	GVYYDSSKEL	IAEVQKQGLN	QWTYQIYQEP	FKNLKTGKYA
AJ_BW_BW21	R.EILKEPVH	GVYYDSAKEL	IAEVQKQGLD	QWTYQIYQEP	FKNLKTGKYA
B_AU_VH_AF	R.EILKEPVH	GVYYDPSKDL	IAEVQKQEQG	QWTYQIYQEP	FKNLKTGKYA
B_CN_RL42	R.EILKESVH	GVYYDPSKDL	IAEIQKQGLG	QWTYQIYQEP	YKNLKTGKYA
B_DE_D31_U	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGQG	QWTYQIYQEP	FKNLKTGKYA
B_DE_HAN_U	R.EILKEPVH	GVYCDPSKDL	VAEIQKQGE	QWTYQIYQEP	FKNLKTGKYA
B_FR_HXB2	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGQG	QWTYQIYQEP	FKNLKTGKYA
B_GA_OYI	R.EILKEPVH	GVYYDPSKDL	VAELQKQGQG	QWTYQIYQEP	FKNLKTGKYA
B_GB_CAM1	R.EILKEPVH	GVYYDPSKDL	IAELQKQGQG	QWTYQIYQEP	FKNLKTGKYA
B_GB_GB8_A	R.EILKEPVH	GVYYDPSKDL	VAEIQKQGLG	QWTYQIYQEP	FKNLKTGKYA
B_GB_MANC	R.EILKVPVH	GVYYDPSKDL	IAEIQKQGQG	QWTYQIYQEP	FRSLKTGKYA
B_KR_WK_AF	R.EILKEPVH	GVYYDPAKDL	IAEIQKQGQG	QWTYQIYQEP	FKNLKTGKYA
B_NL_3202A	R.EILKEPVH	GVYYDPSKEL	IAEIQKQGQG	QWTYQIYQEP	FKNLKTGKYA
B_TW_TWCYS	R.EILKQPVH	GAYYDPSKDL	VAEIQKQGQG	QWTYQIYQET	FKNLKTGKYA
B_US_BC_L0	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGQG	QWTYQIYQEP	FKNLKTAKYA
B_US_DH123	R.EILKEPVH	GVYYDPSKDI	IAEIQKQGQG	QWTYQIYQEP	FKNLKTGKYA
B_US_JRCSF	R.EILKEPVH	GVYYDPSKDL	IVEIQKQGQG	QWTYQIFQEP	FKNLKTGKYA
B_US_MNCG	R.EILKEPVH	GVYYDPSKDL	IAEVQKQGQG	QWTYQIYQEP	FKNLKTGKYA
B_US_P896	R.EILKEPVH	GVYYDPTKDL	IAELQKQGQG	QWTYQIYQEP	YKNLKTGKYA
B_US_RF_M1	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGQG	QWTYQIYQEP	FKNLKTGKYA
B_US_SF2_K	R.EILKEPVH	EVYYDPSKDL	VAEIQKQGQG	QWTYQIYQEP	FKNLKTGKYA
B_US_WEAU1	R.EILKEPVH	GVYYDPSKDL	IAELQKQGQG	QWTYQIYQEP	FKNLKTGKYA
B_US_WR27	R.EILKEPVH	GVYYDPSKDL	VAELQKQGQG	QWTYQIYQEP	FIXLXTGKYA
B_US_YU2_M	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGQG	QWTYQIYQEP	FKNLKTGKYA
BF1_BR_93B	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGQG	QWTYQIYQEP	YKNLKTGKYA
C_BR_92BR0	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGQN	QWTYQIYQEP	FKNLKTGKYA
C_BW_96BW0	R.EILKEPVH	GVYYDPSKDL	IAEVQKQGH	QWTYQIYQEP	FKNLKTGKYA
C_BW_96BW1	R.EILKEPVH	GVYYDPSKDL	IAEIQKQG	QWTYQIYQEP	FKNLKTGKYA
C_BW_96BW1	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGH	QWTYQIYQEP	FKNLKTGKYA
C_BW_96BW1	R.EILKEPVH	GVYYDPSKDL	VAEIQKQGH	QWTYQIYQEP	FKNLKTGKYA
C_ET_ETH22	R.EILKEPVH	GVFYDPSKDL	IAEIQKQGN	QWTFQFYQEP	FKNLKTGKFA
C_IN_93IN1	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGQD	QWTYQIYQEP	FKNLKTGKYA
C_IN_93IN9	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGQD	QWTYQVYQEP	FKNLKTGKYA
C_IN_93IN9	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGQG	QWTYQIYQEP	FKNLKTGKYA
C_IN_94IN1	R.EILKEPIH	GVYYDPSKDL	IAEIQKQGQD	QWTYQVYQEP	FKNLKTGKYA
C_IN_95IN2	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGQD	QWTYQIYQEP	FKNLKTGKYA
CRF01_AE_C	R.EILKNPVH	GVYYDPSKEL	VAEIQKQGQD	QWTYQIYQEP	FKNLKTGKYA
CRF01_AE_C	R.EILKTPVH	GVYYDPSKDL	VAEIQKQGQD	QWTYQIYQEP	FKNLKTGKYA
CRF01_AE_C	R.EILKNPVH	GVYYDPSKDL	VAEIQKQGH	QWTYQIYQEP	FKNLKTGKYA
CRF01_AE_T	R.EILKTPVH	GVYYDPSKDL	VAEVQKQGQD	QWTYQIYQEP	FKNLKTGKYA
CRF01_AE_T	R.EILRTPVH	GVYYDPSKDL	VAEVQKQGQD	QWTYQIYQEP	FKNLKTGKYA
CRF01_AE_T	R.EILRIPVH	GVYYDPSKDL	VAEVQKQGQD	QWTYQIYQEP	FKNLKTGKYS
CRF01_AE_T	R.EILKTPVH	GVYYDPSKDL	AAEVQKQGQD	QWTYQIYQEP	FKNLKTGKYA
CRF01_AE_T	R.EILKTPVH	GVYYDPSKDL	VAEVQKQGQD	QWTYQIYQEP	FKNLKTGKYA
CRF01_AE_T	R.EILKTPVH	GVYYDPSKDL	VAEVQKQGQD	QWTYQIYQEP	FKNLKTGKYA
CRF02_AG_F	R.EILKEPVH	GVYYDPAKDL	IAEIQKQGQD	QWTYQIYQEP	FKNLKTGKYA
CRF02_AG_F	R.EILKEPVH	GVYYDPAKDL	IAEIQKQGQD	QWTYQIYQEP	FKNLKTGKYA
CRF02_AG_G	R.EILKEPVH	GVYYDPTKDL	IAEIQKQGQD	QWTFQIYQEP	FKNLKTGKYQ
CRF02_AG_N	R.EILKEPVH	GVYYDPTKDL	VAELQKQGQD	QWTYQIYQEP	FKNLKTGKYA
CRF02_AG_S	R.EILKEPVH	GVYYDPTKDL	VAEIQKQGQD	QWTYQIYQEP	FKNLKTGKYA
CRF02_AG_S	R.EILKEPVH	GVYYDPTKDL	IAEIQKQGQD	QWTYQIYQEP	FKNLKTGKYA
CRF03_AB_R	R.EILKEPVH	GVYYDPSKDL	VAEIQKQGQG	QWTYQIYQEP	FKNLKTGKYA

CRF03_AB_R	R.EILKVPVH	GVYYDPSKDL	VAEIQKQGQG	QWTYQIYQEP	FKNLKTGKYA
CRF04_cpx_	R.EILKEPVH	GAYYDPSKDL	IAEIQKQGQG	QWTYQIYQEP	HKNLKTGKYA
CRF04_cpx_	R.EILKEPVH	GAYYDPSKDL	IAKIQKQGQG	QWTYQIYQEP	YKNLKTGKYA
CRF04_cpx_	R.EILKEPVH	GAYYDPSKDL	IAEIQKQGLG	QXTYQIYQEP	YKNLKTGKYA
CRF05_DF_B	R.EILKEPVH	GVYYDPSKDL	IAEVQKQGLG	QWTYQIYQEP	FKNLKTGKYA
CRF05_DF_B	R.EILKEPVH	GVYYDPAKDL	IAEIQKQGQE	QWTYQIYQEP	FKNLKTGKYA
CRF06_cpx_	R.EILKEPVH	GVYYDPSKDL	IAEVQKQGYG	QWTYQIYQEP	HKNLKTGKYA
CRF06_cpx_	R.EILKEPVH	GAYYDPSKDL	IAEIQKQGQG	QWTYQIYQEP	HKNLKTGKYA
CRF06_cpx_	R.EILKEPVH	GVYYDPLKDL	IAELQKQGQG	QWTYQIYQEP	HKNLKTGKYA
CRF06_cpx_	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGQG	QWTYQIYQDT	HKNLKTGKYA
CRF11_cpx_	R.EILKEPVH	GVYYDPSKDL	IAEVQKQGLD	QWTYQIYQEP	FKNLKTGKYA
CRF11_cpx_	R.EILKEPVH	GVYYDPSKDL	IAEVQKQGLD	QWTYQIYQEP	FKNLKTGKYA
D_CD_84ZR0	R.EILKEPMH	GVYYDPSKDL	IAELQKQGQG	QWTYQIYQEP	FKNLKTGKYA
D_CD_ELI_K	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGHG	QWTYQIYQEP	FKNLKTGKYA
D_CD_NDK_M	R.EILKEPVH	GVYYDPSKDL	IAELQKQGDG	QWTYQIYQEP	FKNLKTGKYA
D_UG_94UG1	R.EILKEPVH	GAYYDPSKDL	IAEIQKQGQD	QWTYQIYQEQ	YKNLKTGKYA
F1_BE_VI85	R.EILREPVH	GVYYDPSKDL	IAEIQKQGDG	QWTYQIYQNP	FKNLKTGKYA
F1_BR_93BR	R.EILKEPVH	GAYYDPSKDL	IAEIQKQGQG	QWTYQIYQEP	FKNLKTGKYA
F1_FI_FIN9	R.EILKEPVH	GVYYDPSKDL	IPKLQKQGQG	QWTYQIYREP	FKNLKTGKYA
F1_FR_MP41	R.EILKEPVH	GVYYDPSKDL	IAELQKQGQG	QWTYQIYQEP	FKNLKTGKYA
F2_CM_MP25	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGHG	QWTYQIYQEP	HKNLKTGKYA
F2KU_BE_VI	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGQG	QWTYQIYQEP	YKNLKTGKYA
G_BE_DRCBL	R.EILKEPVH	GVYYDPSKDL	IAEVQKQGLG	QWTYQVYQEP	YKNLKTGKYA
G_NG_92NG0	R.EILKEPVH	GVYHDPKSKEL	IAEVQKQGPD	QWTYQIYQEP	YKNLKTGKYA
G_SE_SE616	R.EILREPVH	GVYYDPSKEL	IAEVQKQGLD	QWTYQIYQEP	YKNLKTGKYA
H_BE_VI991	R.EILKEPVH	GAYYDPSKEL	IAEIQKQGPD	QWTYQIYQEP	FKNLKTGKYA
H_BE_VI997	R.EILREPVH	GVYYDPSKDL	IAEIQKQGPD	QWTYQIYQEP	FKNLKTGKYA
H_CF_90CF0	R.EILREPIH	GVYYDPSKDL	IAEIRKQGQG	QWTYQIYQEP	FKNLKTGKYA
J_SE_SE702	K.EILKEPVH	GVYYDPAREL	IAEVQKQGLD	QWTYQIYQEP	FKNLKTGKYA
J_SE_SE788	K.EILKEPVH	GVYYDSAKEL	IAEVQKQGLD	QWTYQIYQEP	FKNLKTGKYA
K_CD_EQTB1	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGHG	QWTYQIYQEP	YKNLKTGKYA
K_CM_MP535	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGND	QWTYQIYQEP	HKNLKTGKYA
N_CM_YBF30	R.EILKEPLH	GVYYDPKSKEL	VAEIQKQGQG	QWTYQIYQEL	HKNLKTGKYA
O_CM_ANT70	R.ERLKPQVH	GVYYQPDKDL	WVNIQKQGGE	QWTYQIYQEE	HKNLKTGKYT
O_CM_MVP51	R.EKLKEPVH	GVYYQPDKDL	WVSIQKHGEG	QWTYQVYQDE	HKNLKTGKYA
O_SN_99SE_	R.EKLKEPVH	GVYYQPDKDL	WVNIQKQGWG	QWTYQIYQDE	HKNLKTGKYT
O_SN_99SE_	R.EKLKEPVH	GVYYQPDKDL	WVNIQKQGKG	QWTYQIYQDE	HKNLKTGKYT
U_CD___83C	R.EILKEPVH	GVYYDPSKDL	VAEIQKQGQD	QWSYQIYQEP	FKNLKTGKYA

551

600

00BW0762_1	KMRTAHTNDV	KQLTEAVQKI	SRESIVIWG.	KTPKFRLPIQ	KETWETWWTD
00BW0768_2	KMRTAHTNDV	KQLTEAVQKI	AQESIVIWG.	KTPKFRLPIQ	KETWEIWWTD
00BW0874_2	KMRTAHTNDV	KQLAEAVQKI	ATESIVIWG.	KTPKFRLPIQ	RETWETWWTN
00BW1471_2	KKRSAHTNDV	KQLTDAVQKI	AMESIVIWG.	KTPKFRLPIQ	KETWDTWWTD
00BW1616_2	KMRTAHTNDV	KQLTEAVQKI	AMESIVIWG.	KTPKFRLPIQ	KETWEAWWTD
00BW1686_8	KMRTAHTNDV	RQLTEAVQKI	AMESVVIWG.	KTPKFRLPIQ	KETWETWWAD
00BW1759_3	KMRTAHTNDV	KQLTEAVQKI	AMESIVIWG.	KTPKFRLPIQ	KETWETWWTD
00BW1773_2	KMRTAHTNDV	KQLTEAVQKI	ALESIVIWG.	KIPKFRLPIQ	KETWETWWTD
00BW1783_5	KMRTAHTNDV	KQLTEAVQKI	ALESIVIWG.	KVPKSRLPIQ	KETWETWWTD
00BW1795_6	KRRTAHTNDV	KQLTEAVQKI	ALESIVIWG.	KIPKFRLPIQ	KETWETWWTD
00BW1811_3	KMRSAHTNDV	KQLTEAVQKI	AMECIVIWG.	KTPKFRLPIQ	KETWETWWTD
00BW1859_5	KMRTAHTNDV	KQLTEAVQKI	AMESIVIWG.	KAPKFRLPIQ	KETWETWWTD
00BW1880_2	KMRTAHTNDV	KQLTEVVQKI	CIESVVIWG.	RTPKFRLPIQ	RETWETWWTD
00BW1921_1	KKRSAHTNDV	KQLTEAVQKI	AMESIVIWG.	KTPKFRLPIQ	KETWDTWWTD
00BW2036_1	KMRTAHTNDV	KQLTEAVQKI	AMESIVIWG.	KTPKFRLPIQ	KETWETWWTD
00BW2063_6	KRRTAHTNGV	KQLTEAVQKI	AQESIVIWG.	KTPKFRLPIQ	KETWETWWTD
00BW2087_2	KMRTAHTNDV	KQLTEAVQKI	AIESIVIWG.	KTPKFRLPIQ	KETWETWWTD
00BW2127_2	KMRTAHTNDV	KQLTEAVQKI	ALESIVIWG.	KTPKFRLPIQ	KETWETWWTD
00BW2128_3	KMRTAHTNDV	KQSTEAVQKI	AMESIVIWG.	RTPKFRLPIQ	KEMWEARWTD
00BW2276_7	KMRTAHTNDV	KQLTEAVQKI	ALESIVIWG.	KTPKFRLPIQ	KETWETWWTD

00BW3819_3	KMKSHTNDV	KQLTEAVQKI	VMESIVIWG.	KAPKFRLPVQ	KETWETWWTD
00BW3842_8	KMRTAHTNDV	KQLTEAVXKI	AMECIVIWG.	KTPKFRLPIQ	KETWETWWTD
00BW3871_3	KMRNAHTNDV	KQLTEAVQKI	AQESIVIWG.	KTPKFRLPIQ	KETWETWWTD
00BW3876_9	KMRSAHTNDV	KQLAEAVQRI	AKESIVIWG.	KTPKFRLPIQ	KETWETWWTD
00BW3886_8	KMRTAHTNDV	KQLTEAVQKI	AMESIVIWG.	KTPKFRLPIQ	KETWEIWWTD
00BW3891_6	KIRTAHTNDV	KQLTEVVQKI	AQESIVIWG.	KTPKFRLPIQ	KETWEIWWTE
00BW3970_2	KRRTAHTNDV	RQLAEAVQKI	TMESIVIWG.	KTPRFRLPVQ	KETWETWWTD
00BW5031_1	KIRTAHTNDV	RQLTEAVQKI	ALESIVIWG.	KIPKFRLPIQ	KETWETWWTD
96BW01B21	KMRTAHTNDV	KQLTEAVQKI	ATESIVIWG.	KXPKFRLPIQ	KETWETWWTD
96BW0407	KMRTAHTNDV	KQLTEVVQKI	AMESIVIWG.	KTPKFRLPIQ	KDTWETWWTD
96BW0502	KMRTAHTNDV	KQLTEAVQKI	AQESIVIWG.	KTPKFRLPIQ	KETWETWWTD
96BW06_J4	KMRTAHTNDV	KQLTEAVQKI	AMESIVIWG.	KTPKFRLPIQ	KEIWETWWTD
96BW11_06	KMRTAHTNDV	KQLTEAVQKI	SMESIVIWG.	KIPKFRLPIQ	KEAWEAWWTD
96BW1210	KLRTAHTNDV	RQLTEAVQKI	AQECIVIWG.	KTPKFRLPIQ	KETWEAWWTD
96BW15B03	KMRTAHTNDV	KQLTEAVQKI	AMESIVIWG.	KTPKFRLPIQ	KETWETWWTD
96BW16_26	KMRTAHTNDV	KQLAEAVQKI	TMESIVLWG.	KTPKFRLPIQ	KETWETWWTD
96BW17A09	KKKSTHTNDV	KQLTDAVQKI	TMESIVIWG.	KTPKFRLPIQ	KETWDTWWTE
96BWM01_5	KRRTAHTNDV	KQLTEAVQKI	ALESTIVIWG.	KIPKFRLPIQ	KETWDTWWTD
96BWM03_2	KMRTAHTNDV	RQLTEAVQKI	AMESIVIWG.	KTPKFRLPIQ	KETWETWWTD
98BWMC12_2	KMRTAHTNDV	KQLAEAVQKI	AQESIVIWG.	KTPKFRLPIQ	KETWETWWTD
98BWMC13_4	KRRTAHTNDV	KQLTEAVQKI	ALESIVIWG.	KIPKFRLPIQ	KETWETWWTD
98BWMC14_a	KMRTAHTNDV	KQLTEAVQKI	AMESIVIWG.	KTPKFRLPIQ	KETWETWWTE
98BWM014_1	KMRTAHTNDV	KQLTEAVQKI	AIESIVIWG.	KTPKFRLPIQ	KETWETWWTD
98BWM018_d	KMRTAHTNDV	RQLTEAVQKI	TMESIVIWG.	KTPKFRLPIQ	KDTWETWWTD
98BWM036_a	KRRTAHTNDV	KQLTEVVQKI	TMESIVIWG.	KTPKFRLPIQ	KDTWETWWTD
98BWM037_d	KRRTAHTNDV	RQLTEAVQKI	TMESIVIWG.	KTPKFRLPIQ	KETWETWWTD
99BW3932_1	KMRSAHPNDV	KQLTEAVHKI	AMESIVIWG.	KTPKFRLPIQ	KETWETWWTD
99BW4642_4	KMRTAHTNDV	KQLAEAVQKI	AVESIVIWG.	KTPKFRLPIQ	KETWETWWTD
99BW4745_8	KMRTAHTNDV	KQLTEAVQKI	AMESIVIWG.	KTPKFRLPIQ	KETWETWWTD
99BW4754_7	KMRTAHTNDV	KQLAEAVQKV	AIESIVIWG.	KIPKFRLPIQ	KETWETWWTD
99BWMC16_8	KIRTAHTNDV	RQLTEAVQKI	TMESIVIWG.	KTPKFRLSIQ	KDTWETWWTD
A2_CD_97CD	KRSTHTNDV	KQLTEAVQKI	ATESIVIWG.	KIPKFRLPIQ	KETWETWWTE
A2_CY_94CY	KRSTHTNDI	KQLTEAVQKI	TMESIVIWG.	KTPKFRLPIQ	KETWETWWAE
A2D_97KR	KRSTHTNDV	KQLTEAVQKI	VMESIVIWG.	KIPKFRLPIQ	KETWETWWTE
A2G_CD_97C	KRGSHTNDV	KQLTEVVQKI	ATESIVIWG.	KTPKFRLPIR	KETWEVWWTE
A_BY_97BL0	KXSAHTNXV	KQLTAVVQKV	ATESXILXG.	KTPKFRLPIQ	XETXEXWXM
A_KE_Q23_A	RKRSHTNDV	RQLAEVVQKV	VMESIVIWG.	KTPKFRLPIQ	KETWDTWWMD
A_SE_SE659	RKRSVHTNDV	KQLAEMVQKV	VTESIVIWG.	KTPKFRLPIQ	KETWETWWMD
A_SE_SE725	RKRSHTNDV	RQLAEVVQKV	VMESIVIWG.	KTPKFRLPIQ	KETWETWWMD
A_SE_SE753	RKRSHTNDV	KQLAEVVQKV	AMESIVIWG.	KTPRSKLPIQ	KETWETWWID
A_SE_SE853	RKRSHTNDV	KQLAEVVQKV	VMESIVIWG.	KTPKFRLPIQ	KETWETWWME
A_SE_SE889	RKRSHTNDV	RQLAEVVQKV	VMESIVIWG.	KTPKFRLPIQ	KETWETWWMD
A_SE_UGSE8	RKRSHTNDV	RQLAEVVQKV	VMESIVIWG.	KTPKFRLPIQ	KDTWDTWWMD
A_UG_92UG0	RKRSHTNDV	KQLAEVVQKV	VMESIVIWG.	KTPKFRLPIQ	KETWETWWMD
A_UG_U455_	RKRSHTNDV	KQLTEVVQKV	STESIVIWG.	KIPKFRLPIQ	KETWEAWWME
AC_IN_2130	KMRTAHTNDV	KQLTETVQKI	AMESIVIWG.	KTPKFRLPIQ	KETWETWWTD
AC_RW_92RW	KRRTAHTNDV	KQLTEAVQKI	AMESIVIWG.	KTPKFRLPIQ	KETWETWWTD
AC_SE_SE94	KRRTAHTNDV	RQLAEVVQKV	VMESIIIWG.	KTPKFRLPIQ	KETWETWWMD
ACD_SE_SE8	KRRTAHTNDV	KQLAEVVQKV	VMESIVIWG.	KAPKFRLPIQ	KETWETWWMD
ACG_BE_VI1	KRRTAHTNDV	KQLTEAVQKI	AQESIVIWG.	KTPKFRLPIQ	RETWEAWWME
AD_SE_SE69	KVRGHTNDI	KQLTAAVQKI	AQECIVIWG.	KTPKFRLPIQ	KETWETWWTE
AD_SE_SE71	KLRGHTNDI	KQLTAAVQKI	AQECIVIWG.	KTPKFRLPIQ	KETWETWWTE
ADHK_NO_97	RMKSHTNDV	KQLTEAVQKI	SIESIVIWG.	KTPKFRLPIQ	KETWETWWTE
ADK_CD_MAL	RIKSAHTNDV	KQLTEAVQKI	AQESIVIWG.	KTPKFRLPIQ	KETWEAWWTE
AG_BE_VI11	KRRTAHTNDV	KQLAEVVQKV	ATESVVIWG.	KTPKFRLPIQ	RETWEAWWRE
AG_NG_92NG	KRGSHTNDV	KQLTEAVQKI	ATESIVIWG.	KVPKFRLPIR	KETWEVWWTE
AGHU_GA_VI	KRRTAHTNDV	KQLTEAVQKI	ATESIVIWG.	KIPKFRLPIQ	KETWETWWTD
AGU_CD_Z32	RRRTAHTNDV	RQLAEVVQKI	ASESIVIWG.	KTPKFRLPIQ	KETWETWWAD
AJ_BW_BW21	KRRAHTNDV	KQLAEVVQKI	ALESIVIWG.	KTPKFRLPIQ	KETWETWWTE
B_AU_VH_AF	RMKGAHTNDV	KQLTEAVQKI	ATESIVIWG.	KTPKFRLPIQ	KETWEAWWME

B_CN_RL42_	RMGAHTNDV	KQLTEAVQKI	ATESIVIWG.	KTPKFKLPIQ	KETWEAWWTE
B_DE_D31_U	RMGAHTNDV	KQLTEAVQKI	TTESIVIWG.	KTPKFKLPIQ	KETWEAWWTE
B_DE_HAN_U	RMGAHTNDI	KQLTEAVQKI	ATEGIVIWG.	KTPKFRLPIQ	KETWEAWWTE
B_FR_HXB2_	RMGAHTNDV	KQLTEAVQKI	TTESIVIWG.	KTPKFKLPIQ	KETWETWWTE
B_GA_OYI_	RMGAHTNDV	KQLTEAVQKI	TQESIVIWG.	KTPKFKLPIQ	KETWEAWWTE
B_GB_CAM1_	KMRGTHTNDV	KQLTEAVQKI	ATESIVIWG.	KTPKFKLPIQ	KETWDAAWWID
B_GB_GB8_A	KMRGAHTNDV	KQLTEAVQKI	ATESIVIWG.	KTPKFKLPIQ	KETWEAWWME
B_GB_MANC_	KMRGTHTNDV	KQLTEAVQKV	TTESIIIWG.	KIPKFKLPIQ	KETWDAAWWTE
B_KR_WK_AF	RMGAHTNDV	KQLTEAVQKV	AIESIVIWG.	KTPKFKLPIQ	KETWEAWWTE
B_NL_3202A	RMGAHTNDV	KQLTEAVQKI	TTESIVIWG.	KTPKFKLPIQ	KETWEAWWTE
B_TW_TWCYS	RTRGAHTNDV	KQLTEAVQKI	ATESIVIWG.	KTPKFKLPIQ	KETWEAWWTE
B_US_BC_L0	RTRGAHTNDV	KQLTEAVQKI	TTECIIIWG.	KTPKFRLPIQ	KETWETWWTE
B_US_DH123	RTRGAHTNDV	KQLTEVVQKV	TTECIVIWG.	KTPKFRLPIQ	KETWETWWTE
B_US_JRCSF	RTRGAHTNDV	KQLTEAVQKI	ANESIVIWG.	KIPKFKLPIQ	KETWETWWTE
B_US_MNCG_	RMGAHTNDV	KQLTEAVQKI	ATESIVIWG.	KTPKFRLPIQ	KETWETWWTE
B_US_P896_	RMGAHTNDV	KQLTEAVQKI	ATESIVIWG.	KTPKFKLPIQ	KETWEAWWTD
B_US_RF_M1	RMGAHTNDV	KQLTEAVQKV	ATESIVIWG.	KTPKFKLPIQ	KETWEAWWTE
B_US_SF2_K	RMGAHTNDV	KQLTEAVQKV	STESIVIWG.	KIPKFKLPIQ	KETWEAWWME
B_US_WEAU1	RVRGAHTNDV	KQLTEAVQKI	TTESIVIWG.	KTPKFKLPIQ	KETWETWWTE
B_US_WR27_	RTRGAHTNDV	XQLXEAVQKX	ATXSIVIWG.	KTPKXILPIQ	KETWESRWTE
B_US_YU2_M	RTRGAHTNDV	KQLTEAVQKI	ATESIVIWG.	KTPKFKLPIQ	KETWETWWTE
BF1_BR_93B	RMGAHTNDV	KQLTEAVQKI	TTESIVIWG.	KIPKFKLPIQ	KETWEAWWIE
C_BR_92BR0	KMRTAHTNDV	QQLTEAVQKI	ALESIIIWG.	KTPKFRLPIQ	KETWEAWWTD
C_BW_96BW0	KMRTAHTNDV	KQLTEVVQKI	TMESIVIWG.	KTPKFRLPIQ	KDTWETWWTD
C_BW_96BW1	KMRTAHTNDV	KQLTEAVQKI	SMESIVIWG.	KIPKFRLPIQ	KEAWEAWWTD
C_BW_96BW1	KLRTAHTNDV	QQLTEAVQKI	AQECIVIWG.	KTPKFRLPIQ	KETWEAWWTD
C_BW_96BW1	KMRTAHTNDV	KQLTEAVQKI	AMESIVIWG.	KTPKFRLPIQ	KETWETWWTD
C_ET_ETH22	KRGTAHTNDV	KQLTAVVQKI	ALESIVIWG.	KTPKFRLPIQ	KETWEAWWTD
C_IN_93IN1	KRRTAHTNDV	KQLTEAVQKI	AMESIVIWG.	KTPKFRLPIQ	KETWETWWTD
C_IN_93IN9	KMRTAHTNDV	KQLTEAVQKI	AMESIVIWG.	KTPKFRLPIQ	KETWETWWTD
C_IN_93IN9	KMRTAHTNDV	KQLAEAVQKI	AMESIVIWG.	KTPKFRLPIQ	KETWEAWWTD
C_IN_94IN1	KMRTAHTNDV	KQLTEAVQKI	AMESIVIWG.	KTPKFRLPIQ	KETWETWWTD
C_IN_95IN2	KMRTAHTNDV	KQLTEAVQKI	ATESIVIWG.	KTPKFRLPIQ	KETWETWWTD
CRF01_AE_C	RKRSHTNDV	RQLAEVVQKV	ATESIVIWG.	KTPKFRLPIQ	RETWETWWAE
CRF01_AE_C	RKRSHTNDV	RQLAEVVQKV	ATESIVIWG.	KTPKFRLPIQ	RETWETWWME
CRF01_AE_C	RQRSHTNDV	RQLVEVVQKV	STESIVIWG.	KTPKFRLPIQ	RETWETWWME
CRF01_AE_T	RKRSHTNDV	RQLTEVVQKI	ATESIVIWG.	KTPKFRLPIQ	RETWETWWME
CRF01_AE_T	RKRSHTNDV	RQLTEVVQKI	ATESIVIWG.	KTPKFRLPIQ	RETWETWWME
CRF01_AE_T	RKRSHTNDV	RQLTEVVQKI	ATESIVIWG.	KTPKFRLPIQ	RETWETWWME
CRF01_AE_T	RKRSHTNDV	RQLTEVVQKI	ATESIVIWG.	KTPKFRLPIQ	RETWETWWME
CRF01_AE_T	RNRSHTNDV	RQLTEVVQKI	ATESIVIWG.	KTPKFRLPIQ	KETWETWWME
CRF01_AE_T	RRGSAHTNDV	RQLTEVVQKV	ATESIVIWG.	KTPKFRLPIQ	RETWETWWME
CRF01_AE_T	RKRSHTNDV	RQLTEVVQKI	ATESIVIWG.	KTPKFKLPIQ	KETWETWWME
CRF02_AG_F	KRRSAHTNDV	QQLAEVVQKV	VTESIVIWG.	KTPKFRLPIQ	RETWEAWWME
CRF02_AG_F	KRRSAHTNDV	KQLTEVVQKV	ATESIVIWG.	KTPKFSLPIQ	RETWEAWWME
CRF02_AG_G	ERVAPYDLSI	TELTEVVQKV	TTESIIIWG.	KTPKFRLPIQ	RETWEAWWME
CRF02_AG_N	KKRSHTNDV	KQLTEVVQKV	AMESIVIWG.	KTPKFRLPIQ	RETWETWWME
CRF02_AG_S	KKRSHTNDV	KQLTEVVQKV	ATESIVIWG.	KTPKFRLPIQ	RETWEAWWME
CRF02_AG_S	KKRSHTNDV	KQLTEVVQKV	ATESIVVWG.	KTPKFRLPIQ	RETWEAWWME
CRF03_AB_R	RLRGAHTNDV	KQLTEAVQKI	ATESIVIWG.	KTPKFKLPIQ	KETWETWWTE
CRF03_AB_R	RLRSAHTNDV	KQLTEAVQKI	ATESIVIWG.	KTPKFKLPIQ	KETWETWWAE
CRF04_cpx_	RTRSAHTNDV	RQLTEAVQKI	AMECIVIWG.	KTPKFRLPIQ	KETWDTWWTE
CRF04_cpx_	RTRSAHTNDV	RQLTEVVQKI	AMECIVIWG.	KTPKFRLPIQ	KETWDTWWTE
CRF04_cpx_	KTRSAHTNDV	RQLTEAVQKI	AMECIVIWG.	KTPKFRLPIQ	KETWDTWWME
CRF05_DF_B	RARGVHTNDV	QQLAEAVQKI	ATESIVIWG.	KTPKFRLPIQ	KETWEIWWTE
CRF05_DF_B	RTRNAHTNDV	QQLAEAVQKI	ATESIVIWG.	KTPKFRLPIQ	KETWETWWTE
CRF06_cpx_	RIKSAHTNDV	KQLTEAVQKI	ALESIVIWG.	KTPKFRLPIQ	KETWETWWTE
CRF06_cpx_	KIKSTHTNDV	KQLTEAVQKI	ARESIVIWG.	KTPKFRLPIQ	KETWETWWTE
CRF06_cpx_	RMRSAHTNDI	KQLTEAVQKI	ALEAIVIWG.	KIPKFRLPIQ	KETWETWWTE
CRF06_cpx_	RTKSAHTNDV	RQLTEAVQKI	ALESIVIWG.	KTPKFRLPIH	KETWETWWTE
CRF11_cpx_	KRRSAHTNDV	RQLTEVIQKI	CLEAIVIWG.	KTPKFRLPIQ	RETWETWWTD

CRF11_cpx_	KRRTAHTNDV	RQLAEVVQKI	ALEGIVIWG.	KIPKFRLPIQ	KETWETWWTD
D_CD_84ZR0	RMRGAHTNDV	KQLTEAVQKI	AIESIVIWG.	KTPKFRLPIQ	KETWETWWID
D_CD_ELI_K	RMRGAHTNDV	KQLAEAVQRI	STESIVIWG.	RTPKFRLPIQ	KETWETWWAE
D_CD_NDK_M	RTRGAHTNDV	KQLTEAVQKI	ATESIVIWG.	KTPKFRLPIQ	KETWETWWIE
D_UG_94UG1	KMRGTHTNDV	KQLTEAVQKI	AQECIVIWG.	KTPKFRLPIQ	KETWETWWTE
F1_BE_VI85	KVRSHTNDV	KQLTEAVQKI	ALESIVIWGK	RSPKFRLPIL	KETWDTWWTD
F1_BR_93BR	KMRSHTNDV	KQLTEAVQKI	SLESIVIWG.	KTPKFRLPIL	KETWDTWWTE
F1_FI_FIN9	KMRSHTNDV	KQLTEAVQKI	ALESIVIWG.	KTPKFRLPIL	KETWDTWWTE
F1_FR_MP41	KTRSHTNDI	KELTDAVQKV	ARECIVIWG.	KSPKFRLPIQ	KETWEAWWTD
F2_CM_MP25	RRKSAHTNDV	KQLTEVVQKV	ATEGIVIWG.	KVPKFRLPIQ	KETWEIWWTE
F2KU_BE_VI	RMRSHTNDV	KQLTEAVQKI	ATEGIVIWG.	KTPKFRLPIQ	KETWETWWTE
G_BE_DRCBL	KGGSHTNDV	KQLTEVVQKI	ATEGIIIWG.	KIPKFRLPIK	KETWEVWWTE
G_NG_92NG0	KRGSHTNDV	KQLTEVVQKI	ATEGIVIWG.	KIPKFRLPIR	KETWEVWWTE
G_SE_SE616	KRGSHTNDV	KQLTEVVQKI	ATESIVIWG.	KTPKFRLPIR	KETWEIWWTD
H_BE_VI991	KMRSHTNDV	KQLTEVVQKI	ATESIVIWG.	KIPKFRLPIQ	KETWETWWTE
H_BE_VI997	KMRNAHTSDV	KQLTEAVQKI	ATESIVIWG.	KIPKFRLPIQ	KETWETWWTE
H_CF_90CF0	KMRTAHTNDI	KQLTEAVQKI	STESIVIWG.	KIPKFRLPIQ	KETWETWWTE
J_SE_SE702	KRRSAHTNDV	KQLSQVVQKI	ALEAIVIWG.	KTPKFRLPIQ	KETWETWWTD
J_SE_SE788	KRRSAHTNDV	KQLAEVVQKI	ALEAIVIWG.	KTPKFRLPIQ	RETWETWWTD
K_CD_EQTB1	RIRSAHTNDV	KQLTEVVQKV	AMESIVIWG.	KTPKFRLPIQ	KETWGTWWTE
K_CM_MP535	RMRSHTNDV	KQLTEAVQKI	ATEGIVIWG.	KTPKFRLPIQ	KETWETWWTE
N_CM_YBF30	KMRSHTNDI	KQLVEVVVRKV	ATESIVIWG.	KTPKFRLPVQ	KEVWEAWWTD
O_CM_ANT70	RQKASHTNDI	RQLAEVIQKV	SQESIIIWG.	KLPKFRLPVT	RETWETWWAD
O_CM_MVP51	RQKASHTNDI	RQLAEVVQKV	SQEAIVIWG.	KLPKFRLPVT	RETWETWWAE
O_SN_99SE_	RQKASHTNDI	RQLAEVLQRV	SQEAIIIWG.	KLPKFRLPIT	RETWETWWAD
O_SN_99SE_	KQKASHTNDI	RQLAEVLQKV	SQEAIIIWG.	KLPKFRLPIT	RETWETWWAD
U_CD___83C	KRRSAHTNDV	KQLTEAVQKI	SMESIVIWG.	KIPKFRLPIQ	KETWESWWTD

601

650

00BW0762_1	YWQATWIPEW	EFVNTPLPVK	LWYQLEKDPL	VGVEFYVDG	AANRDTKIGK
00BW0768_2	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	LGAETFYVDG	AANRETKKGGK
00BW0874_2	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	AGAETFYVDG	AANRETKLGGK
00BW1471_2	YWQAT.IPEW	EFVNAPPLVK	LWYQLEKDPI	AGAETFYVDG	AANRETKLGGK
00BW1616_2	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	IGIETFYVDG	AANRETKLGGK
00BW1686_8	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	VGAETFYVDG	AANRETKAGK
00BW1759_3	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	AGAETFYVDG	AANRDTKKGK
00BW1773_2	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	AGVETFYVDG	AANRETKIGK
00BW1783_5	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	VGAETYYVDG	AANRETKMGR
00BW1795_6	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPV	AGVETFYVDG	AANRETKMGK
00BW1811_3	YWQATWIPEW	EFVNTPLPVK	LWYQLEEEPI	AGAETFYVDG	AANRETKIGK
00BW1859_5	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	VGAETFYVDG	AAHRETKVEK
00BW1880_2	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPM	MGVETFYVDG	AANRETKIGK
00BW1921_1	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	VGAETFYVDG	AANRETKLGGK
00BW2036_1	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	IGAETFYVDG	AANRETKLGGK
00BW2063_6	YWQATWIPEW	EFVNTPLPVK	LWYQLEKDPI	LGVEFYVDG	AANRETKMGK
00BW2087_2	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	AGAETFYVDG	AANRETKIGK
00BW2127_2	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	AGVETFYVDG	AVNRETKVGK
00BW2128_3	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	VGAETFYVDG	AANRETKKGGK
00BW2276_7	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	AGAETFYVDG	AANRETKIGK
00BW3819_3	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	AGVETFYVDG	AANRDTKVGK
00BW3842_8	YWQATWIPDW	EFVNTLPLVK	LWYQLEKEPI	IGAETFYVDG	AANRDTKIGK
00BW3871_3	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	VGAETFYVDG	AANRETKAGK
00BW3876_9	YWQATWIPDW	EFVNTPLPVK	LWYQLEKEPI	VRAETFYVDG	AANRETKIGK
00BW3886_8	YWQATWIPEW	EFVNTPLPVK	LRYQLEKEPI	AGVETFYVDG	AANRETKVGK
00BW3891_6	YWQATWIPEW	EFVNTPLPVK	LWYQLEKDPI	AEVETFYVDG	AANRETKRGK
00BW3970_2	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPM	AGVETFYVDG	AANRETKIGR
00BW5031_1	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPV	AGVETFYVDG	AANRETKIGK
96BW01B21	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	VGAETFYVDG	AANRETKIGK
96BW0407	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	AGAETFYVDG	AANRETKLGGK
96BW0502	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	PGVETFYVDG	AANRETKLGGK

96BW06_J4	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	MGAETFYVDG	AANRETKAGK
96BW11_06	Y.QATWIPEW	EFVNTPLPVK	LWYQLETEPM	AGAETFYVDG	AANRETKIGK
96BW1210	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	AGVETFYVDG	AANRETKMGK
96BW15B03	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	IGAETFYVDG	AANRETKIGK
96BW16_26	YWQATWIPKW	EFVNTPLPVK	LWYQLEKEPI	VGAETFYVDG	AANRETKLGK
96BW17A09	YWQATWIPEW	EFVNTPLPVK	LWYQLEKDPI	AGAETFYVDG	AANRETKLGK
96BWM01_5	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	LGAETFYVDG	AANRETKMGK
96BWM03_2	YWQATWIPEW	EFVNTPLPVK	LWYQLEKGPI	AGAETFYVDG	ASNRETKLGK
98BWMC12_2	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	AGAETLYVDG	AANRETKLGK
98BWMC13_4	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	LGVETFYVDG	AANRETKLGK
98BWMC14_a	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	IGVETFYVDG	AANRETKAGK
98BWM014_1	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	PGAETFYVDG	AANRETKTGK
98BWM018_d	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	GGAETFYVDG	AANRETKMGK
98BWM036_a	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	AGAETFYVDG	AASRETKKGGK
98BWM037_d	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	AGVETFYVDG	AASRDTKIGK
99BW3932_1	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	GGVETFYVDG	AANRETKVGGK
99BW4642_4	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	VGAETFYVDG	AANRETKKGGK
99BW4745_8	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	AGVETFYVDG	ATNRETKRGN
99BW4754_7	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	VGvetFYVDG	AANRDTKLGK
99BWMC16_8	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	VGAETFYVDG	AANRETKKGGK
A2_CD_97CD	WWQATWIPEW	EFVNTPLPVK	LWYQLETEPI	AGAETFYVDG	AANRETKLGK
A2_CY_94CY	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	AGAETFYVDG	AANRETKLGK
A2D_97KR	YWQATWIPEW	EFVNTPLPVK	LWYQLETEPI	TGAETFYVDG	AANRETKLGK
A2G_CD_97C	YWQATWIPDW	EFVNTPLPVK	LWYRLETEPI	PGAETYYVEG	AANRETKLGK
A_BY_97BL0	XWQATXIPE.	EFVNTPLPVK	LWYQLEKEPI	VRAETFYVDR	AANRETKIGK
A_KE_Q23_A	YWQATWILEW	EFVNTPLPVK	LWYQLEKDPI	AGAETFYVDG	AANRETKLGK
A_SE_SE659	YWQATWIPEW	EFVNTPLVL	WWYLLLEEDPI	VGADSFVEG	AAKEKTLXGT
A_SE_SE725	YWQATWIPEW	EFVNTPLPVK	LWYQLEKDPI	AGAETFYVDG	AANRETKLGK
A_SE_SE753	YWQATWIPEW	EFVNTPLPVK	LWYQLEKDPI	VGAETFYVDG	AANRETKLGK
A_SE_SE853	YWQATWIPEW	EFVNTPLPVK	LWYQLEKDPI	AGAETFYVDG	AANRETKLGK
A_SE_SE889	YWQATWIPEW	EFVNTPLPVK	LWYQLEKDPI	VGAETFYVDG	AANRETKLGK
A_SE_UGSE8	YWQATWIPEW	EFVNTPLPVK	LWYQLEKDPI	AGVETFYVDG	AANRETKLGK
A_UG_92UG0	YWQAT.IPEW	EFVNTPLPVK	LWYQLEKDPI	AGAETFYVDG	AANRETKLGK
A_UG_U455_	YWQATWIPEW	EFVNTPLPVK	LWYQLEKDPI	AGAETFYVDG	AANRETKLGK
AC_IN_2130	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPM	AGAETFYVDG	AANRETKIGK
AC_RW_92RW	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	LGAETFYVDG	AANRETKIGK
AC_SE_SE94	YWQATWIPEW	EFVNTPLPVK	LWYQLEKDPI	IGAETFYVDG	AANRETKLGK
ACD_SE_SE8	YWQATWIPEW	EFVNTPLPVK	LWYQLEKDPI	IGAETFYVDG	AANRETKLGK
ACG_BE_VI1	YWQATWIPEW	EFVNTPLPVK	LWYQLEKDPI	VGAETFYVDG	AASRETKLGK
AD_SE_SE69	YWQATWIPEW	EFVNTPLPVK	LWYQLEKDP	VGAETFYVDG	AANRETKLGK
AD_SE_SE71	YWQATWIPEW	EFVNTPLPVK	LWYQLEKDPI	AGVETFYVDG	AANRETKLGK
ADHK_NO_97	YWQATWIPEW	EFVNTPLPVK	LWYQLETEPI	VGAETFYVDG	AANRETKKGGK
ADK_CD_MAL	YWQATWIPEW	EFVNTPLPVK	LWYQLETEPI	VGAETFYVDG	AANRETKKGGK
AG_BE_VI11	YWQATWIPEW	EFVNTPLPVK	LWYQLEKDPI	AGAETFYVDG	AANRETKLGK
AG_NG_92NG	YWQATWIPDW	EFVNTPLPVK	LWYRLETEPI	PGAETYYVDG	AANKETKLGK
AGHU_GA_VI	HWQATWIPEW	EFVNTPLPVK	LWYQLETEPI	VGAETFYVDG	AANRETKQGGK
AGU_CD_Z32	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	IGAETFYVDG	AANRETKQGGK
AJ_BW_BW21	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	VGAETFYVDG	ASNRETKLGK
B_AU_VH_AF	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	VGAETFYVDG	AANRETKLGK
B_CN_RL42_	YWQATWIPEW	EFINTSPLVK	LWYQLEKEPI	EEAETFYVDG	AANRETKLGK
B_DE_D31_U	YWQATWIPEW	EFVNTPLPVK	LWYQLETEPI	VGAETFYVDG	AANRETKLGK
B_DE_HAN_U	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	VGAETFYVDG	AANRETKLGK
B_FR_HXB2_	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	VGAETFYVDG	AANRETKLGK
B_GA_OYI_	YWQATWIPEW	EFVNTPLPVK	LWYQLEKDPI	VGAETFYVDG	AANRETKLGK
B_GB_CAM1_	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	VGAETFYVDG	AANRETRLGK
B_GB_GB8_A	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	IGAETFYVDG	AANRETKLGK
B_GB_MANC_	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	VGAETFYVDG	AANRETKLGK
B_KR_WK_AF	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	VGAETFYVDG	AANRETKLGK
B_NL_3202A	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	VGAETFYVDG	AANRETKLGK
B_TW_TWCYS	YWQATWIPEW	EFVNTPLPVK	LWYQLEKEPI	IGAETFYVDG	AANRETKLGK

B_US_BC_L0	YWQATWIPeW	EFVNTpPLVK	LWYQLEKEPI	EGAETfYVDG	AANRETKLGK
B_US_DH123	YWQATWIPeW	EFVNTpPLVK	LWYQLEKEPI	VGAETfYVDG	AASRETRLGK
B_US_JRCSF	YWQATWIPeW	EFVNTpPLVK	LWYQLEKEPI	VGAETfYVDG	AANRETKLGK
B_US_MNCG_	YT.ATWIPeW	EVVNTpPLVK	LWYQLEKEPI	VGAETfYVDG	AANRETKKGK
B_US_P896_	YWQATWIPeW	EFVNTpPLVK	LWYQLEKEPI	VGAETfYVDG	AANRDtKSGK
B_US_RF_M1	YWQATWIPeW	EFVNTpPLVK	LWYQLEKEPI	IGAETfYVDG	AANRETKLGK
B_US_SF2_K	YWQATWIPeW	EFVNTpPLVK	LWYQLEKEPI	VGAETfYVDG	AANRETKLGK
B_US_WEAU1	YWQATWIPeW	EFVNTpPLVK	LWYQLEKEPI	VGAETfYVDG	AANKETKLgK
B_US_WR27_	YWQATWIPeW	EXVNTpPLVK	LWYQLEKEPI	VGAETfYVDG	AASRETKLGK
B_US_YU2_M	YWQATWIPeW	EFVNTpPLVK	LWYQLEKEPI	IGAETfYVDG	AANRETKLGK
BF1_BR_93B	YWQATWIPeW	EFVNTpPLVK	LWYQLEKEPI	VGAETfYVDG	AANRETKLGK
C_BR_92BR0	YWQAT.WIPeW	EFVNTpPLVK	LWYQLEKEPI	AGAETfYVDG	AANREIKMGK
C_BW_96BW0	YWQATWIPeW	EFVNTpPLVK	LWYQLEKEPI	AGAETfYVDG	AANRETKLGK
C_BW_96BW1	YWQATWIPeW	EFVNTpPLVK	LWYQLETEPM	AGAETfYVDG	AANRETKIGK
C_BW_96BW1	YWQATWIPeW	EFVNTpPLVK	LWYQLEKEPI	AGVETfYVDG	AANRETKMGK
C_BW_96BW1	YWQATWIPeW	EFVNTpPLVK	LWYQLEKEPI	IGAETfYVDG	AANRETKIGK
C_ET_ETH22	YWQATWIPeW	EFVNTpPLVK	LWYQLEKEPI	AGVETfYVDG	AANRETKIGK
C_IN_93IN1	YWQATWIPeW	EFVNTpPLVK	LWYQLEKDPI	AGVETfYVDG	AANRETKLGK
C_IN_93IN9	YWQATWIPeW	EFVNTpPLVK	LWYQLEKDPI	AGVETfYVDG	AANRETKKGK
C_IN_93IN9	YWQATWIPeW	EFVNTpPLVK	LWYRLEKEPI	AGVETfYVDG	AANRETKIGK
C_IN_94IN1	YWQATWIPeW	EFVNTpPLVK	LWYQLEKDPI	AGAETfYVDG	AANRDtKIGK
C_IN_95IN2	YWQATWIPeW	EFVNTpPLVK	LWYQLEKEPI	AGAETfYVDG	AANRETKIGK
CRF01_AE_C	YWQATWIPeW	EFVNTpPLVK	LWYQLEKDPI	AGAETLYVDG	AASRENKLgK
CRF01_AE_C	YWQATWIPeW	EFVNTpPLVK	LWYQLEKDPI	MGAETfYVDG	AASRETKQgK
CRF01_AE_C	YWQATWIPeW	EFVNTpPLVK	LWYQLEKDPI	AGAETfYVDG	AASRETKLGK
CRF01_AE_T	YWQATWIPeW	EFVNTpPLVK	LWYQLEKDPI	VGAETfYVDG	AASRETKLGK
CRF01_AE_T	YWQATWIPeW	EFVNTpPLVK	LWYQLEKDPI	VGAETfYVDG	AASRETKLGK
CRF01_AE_T	YWQATWIPeW	EFVNTpPLVK	LWYQLEKDPI	VGAETfYVDG	AASRETKLGK
CRF01_AE_T	YWQATWIPeW	EFVNTpPLVK	LWYQLEKEPI	IGAETfYVDG	AASRETKLGK
CRF01_AE_T	YWQATWIPeW	EFVNTpPLVK	LWYQLEKDPI	VGAETfYVDG	AASRETKLGK
CRF01_AE_T	YWQATWIPeW	EFVNTpPLVK	LWYQLEKDPI	VGAETfYVDG	AASRETKLGK
CRF02_AG_F	YWQATWIPDW	EFVNTpPLVK	LWYQLEKDPI	VGAETfYVDG	AANRETKLGK
CRF02_AG_F	YWQATWIPDW	EFVNTpPLVK	LWYQLEKDPI	VGAETfYVDG	AANKETKLgK
CRF02_AG_G	YWQATWIPeW	EFVNTpPLVK	LWYQLEKDPI	VGAETfYVDG	AANRETKLGK
CRF02_AG_N	YWQATWIPeW	EFVNTpPLVK	LWYQLEKDPI	VGAETfYVDG	AANRETKIGK
CRF02_AG_S	YWQATWIPeW	EFVNTpPLVK	LWYQLEKDPI	VGAETfYVDG	AANRETKIGK
CRF02_AG_S	YWQATWIPeW	EFVNTpPLVK	LWYQLEKDPI	IGAETfYVDG	AANRETKLGR
CRF03_AB_R	YWQATWIPeW	EFVNTpPLVK	LWYQLEKEPI	VGAETfYVDG	AANRETKSGK
CRF03_AB_R	YWQATWIPeW	EFVNTpPLVK	LWYQLEKEPI	VGAETfYVDG	AANRETKSGK
CRF04_cpx_	YWQATWIPeW	EFVNTpPLVK	LWYQLETDPI	AGAETfYVDG	AANRETKQgK
CRF04_cpx_	YWQATWIPeW	EFVNTpPLVK	LY.QLEPDPI	AGAETfYVDG	AASRETRRGK
CRF04_cpx_	YWQATWIPeW	EFVNTpPLVK	LWYQLETEPI	AGAETfYVDG	AASRETNQgK
CRF05_DF_B	YWQATWIPeW	EFVNTpPLVK	LWYQLEKEPI	LGAETfYVDG	AANRETKLGK
CRF05_DF_B	YWQATWIPeW	EFVNTpPLVK	LWYQLEKEPI	MGAETfYVDG	AANRETKLGK
CRF06_cpx_	YWQATWIPeW	EFVNTpPLVK	LWYQLETEPI	VGAETfYVDG	AANRETKQgK
CRF06_cpx_	YWQATWIPeW	EFVNTpPLVK	LWYQLETEPI	VGAETfYVDG	AANRETKKGK
CRF06_cpx_	YWQATWIPeW	EFVNTpPLVK	LWYQLETEPI	VGAETfYVDG	AANKETKKgK
CRF06_cpx_	YWQATWIPeW	EFVNTpPLVK	LWYQLETEPI	IGAETfYVDG	AANRETKIGK
CRF11_cpx_	YWQATWIPeW	EFVNTpPLVK	LWYQLEQGPI	LGAETfYVDG	AANRETKIGK
CRF11_cpx_	YWQATWIPeW	EFVNTpPLVK	LWYQLEKEPI	IGAETfYVDG	AANRETKLGK
D_CD_84ZR0	YWQATWIPeW	EFVNTpPLVK	LWYQLEKEPI	IGAETfYVDG	AANKETKLgK
D_CD_ELI_K	YWQATWIPeW	EFVNTpPLVK	LWYQLEKEPI	IGAETfYVDG	AANRETKLGK
D_CD_NDK_M	YWQATWIPeW	EFVNTpPLVK	LWYQLEKEPI	IGAETfYVDG	AANRETKLGK
D_UG_94UG1	YWQATWIPeW	EYVNTpPLVK	LWYQLEKEPI	VGAETfYVDG	AANRETKIGK
F1_BE_VI85	YWQATWIPeW	EFVNTpPLVK	LWYQLETEPI	AGADTFYVDG	ASNRETKKGK
F1_BR_93BR	YWQATWIPeW	EFVNTpPLVK	LWYQLETEPI	VGAETfYVDG	ASNRETKKGK
F1_FI_FIN9	YWQATWIPeW	EFVNTpPLVK	LWYQLETEPI	AGAETfYVDG	ASNRETKKGK
F1_FR_MP41	YWQATWIPeW	EFVNTpPLVK	LWYQLETEPI	IGAETfYVDG	ASNRETKKGK
F2_CM_MP25	YWQATWIPeW	EFVNTpPLVK	LWYQLETEPI	IGAETfYVDG	AANRETKLGK
F2KU_BE_VI	YWQATWIPeW	EFVNTpPLVK	LWYQLETDPI	AGAETfYVDG	AANRETKKGR

G_BE_DRCBL	YWQATWIPEW	EFVNTPLPLVK	LWYQLETEPI	PGVETYYVDG	AANRETKLKG
G_NG_92NG0	YWQAAWIPEW	EFVNTPLPLVK	LWYQLETEPI	PGAETYYVDG	AANRETKLKG
G_SE_SE616	YWQATWIPEW	EFVNTPLPLVK	LWYRLETEPI	PGAETYYVDG	AANRETKLKG
H_BE_VI991	HWQATWIPEW	EFVNTPHLVK	LWYQLETEPI	EGAETYYVDG	AANRETKMGK
H_BE_VI997	HWQATWIPE.	EFVNTPHLVK	LWYQLEAEPI	AGAETYYVDG	AANRETKIGK
H_CF_90CF0	YWQATWIPEW	EFVNTPHLVK	LWYQLETEPI	AGAETYYIDG	AANRETKLKG
J_SE_SE702	YWQATWIPEW	EFVNTPLPLVK	LWYQLEKEPI	MGAETFYVDG	ASNRETKVKG
J_SE_SE788	YWQATWIPEW	EFVNTPLPLVK	LWYQLEKEPI	MGAETFYVDG	ASNRETKTGK
K_CD_EQTB1	YWQATWIPEW	EFVNTPLPLVK	LWYQLETEPI	VGAETFYVDG	AANRETKQ GK
K_CM_MP535	YWQATWIPEW	EFVNTPLPLVK	LWYQLETEPI	VGAETFYVDG	AAHRETKKGR
N_CM_YBF30	HWQATWIPEW	EFVNTPLPLVK	LWYQLETEPI	SGAETFYVDG	AANRETKLKG
O_CM_ANT70	YWQATWIPEW	EFVSTPPLIK	LWYRLESEPI	MGAETYYVDG	AANRETKLKG
O_CM_MVP51	YWQATWIPEW	EFVSTPPLIK	LWYQLETEPI	VGAETFYVDG	AANRNTKLKG
O_SN_99SE_	YWQATWIPEW	EFVSTPPLIK	LWYQLESEPI	MGAETYYVDG	AANRDTKLKG
O_SN_99SE_	YWQATWIPEW	EFVSTAPLIK	LWYQLESEPI	IGAETYYVDG	AANRDTKLKG
U_CD___83C	YWQATWIPEW	EFVNTPLPLVK	LWYQLEKDPI	MGAETFYVDG	AANRETKKKG

	651				700
00BW0762_1	AGYVTDKGRR	KVITLTETTN	QKTELQAIQL	ALQDSGPEVN	IVTDSQYALG
00BW0768_2	AGYVTDGRGR	KIVPLTETTN	QKTELHAIQL	ALQDSGSEVN	IVTDSQYALG
00BW0874_2	AGYVTDGRGR	KIVSLTETTN	QKTELQAIHL	ALQDSGSEVN	IVTDSQYAFG
00BW1471_2	AGYVTDKGRQ	KVVSLTETTN	QKTELQAIKL	ALQDSGSEVN	IVTDSQYALG
00BW1616_2	AGYVTDGRGR	KIVSLAETTN	QKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
00BW1686_8	AGYVTDGRGR	KVISITETTN	QKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
00BW1759_3	AGYVTDGRGR	KIVSLTETTN	QKTELQAIQL	ALQDSGLEVN	IVTDSQYALG
00BW1773_2	AGYVTDGRGR	KIVSLTETTN	QKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
00BW1783_5	AGYVTDGRGR	KVISLTETTN	QKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
00BW1795_6	AGYVTDGRGR	KIISLTETTN	QKTELHAIQL	ALQDSGPEVN	IVTDSQYALG
00BW1811_3	AGYVTDKGRQ	KTVSLTETTN	QKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
00BW1859_5	AGYVTDGRGR	KIVNLTETTN	QKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
00BW1880_2	AGYVTDGRGR	KVVTLTETTN	QKTELQAIQL	ALQDSGPEVN	IVTDSQYALG
00BW1921_1	AGYVTDKGRQ	KVITLTETTN	QKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
00BW2036_1	AGYVTDGRGR	KIISLTETTN	QKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
00BW2063_6	AGYVTDGRGR	KVVSLTGTTN	QKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
00BW2087_2	AGYVTDKGRQ	KIVCLNETTN	QKTELHAIQL	ALQDSGLEVN	IVTDSQYALG
00BW2127_2	AGYVTDGRGR	KVISINETTN	QKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
00BW2128_3	AGYVTDKGRQ	KVVSLTETTN	QKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
00BW2276_7	AGYVTDGRGR	KIVSLSETTN	QKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
00BW3819_3	AGYVTDGRGR	KIVSINGTTN	QKTELRAIYL	ALQDSGSEVN	IVTDSQYALG
00BW3842_8	AGYVTDGRGR	KVVSLTETTN	QKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
00BW3871_3	AGYVTDGRGR	KVISLTETTN	QKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
00BW3876_9	AGYVTDGRGR	KIVSLTETTN	QKSELQAIHL	ALQDSGSEVN	IVTDSQYALG
00BW3886_8	AGYVTDGRGR	KVITLTETTN	QKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
00BW3891_6	AGYVTDGRGR	KIVSLTETTN	QKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
00BW3970_2	AGYVTDGRGR	KIITLNETTN	QKTELQAIKL	ALQDSGSEVN	IVTDSQYALG
00BW5031_1	AGYVTDGRGR	KIVSLTETTN	QKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
96BW01B21	AGYVTDGRGR	KIISLTETTN	QKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
96BW0407	AGYVTNKGRQ	KIVPLTETTN	QKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
96BW0502	AGYVTDGRGR	KIVSLTETTN	QKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
96BW06_J4	AGYVTDGRGR	KVISLTETTN	QKTELQAIQL	ALQDSGLEVN	IVTDSQYALG
96BW11_06	AGYVTDKGRQ	KVVTLTETTN	QKTELQAIQL	ALQDSGPEVN	IVTDSQYALG
96BW1210	AGYVTDGRGR	KIVSLNETTN	QKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
96BW15B03	AGYVTDGRGR	KIVSLTETTN	QKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
96BW16_26	AGCVTDGRGR	KIVSLTETTN	QKTELQAIQL	ALQDSGAEVN	IVTDSQYALG
96BW17A09	AGYVTDKGRQ	KVVSLTETTN	QKTELQAIKL	ALQDSGSEVN	IVTDSQYALG
96BWM01_5	AGYVTDGRGR	KVVPLTETTN	QKTELQAIQL	ALQDSGSEVN	IVTDSQYALK
96BWM03_2	AGYVTDGRGR	KVVSLNETTN	QKTELQAIQL	ALQDSGTEVN	IVTDSQYALG
98BWMC12_2	AGYVTDKGRQ	KVVSLTETTN	QKTELHAIQL	ALQDSGSEVN	IVTDSQYALG
98BWMC13_4	AGYITDRGRQ	KVVSLTETTN	QKTELQAIQL	ALQDSGPEVN	IVTDSQYALG
98BWMC14_a	AGYVTDGRGR	KVISLTETAN	QKTELQAIQL	ALQDSGSEVN	IVTDSQYALG



98BWM014_1	AGYVTDKGRQ	KIVSLNETTN	QKAELQAIQL	ALQDSGLEVN	IVTDSQYALG
98BWM018_d	AGYVTDKGRQ	KIVALTETTN	QKAELQAIQL	ALQDSGSEVN	IVTDSQYALG
98BWM036_a	AGYVTDGRGRQ	KCVTLTETTN	QKTELQAIQL	ALQDSGPEVN	IVTDSQYALG
98BWM037_d	AGYVTDGRGKQ	KIITLTETTN	QKTELQAIQL	ALQDSGPEVN	IVTDSQYALG
99BW3932_1	AGYVTDKGRQ	KVITINETTN	QKTELQAIYL	ALQDSGSEVN	IVTDSQYALG
99BW4642_4	AGYVTDGRGRQ	RIVNLTETTN	QKTELQAIHL	ALQDSGLEVN	IVTDSQYALG
99BW4745_8	AGYVTDGRGRQ	KIVSLTETTN	QKAELQAIQL	ALQDSGSEVN	IVTDSQYALG
99BW4754_7	AGYVTDGRGRQ	KVVSLTETTN	QKTELQAIHL	ALQDSGPEVN	IVTDSQYALG
99BWMC16_8	AGYVTDGRGRQ	KVVTLTETTN	QKTELQAIQL	ALQDSESEVN	IVTDSQYALG
A2_CD_97CD	AGYVTDGRGRQ	KIVPLTETTN	QKTELHAIYL	ALQDSGSEVN	IVTDSQYALG
A2_CY_94CY	AGYVTDGRGRQ	KIVSLTETTN	QKTELHAIYL	ALQDSGLEVN	IVTDSQYALG
A2D_97KR	AGYVTDKGRQ	KIVSLTDTTN	QKTELHAIYL	ALQDSGLEVN	IVTDSQYALG
A2G_CD_97C	AGYVTDKGKQ	KIINLTETTN	QKTELHAIQL	ALQDSGSEVN	IVTDSQYALG
A_BY_97BL0	AGYVTDGRGRQ	KVVPLTETTN	QKTELHAIHL	VLQDSGSEVD	IVTDSQYALG
A_KE_Q23_A	AGYVTDKGRQ	KVVSLTETTN	QKTELHAIHL	ALQDSGSEVN	IVTDSQYALG
A_SE_SE659	GWFAEGGRQ	VVVPLAKTTH	QTTELPALHP	SLQDSGSVVI	IVNDSQSAGG
A_SE_SE725	AGYVTDGRGRQ	KVVSLTETTN	QKTELHAIHL	ALQDSGSEVN	IVTDSQYALG
A_SE_SE753	AGYVTNRGRQ	KVVSLTETTN	QKTELHAILL	ALQDSGSEVN	IVTDSQYALG
A_SE_SE853	AGYVTDGRGRQ	KVVSLTETTN	QKTEVHAIHL	ALQDSGSEVN	IVTDSQYALG
A_SE_SE889	AGYVTDGRGRQ	KVVTLAETTN	QKTELHAIYL	ALQDSGSEVN	IVTDSQYALG
A_SE_UGSE8	AGYVTDGRGRQ	KVVSLTETTN	QKTELHAIHL	ALQDSGSEVN	IVTDSQYALG
A_UG_92UG0	AGYVTDGRGRQ	KVVSLTETTN	QKTELHAIHL	ALQDSGSEVN	IVTDSQYALG
A_UG_U455	AGYVTDGRGRQ	KVVSLTETTN	QKTELHAIHL	ALQDSGSEVN	IVTDSQYALG
AC_IN_2130	AGYATDRGRQ	KIVTLTETTN	QKTELQAIYL	ALQDSGSEVN	IVTDSQYALG
AC_RW_92RW	AGYVTDGRGRQ	KIVSLTETTN	QKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
AC_SE_SE94	AGYVTDGRGRQ	KVVSLTETTN	QKTELHAIQL	ALQDSGSEVN	IVTDSQYALG
ACD_SE_SE8	AGYVTDGRGRQ	KVVSLTETTN	QKTELHAIYL	ALQDSGSEVN	IVTDSQYALG
ACG_BE_VI1	AGYVTDGRGRQ	KAITLTETTN	QKTELHAIHL	ALQDSGSEVN	IVTDSQYALG
AD_SE_SE69	AGYVTDGRGRQ	KVVPLTETTN	QKTELHAIHL	ALQDSGSEVN	IVTDSQYALG
AD_SE_SE71	AGYITDRGRQ	KVVSLTDTTN	QKTELQAINL	ALQDSGPEVN	IVTDSQYALG
ADHK_NO_97	AGYVTDGRGRQ	KVVFLTETTN	QKTELQAIHL	ALQDSGSEVN	IVTDSQYALG
ADK_CD_MAL	AGYVTDGRGRQ	KVVSLTETTN	QKTELQAIHL	ALQDSGSEVN	IVTDSQYALG
AG_BE_VI11	AGYVTDGRGRQ	KAVSLTETTN	QKTELHAIQL	ALQDSGSEVN	IVTDSQYALG
AG_NG_92NG	AGYVTDGRGKQ	KIITIQUETTN	QKTELHAIQL	ALQDSGSEVN	IVTDSQYALG
AGHU_GA_VI	AGYVTDGRGRQ	KIVSLTETTN	QKTELQAIHL	ALQDSGPEVN	IVTDSQYALG
AGU_CD_Z32	AGYITDKGRQ	KVITLTETTN	QKTELEAIHL	ALQDSGLEVN	IVTDSQYALG
AJ_BW_BW21	AGYVTDGRGRQ	KIVSLTETTN	QKTELHAIYL	ALQDSGSEVN	IVTDSQYALG
B_AU_VH_AF	AGYVTDGRGRQ	KVVPLSDTTN	QKTELQAIQL	ALQDSGLEVN	IVTDSQYALG
B_CN_RL42	AGYVTNKGGRQ	KVVTLTDTTN	QKTELQAIYL	ALQDSGSEVN	IVTDSQYALG
B_DE_D31_U	AGYVTDGRGRQ	KVVSLTDTTN	QKTELQAIHL	ALQDSGLEVN	IVSDSQYAIG
B_DE_HAN_U	AGYVTDGRGRQ	KVVSLNDTTN	QKTELQAIHL	ALQDSGLEVN	IVTDSQYALG
B_FR_HXB2	AGYVTNRGRQ	KVVTLTDTTN	QKTELQAIYL	ALQDSGLEVN	IVTDSQYALG
B_GA_OYI	AGYVTDGRGRQ	KVVSLTDTTN	QKTELQAIHL	ALQDSGLEVN	IVTDSQYALG
B_GB_CAM1	AGYVTDGRGRQ	KVVPLTDTTN	QKTELQAIYL	ALQDSGLEVN	IVTDSQYALG
B_GB_GB8_A	AGYVTDGRGRQ	KVVPLTDTTN	QKTELQAIHL	ALQDSGLEVN	IVTDSQYALG
B_GB_MANC	AGYVTDGRGRQ	KVISLTDTTN	QKTELQAIHL	ALQDSGLEVN	IVSDSQYALG
B_KR_WK_AF	AGYVTDGRGRQ	KVVPLTDTTN	QKTELQAIHL	ALQDSGLEVN	IVTDSQYALG
B_NL_3202A	AGYVTDGRGRQ	KVVSLNDTTN	QKTELQAINL	ALQDSGLEVN	IVTDSQYALG
B_TW_TWCYS	AGYVTDKGRQ	KVVSLTDTTN	QKTELQAIHL	ALQDSGLEVN	IVTDSQYALG
B_US_BC_L0	AGYVTNKGGRQ	KVVTLTDTTN	QKTELEAIHL	ALQDSGLEVN	IVTDSQYALG
B_US_DH123	AGYVTNRGRQ	KVVSLTDTTN	QKTELQAIYL	ALQDSGLEVN	IVTDSQYALG
B_US_JRCSF	AGYVTSRGRQ	KVVSLTDTTN	QKTELQAIHL	ALQDSGLEVN	IVTDSQYALG
B_US_MNCG	AGYVTNRGRQ	KVVSLTDTTN	QKTELQAIHL	ALQDSGLEVN	IVTDSQYALG
B_US_P896	AGYVTDGRGRQ	KVVSLADTTN	QKTELQAIHL	ALQDSGLEVN	IVTDSQYALG
B_US_RF_M1	AGYVTDGRGRQ	KVVSLTDTTN	QKTELQAIHL	ALQDSGLEVN	IVTDSQYALG
B_US_SF2_K	AGYVTDGRGRQ	KVVSIADTTN	QKTELQAIHL	ALQDSGLEVN	IVTDSQYALG
B_US_WEAU1	AGYVTNRGRQ	KVVSLTDTTN	QKTELQAIHL	ALQDSGLEVN	IVTDSQYALG
B_US_WR27	AGYVTDGRGRQ	KVVSLNDTTN	QKTELQAIHL	ALQDSGLEVN	IVTDSQYALG
B_US_YU2_M	AGYVTNKGGRQ	KVVSLTDTTN	QKTELQAIYL	ALQDSGLEVN	IVTDSQYALG
BF1_BR_93B	AGYVTDGRGRQ	KVVPLTDTTN	QKTELQAIHL	ALQDSGLEVN	IVTDSQYALG

C_BR_92BR0	AGYVTDGRGQ	KIVSITETTN	QKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
C_BW_96BW0	AGYVTDKGRQ	KIVPLTETTN	QRAELQAIQL	ALQDSGSEVN	IVTDSQYALG
C_BW_96BW1	AGYVTDKGRQ	EVVTLTETTN	QKAELQAIQL	ALQDSGPEVN	IVTDSQYALG
C_BW_96BW1	AGYVTDGRGQ	KIVSLNETTN	QKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
C_BW_96BW1	AGYVTDGRGQ	KIVSLTETTN	QKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
C_ET_ETH22	AGYVTDGRGQ	KIVSLTETTN	QKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
C_IN_93IN1	AGYVTDGRGQ	KIVSLTETTN	QKTELQAIYL	ALQDSGSEVN	IVTDSQYALG
C_IN_93IN9	AGYVTDGRGQ	KIVSLTETTN	QKTELQAICL	ALQDSGSEVN	IVTDSQYALG
C_IN_93IN9	AGYVTDGRGQ	KIVPLTETTN	QKTELQAIYL	ALQDSGSEVN	IVTDSQYALG
C_IN_94IN1	AGYVTDGRGQ	KIVSLTETTN	QKTELQAICL	ALQDSGSEVN	IVTDSQYALG
C_IN_95IN2	AGYVTDKGRN	KIVSLTETTN	QKTELQAICL	ALQDSGSEVN	IVTDSQYALG
CRF01_AE_C	AGYVTDGRGQ	KVVSLTETTN	QKTELHAIHL	ALQDSGSDVN	IVTDSQHALG
CRF01_AE_C	AGYVTDGRGQ	KVVSLTETTN	QKTELHAIHL	ALQDSGPEVN	IVTDSQYALG
CRF01_AE_C	AGYATDRGRH	KVVSLTETTN	QKTELHAIHL	ALRDSGSEVN	IVTDSQYALG
CRF01_AE_T	AGYVTDGRGQ	KVVSLTETTN	QKTELHAIHL	ALQDSGSEVN	IVTDSQYALG
CRF01_AE_T	AGYVTDGRGQ	KVVSLTETTN	QKTELHAIHL	ALQDSGSEVN	IVTDSQYALG
CRF01_AE_T	AGYVTDGRGQ	KVISLTETTN	QKTELHAIHL	ALQDSGSEVN	IVTDSQYALG
CRF01_AE_T	AGYVTDGRGQ	KVVSLTETTN	QKTELHAIHL	ALQDSGSEVN	IVTDSQYALG
CRF01_AE_T	AGYVTDGRGQ	KVVSLTETTN	QKTELHAIHL	ALQDSGSEVN	IVTDSQYALG
CRF01_AE_T	AGYVTDGRGQ	KVVSLTETTN	QKTELHAIHL	ALQDSGSEVN	IVTDSQYALG
CRF01_AE_T	AGYVTNRGRQ	KVVSLTETTN	QKSELHAIHL	ALQDSGSEVN	IVTDSQYALG
CRF02_AG_F	AGYVTDGRGQ	KVVSLTETTN	QKTELHAIYL	ALQDSGSEVN	IVTDSQYALG
CRF02_AG_F	AGYVTDGRGQ	KVVSLTETTN	QKTELHAIYL	ALQDSGSEVN	IVTDSQYALG
CRF02_AG_G	AGYVTDGRGQ	KVVSLTETTN	QKTELHAIHL	ALQDSGSEVN	IVTDSQYALG
CRF02_AG_N	AGYVTDGRGQ	KVVSLTETTN	QKTELHAIHL	ALQDSGSEVN	IVTDSQYALG
CRF02_AG_S	AGYVTDGRGQ	KVVSLAETTN	QKTELHAIHL	ALQDSGSEVN	IVTDSQYALG
CRF02_AG_S	AGYVTDGRGQ	NVVSLTETTN	QKTELHAILL	ALQESGSEVN	IVTDSQYALG
CRF03_AB_R	AGYVTDGRGQ	KVVSLTDTTN	QKTELQAIHL	ALQDSGLEVN	IVTDSQYALG
CRF03_AB_R	AGYVTDGRGQ	KVVSLTDTTN	QKTELHAIHL	ALQDSGLEVN	IVTDSQYALG
CRF04_cpx_	AGYVTDGRGQ	KVVSLSETTN	QKTELQAIYL	ALQDSGSEVN	IVTDSQYAIG
CRF04_cpx_	AGYVTDGRGQ	KVVSLSETTN	QKTELQAIYL	ALKDSGSEVN	IVTDSQYAIG
CRF04_cpx_	AGYVTDGRGQ	KVITLPETTN	QKTELQAIYL	ALQDSGSEVN	IVTDSQYAMG
CRF05_DF_B	AGYITDKGRQ	KAVSLTETTN	QKAELQAIHL	ALQDSGLEVN	IVTDSQYALG
CRF05_DF_B	AGYVTDKGRQ	KAVSLTETTN	QKTELHAIYL	ALQDSGSEVN	IVTDSQYALG
CRF06_cpx_	AGYVTDGRGQ	KVVTLTETTN	QKTELQAINL	ALQDSGPEVN	IVTDSQYALG
CRF06_cpx_	AGYVTDGRGQ	KVVSLAETTN	QKTELQAINL	ALQDSGSEVN	IVTDSQYALG
CRF06_cpx_	AGYVTDKGRQ	RVISLTETTN	QKTELQAINL	ALQDSGSEVN	IVTDSQYALG
CRF06_cpx_	AGYVTDGRGQ	KVVSLTETTN	QKTELQAINL	ALQDSGSEVN	IVTDSQYALG
CRF11_cpx_	AGYVTDKGRQ	KVITLTETTN	QKTELEAIHL	ALQDSGLEVN	IVTDSQYALG
CRF11_cpx_	AGYVTNKGRQ	KVITPIETTN	QKTELEAIHL	ALKDSGLEVN	IVTDSQYALG
D_CD_84ZR0	AGYVTDGRGQ	KVVPFTDTTN	QKTELQAINL	ALQDSGLEVN	IVTDSQYALG
D_CD_ELI_K	AGYVTDGRGQ	KVVPLTDTTN	QKTELQAINL	ALQDSGLEVN	IVTDSQYALG
D_CD_NDK_M	AGYVTDGRGQ	KVVPFDTDTN	QKTELQAINL	ALQDSGLEVN	IVTDSQYALG
D_UG_94UG1	AGYVTDGRGQ	KVVSLTDTTN	QKTELQAINL	ALQDSGLEVN	IVTDSQYALG
F1_BE_VI85	AGYVTDKGRQ	KVVSLTETTN	QKAELQAIYL	ALQDSGSEVN	IVTDSQYALG
F1_BR_93BR	AGYVTDGRGQ	KAVSLTETTN	QKAELQAIQL	ALQDSGSEVN	IVTDSQYALG
F1_FI_FIN9	AGYVTDGRGQ	KVVSLTETTN	QKAELQAIHL	ALQDSGSEVN	IVTDSQYALG
F1_FR_MP41	AGYVTDGRGQ	KAVILTETTN	QKAELQAIHL	ALQDSGSEVN	IVTDSQYVLG
F2_CM_MP25	AGYITDRGRQ	KVVSLTETTN	QKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
F2KU_BE_VI	AGYVTDKGRQ	KVVSLTETTN	QKTELQTIYL	ALQDSGSEVN	IVTDSQYAIG
G_BE_DRCBL	AGYVTDKGRQ	IIITLTETTN	QKAELHAIQL	ALQDSQSEVN	IVTDSQYALG
G_NG_92NG0	AGHVTDKGRQ	KIITLTETTN	QKAELHAIQL	ALQDSRPEVN	IVTDSQYALG
G_SE_SE616	AGYVTDKGRQ	KIITLTETTN	QKAELQAIQL	ALQDSRSEVN	IVTDSQYALG
H_BE_VI991	AGYVTDGRGQ	KIVSLTETTN	QKTELQAIYL	ALQESGPEVN	IVTDSQYALG
H_BE_VI997	AGYVTDKGRQ	KVVALTETTN	QKTELQAIYL	ALQDSGLEVN	IVTDSQYALG
H_CF_90CF0	AGYVTDGRGQ	KVVSLTETTN	QKTELQAIYL	ALQDSGLEVN	IVTDSQYALG
J_SE_SE702	AGYVTDKGRQ	KVITLTDTTN	QKTELQAIYL	ALQDSGIEVN	IVTDSQYALG
J_SE_SE788	AGYVTDKGRQ	KVVTLTDTTN	QKTELHAIYL	ALRDSGLEVN	IVTDSQYALG
K_CD_EQTB1	AGYVTDKGRQ	KVISITETTN	QKTELQAIHL	ALQDSGSEVN	IVTDSQYALG
K_CM_MP535	AGYVTDGRGQ	KVVSIETTN	QKAELQAICL	ALQDSGSEVN	IVTDSQYALG
N_CM_YBF30	AGFVTDGRGQ	KVVSIADTTN	QKAELQAILM	ALQESGRDVN	IVTDSQYAMG

O_CM_ANT70	AGYVTEQGKQ	KIIKLEETTN	QKAELMAILL	ALQDSKETVN	IVTDSQYALG
O_CM_MVP51	AGYVTEQGKQ	NIIKLEETTN	QKAELMAVLI	ALQDSKEQVN	IVTDSQYVLG
O_SN_99SE_	AGYVTEKGRQ	KIIKLEETTN	QRAELMAVLL	ALQDSKETVN	IVQDSQYVLG
O_SN_99SE_	AGYVTEKGKQ	KIVKLEETTN	QKAELMAVLL	ALQDSKETVN	IVTDSQYVLG
U_CD___83C	AGYVTDRGRQ	KVISLTETTN	QKAELQALYL	ALQDSGLEAN	IVTDSQYALG

	701				750
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00BW0768_2	IIQAQPDKSE	SELVNQIIEQ	LIKKERVYLS	WVPAHKGIGG	NEQVDKLVSK
00BW0874_2	IIQAQPDKSE	SELVNQIIEQ	LINKERVYLS	WVPAHKGIGG	NEQVDKLVSS
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00BW1616_2	IIQAQPDKSE	SELVNQIIEQ	LINKERIYLS	WVPAHKGIGG	NEQVDKLVSS
00BW1686_8	IIQAQPDKSE	SELVNQIIEQ	LINKERVYLS	WVPAHKGIGG	NEQVDKLVSS
00BW1759_3	IIQAQPDKSE	SELVNQIIEE	LIKKERVYLS	WVPAHKGIGG	NEQVDKLVSS
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00BW1795_6	IIQAQPDKSE	SELVSQIIEQ	LINKERVYLS	WVPAHKGIGG	NEQVDKLVSS
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00BW1880_2	ITQAQPDKSE	SELVNQIIEQ	LIKKEKVYLS	WVPAHKGIGG	NEQVDKLVSN
00BW1921_1	IIQAQPDKSE	SELVNQIIEE	LIKKERVYLS	WVPAHKGIGG	NEQVDKLVSS
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00BW2063_6	IIQAQPDKSE	SELVNQIIEQ	LIKKERVYLS	WVPAHKGIGG	NEQVDKLVSS
00BW2087_2	IIQAQPDKSE	SELVNQIIEQ	LINKERIYLS	WVPAHKGIGG	NEQVDKLVSN
00BW2127_2	IIQAQPDKSE	SELVNQIIEQ	LIKKDRVYLS	WVPAHKGIGG	NEQVDKLVSS
00BW2128_3	IIQAQPDKSE	SELVNQIIEQ	LIKKERVYLS	WVPAHKGIGG	NEQVDKLVSN
00BW2276_7	IIQAQPDKSE	SELVNQIIEQ	LIKKEKVYLS	WVPAHKGIGG	NEQVDKLVSK
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00BW3871_3	IIQAQPDKSE	SELVNQIIEE	LIKKERVYLS	WVPAHKGIGG	NEQVDKLVSS
00BW3876_9	IIQAQPDKSE	SELVNQIIEQ	LIKKEKVYLS	WVPAHKGIGG	NEQVDKLVSS
00BW3886_8	IIQAQPDKSE	SELVNQIIEQ	LIKKEGVYLS	WVPAHKGIGG	NEQVDKLVSK
00BW3891_6	IIQSQPGKSE	SELVNQKIEQ	LIKKERVYLS	WVPAHKGIGG	NEQVDKLVSK
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96BW0407	IIQAQPDKSE	SELVTQIIEQ	LIKKERIYLS	WVPAHKGIGG	NEQVDKLVSS
96BW0502	IIQAQPDKSE	SELVNQIIEQ	LIQKEWVYLS	WVPAHKGIGG	NEQVDKLVSS
96BW06_J4	IIQAQPDKSE	SELVNQIIEQ	LINKERVYLS	WVPAHKGIGG	NEQVDKLVSN
96BW11_06	IIQAQPDKSE	SELVNQIIEQ	LIKKEKVYLS	WVPAHKGIGG	NEQVDKLVSS
96BW1210	IIQAQPDKSE	SELVNQIIEQ	LICKERVYLS	WVPAHKGIGG	NEQVDKLVSS
96BW15B03	IIQAQPDKSE	SELVNQIIEQ	LIKKEKVYLS	WVPAHKGIGG	NEQIDKLVSK
96BW16_26	IIQAQPDKSE	SELVNQIIEQ	LINKERIYLS	WVPAHKGIGG	HEQVDKLVSS
96BW17A09	IIQAQPDSE	SELVNQIIEQ	LIQKDKVYLS	WVPAHKGIGG	NEQVDKLVSS
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98BWMC13_4	IIQAQPDKSE	SELVNQIIEQ	LIKKERVYLS	WVPAHKGIGG	NEQVDKLVSS
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98BWM018_d	IIQAQPDKSE	SEIVNQIIEQ	LINKERVYLS	WVPAHKGIGG	NEQVDKLVSR
98BWM036_a	IIQAQPDKSE	SELVNQIIEQ	LINKERIYLS	WVPAHKGIGG	NEQVDKLVSS
98BWM037_d	IIQAQPDNSE	SELVNQIIEQ	LIQKERVYLS	WVPAHKGIGG	NEQVDKLVSK
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99BW4754_7	IIQAQPDKSE	SELVNQIIEQ	LIKKKKVYLS	WVPAHKGIGG	NEQVDKLVSS
99BWMC16_8	IIQAQPDKSE	SELVNQIIEG	LIKKERVYLS	WVPAHKGIGG	NEQVDKLVSN
A2_CD_97CD	IIQAQPDSSSE	SELVNQIIEK	LIEKERVYLS	WVPAHKGIGG	NEQVDKLVSC
A2_CY_94CY	IIQAQPERSE	SEIVNQIIEK	LIEKERVYLS	WVPAHKGIGG	NEQVDKLVSS

A2D__97KR	IIQAQPDRSE	SEIVNLIIEK	LIEKERVYLS	WVPAHKGIGE	NEQVDKLVSS
A2G_CD_97C	IIQAQPDSSSE	AEIVNQIIEQ	LIRKEKVYLS	WVPAHKGIGG	NEQVDKLVSS
A_BY_97BL0	IISAQPDRSE	SEIVNKIIEK	LIKKEKVYLS	.VPAHKRIX	NEQVDKLVSN
A_KE_Q23_A	IIQAQPDKSE	SEIVNQIIEK	LIEKDKVYLS	WVPAHKGIGG	NEQVDKLVSS
A_SE_SE659	IIQAQPDRSE	SEIVNQIIEK	LVGKDKVYLA	WVPAHKGIGG	NEQVDKLVSS
A_SE_SE725	IIQAQPDSSSE	SEIVNQIIEK	LIGKDKVYLS	WVPAHKGIGG	NEQVDKLVSS
A_SE_SE753	IIQAQPDRSE	SEIVNQIIEK	LIGKDKVYLS	WVPAHKGIGG	NEQVDKLVSS
A_SE_SE853	IIQAQPDSSSE	SEIVNQIIEK	LIGKDKVYLS	WVPAHKGIGG	NEQVDKLVSS
A_SE_SE889	IIQAQPDRSE	SEIVNQIIEK	LIGKDKVYLS	WVPAHKGIGG	NEQVDKLVSA
A_SE_UGSE8	IIQAQPDKSE	SEIVNQIIEK	LIEKDKVYLS	WVPAHKGIGG	NEQVDKLVSS
A_UG_92UG0	IIQAQPDRSE	SEIVNQIIEK	LIEKDKVYLS	WVPAHKGIGG	NEQVDKLVSS
A_UG_U455_	IIQAQPDRSE	SEIVNQIIEK	LIEKEKVYLS	WVPAHKGIGG	NEQVDKLVSS
AC_IN_2130	IIQAQPDKSE	SEIVNQIIEQ	LIKKEKVYLS	WVPAHKGIGG	NEQVDKLVSS
AC_RW_92RW	IIQAQPDSSSE	SEAVNQIIEK	LIKKEKVYLS	WVPAHKGIGG	NEQVDKLVSS
AC_SE_SE94	IIQAQPDRSE	SEIVNQIIEK	LIQKDKVYLS	WVPAHKGIGG	NEQVDKLVSS
ACD_SE_SE8	IIQAQPDRSE	SEIVNQIIEK	LIGKDKVYLS	WVPAHKGIGG	NEQVDKLVSS
ACG_BE_VI1	IIQAQPDKSE	SEIVNQIIEQ	LIRKDRVYLS	WVPAHKGIGG	NEQVDKLVSS
AD_SE_SE69	IIQAQPDKSE	SELVSIIEQ	LIKKEKVYLS	WVPAHKGIGG	NEQVDKLVSN
AD_SE_SE71	IIQAQPDRSE	SEIVNQIIEK	LIGKDKVYLS	WVPAHKGIGG	NEQVDKLVSS
ADHK_NO_97	IIQAQPDKSE	SDLVNQIIEQ	LIQKDKVYLT	WVPAHKGIGG	NEQVDKLVSS
ADK_CD_MAL	IIQAQPDKSE	SEIVNQIIEQ	LIQKDKVYLS	WVPAHKGIGG	NEQVDKLVSS
AG_BE_VI11	IIQAQPDRSE	SEIVNQIIEK	LIEKDKVYVS	WVPAHKGIGG	NEQVDKLVSS
AG_NG_92NG	IIQAQPDRSE	SEIVNQIIEQ	LIKKEKVYLT	WVPAHKGIGG	NEQVDKLVSS
AGHU_GA_VI	IIQAQPDKSE	SEIVNQIIEK	LIQKNKVYLS	WVPAHKGIGG	NEQVDKLVSA
AGU_CD_Z32	IIQAQPDKSE	SELVSIIEQ	LIKKEKVYLS	WVPAHKGIGG	NEQVDKLVSS
AJ_BW_BW21	IIQAQPDKSE	SELVSIIEE	LIKKEKVYLS	WVPAHKGIGG	NEQVDKLVSS
B_AU_VH_AF	IIQAQPDKSE	SEIVNQIIEQ	LIKKEKIYLA	WVPAHKGIGG	NEQVDKLVSA
B_CN_RL42_	IIQAQPDKSE	SELVSIIEQ	LIKKEKVYLA	WVPAHKGIGG	NEQVDKLVSA
B_DE_D31_U	IIQAQPDKSE	SELVSIIEQ	LIKKEKVYLT	WVPAHKGIGG	NEQVDKLVSA
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B_FR_HXB2_	IIQAQPDQSE	SEIVNQIIEQ	LIKKEKVYLA	WVPAHKGIGG	NEQVDKLVSA
B_GA_OYI_	IIQAQPDKSE	SELVSIIEQ	LIKKEKVYLA	WVPAHKGIGG	NEQVDKLVSA
B_GB_CAM1_	IIQAQPDKSE	SEIVNQIIEE	LIKKEKVYLA	WVPAHKGIGG	NEQVDKLVSA
B_GB_GB8_A	IIQAQPDRSE	SEIVNQIIEQ	LIKKEKVYLA	WVPAHKGIGG	NEQVDKLVSS
B_GB_MANC_	IIQAQPDKSE	SELVSIIEQ	LIKKEKVYLA	WVPAHKGIGG	NEQVDKLVSA
B_KR_WK_AF	IIQAQPDKSE	SELVSIIEQ	LIKKEKVYLA	WVPAHKGIGG	NEQVDKLVSA
B_NL_3202A	IIQAQPDKSE	SELVSIIEQ	LIKKEKVYLA	WVPAHKGIGG	NEQVDKLVSA
B_TW_TWCYS	IIQAQPDKSE	SELVSIIEE	LIKKEKVYLT	WVPAHKGIGG	NEQVDKLVSA
B_US_BC_L0	IIQAQPDKSE	SELVSIIEQ	LIKKEKVYLA	WVPAHKGIGG	NEQVDKLVSA
B_US_DH123	IIQAQPDKSE	SEIVNQIIEQ	LIKKEKVYLA	WVPAHKGIGG	NEQVDKLVST
B_US_JRCSF	IIQAQPDKSE	SELVSIIEQ	LIKKEKVYLA	WVPAHKGIGG	NEQVDKLVSA
B_US_MNCG_	IIQAQPDKSE	SELVSIIEQ	LIKKEKVYLA	WVPAHKGIGG	NEQVDKLVSA
B_US_P896_	IIQAQPDKSE	SELVSIIEQ	LIKKEKVYLA	WVPAHKGIGG	NEQVDKLVSA
B_US_RF_M1	IIQAQPDKSE	SELVSIIEQ	LIKKEKVYLA	WVPAHKGIGG	NEQVDRLVST
B_US_SF2_K	IIQAQPDKSE	SELVSIIEQ	LIKKEKVYLA	WVPAHKGIGG	NEQVDKLVSA
B_US_WEAU1	IIQAQPDQSE	SELVSIIEQ	LIKKEKVYLA	WVPAHKGIGG	NEQVDKLVSS
B_US_WR27_	IIQAQPDKSE	SELVSIIEQ	LIXKXXVYLA	WVPAHKGIGG	NEQVDKLVSS
B_US_YU2_M	IIQAQPDRSE	SELVSIIEQ	LIKKEKVYLA	WVPAHKGIGG	NEQVDKLVSA
BF1_BR_93B	IIQAQPDKSE	LEIVNQIIEQ	LIKKEKIYLA	WVPAHKGIGG	NEQVDKLVSS
C_BR_92BR0	IIQAQPDKSE	SEIVNQIIEQ	LIKKEKVYLS	WVPAHKGIGG	NEQVDKLVSS
C_BW_96BW0	IIQAQPDKSE	SELVTQIIEQ	LIKKEKVYLS	WVPAHKGIGG	NEQVDKLVSS
C_BW_96BW1	IIQAQPDKSE	SEIVNQIIEQ	LIKKEKVYLS	WVPAHKGIGG	NEQVDKLVSS
C_BW_96BW1	IIQAQPDKSE	SEIVNQIIEQ	LICKERVYLS	WVPAHKGIGG	NEQVDKLVSS
C_BW_96BW1	IIQAQPDKSE	SEIVNQIIEQ	LIKKEKVYLS	WVPAHKGIGG	NEQVDKLVSK
C_ET_ETH22	IIQAQPDKSE	SEIVNQIIEQ	LISKERVYLS	WVPAHKGIGG	NEQVDKLVSS
C_IN_93IN1	IIQAQPDKSE	SEIVNQIIEQ	LIKKEKVYLS	WVPAHKGIGG	NEQVDKLVSS
C_IN_93IN9	IIQAQPDKSE	SEIVNQIIEQ	LIKKEKVYLS	WVPAHKGIGG	NEQVDKLVSS
C_IN_93IN9	IIQAQPDKSE	SEIVNQIIEQ	LIKKEKVYLS	WVPAHKGIGG	NEQVDKLVSS
C_IN_94IN1	IIQAQPDKSE	SEIVNQIIEQ	LINKERVYLS	WVPAHKGIGG	NEQVDKLVSS
C_IN_95IN2	IIQAQPNKSE	SEIVNQIIEQ	LIKKEKVYLS	WVPAHKGIGG	NEQVDKLVSS

CRF01_AE_C	IIQAQPDRSE	SEIVNQIIEK	LIEKERVYLS	WVPAHKGIGG	NEQVDKLVSS
CRF01_AE_C	IIQAQPDRSE	SDIVNQIIEK	LIEKEKVYLS	WVPAHKGIGG	NEQVDKLVSS
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CRF02_AG_F	IIQAQPDRSE	SELVNQIIEK	LIEKDKVYLS	WVPAHKGIGG	NEQVDKLVSN
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CRF03_AB_R	IIQAQPDKSE	SELVSQIIEQ	LIKKEKVYLA	WVPAHKGIGG	NEQVDKLVSA
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CRF04_cpx_	IIQAQPDRSE	SDLVNQIIEQ	LIRKDKVYLS	WVPAHKGIGG	NEQVDKLVSN
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CRF05_DF_B	IIQAQPDKSE	SELVNQIIEQ	LIEKKKVYLS	WVPAHKGIGG	NEQVDKLVSA
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CRF11_cpx_	IIQAQPDKSE	SELVSQIIEQ	LIKKEKVYLT	WVPAHKGIGG	NEQIDKLVSS
CRF11_cpx_	IIQAQPDKSE	SELVSQIIEQ	LIKKEKVYLS	WVPAHKGIGG	NEQVDKLVSS
D_CD_84ZR0	IIQAQPDKSE	SELVSQIIEQ	LIKKEKVYLA	WVPAHKGIGG	NEQVDKLVSS
D_CD_ELI_K	IIQAQPDKSE	SELVNQIIEQ	LIKKEKVYLA	WVPAHKGIGG	NEQVDKLVSQ
D_CD_NDK_M	IIQAQPDKSE	SELVSQIIEQ	LIKKEKVYLA	WVPAHKGIGG	NEQVDKLVSQ
D_UG_94UG1	IIQAQPDKSE	SEVVSQIIEQ	LIKKEKVYLS	WVPAHKGIGG	NEQVDKLVSN
F1_BE_VI85	IIQAQPDKSE	SEIVNQIIEQ	LIQKERVYLS	WVPAHKGIGG	NEQVDKLVSA
F1_BR_93BR	IIQAQPDKSE	SELVNQIIEQ	LIKKEKVYLS	WVPAHKGIGG	NEQVDKLVSA
F1_FI_FIN9	IIQAQPDKSE	SELVNQIIEQ	LIQKEKIYLS	WVPAHKGIGG	NEQVDKLVSA
F1_FR_MP41	IIQAQPDKSE	SEIVNQIIEK	LIQKERVYLS	WVPAHKGIGG	NEQVDRLVSA
F2_CM_MP25	IIQAHPDKSE	SEIVNQIIEQ	LIQKERVYLS	WVPAHKGIGG	NEQVDKLVST
F2KU_BE_VI	IIQAQPDKSE	SELVNQIIEQ	LIQKQIYLS	WVPAHKGIGG	NEQVDKLVSS
G_BE_DRCBL	IIQAQPDRSE	SEIVNQIIEQ	LIKKEKVYLS	WVPAHKGIGG	NEQVDKLVSS
G_NG_92NG0	IIQAQPDRSG	SELVNQIIEQ	LIKKEKVYLS	WVPAHKGIGG	NEQVDKLVSS
G_SE_SE616	IIQAQPDRSE	AELVNQIIEQ	LIKKEKVYLS	WVPAHKGIGG	NEQVDKLVSS
H_BE_VI991	IIQAQPDKSE	SELVNQIIEE	LIKKEKFYLS	WVPAHKGIGG	NEQVDKLVSS
H_BE_VI997	IIQAQPDKSE	SELVNQIIEE	LIKKEKVYLS	WVPAHKGIGG	NEQVDKLVSS
H_CF_90CF0	IIQAQPDKSE	SELVNQIIEE	LIKKEKVYLS	WVPAHKGIGG	NEQVDKLVSS
J_SE_SE702	IIQAQPDKSE	SELVNQIIEE	LIKKEKVYLS	WVPAHKGIGG	NEQVDKLVSS
J_SE_SE788	IIQAQPDKSE	SELVNQIIEE	LIKKEKVYLS	WVPAHKGIGG	NEQVDKLVSS
K_CD_EQTB1	IIQAQPDKSE	SELVNQIIEQ	LIKKDRVYLS	WVPAHKGIGG	NEQVDKLVSS
K_CM_MP535	IIQAQPDKSE	SDLVNQIIEQ	LIKKERIYLS	WVPAHKGIGG	NEQVDKLVSA
N_CM_YBF30	IIHSQPDKSE	SELVSQIIEE	LIKKERVYLS	WVPAHKGIGG	NEQVDKLVSS
O_CM_ANT70	VISSQPTQSE	SPIVQIIEE	LTKKEQVYLT	WVPAHKGIGG	NEKIDKLVSK
O_CM_MVP51	IISSQPTQSD	SPIVQIIEE	LTKKERVYLT	WVPAHKGIGG	NEKIDKLVSK
O_SN_99SE_	IISSQPTQSE	SSLVQIIEE	LTKKEQVYLT	WVPAHKGIGG	NEKIDKLVSK
O_SN_99SE_	IISSQPTQSE	SPLVQIIEE	LTQKEQVFLT	WVPAHKGIGG	NEKIDKLVSK
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751

800

00BW0762_1	GIRKVLFLDG	IDKAQDEHEK	YHSNWRAMAN	EFNLPPIVAK	EIVASCDKCQ
00BW0768_2	GIRRVFLFLDG	IDKAQEEHEK	YHSNWRAMAS	EFNLPPIVAK	EIVASCDKCQ
00BW0874_2	GIRKALFLDG	IDKAQEEHEK	YHSNWRAMAS	EFNLPPIVAK	EIVASCDKCQ
00BW1471_2	GIRKVLFLDG	IDKAQEEHER	YHSNWRAMAN	EFNLPPIVAK	EIVASCDKCQ

00BW1616_2	GIRKVLFLDG	IDKAEHEK	YHSSWRAMAN	EFNLPPIVAK	EIVASCDKCQ
00BW1686_8	GIRKVLFLDG	IDKAEHEK	YHSNWRAMAS	EFNLPPVVA	EIVASCDKCQ
00BW1759_3	GIRKVLFLDG	IDKAGGSEK	YHSNWRAMAS	EFNLPPIVAK	EIVASCDKCQ
00BW1773_2	GIRKVLFLDG	IDKAEHEK	YHNNWRAMAS	DFNLPPVVA	EIVASCDKCQ
00BW1783_5	GIRKVLFLDG	IDKAQEDHEK	YHSNWRAMAN	EFNLPPIVAK	EIVASCDKCQ
00BW1795_6	GIRKVLFLDG	IDKAEHEK	YHSNWRAMAN	EFNLPPIVAK	EIVASCDKCQ
00BW1811_3	GIRKVLFLDG	IDKAEHEK	YHSNWRAMAS	EFNLPPVVA	EIVASCDKCQ
00BW1859_5	GIRKVLFLDG	IDKAEHEK	YHSNWRAMAN	EFNLPPIVAK	EIVASCDKCQ
00BW1880_2	GIRKVLFLDG	IDKAEHEK	YHSNWRAMAS	EFNLPPVVA	EIVASCDKCQ
00BW1921_1	GIRKVLFLDG	IDKAEHEK	YHSNWRAMAS	EFNLPPVVA	EIVASCDKCQ
00BW2036_1	GIRKVLFLDG	IDKAEHEK	YHSNWRAMAS	EFNLPPIVAK	EIVASCDKCQ
00BW2063_6	GIRKVLFLDG	IDKAQEDHER	YHSNWRTMAS	EFNLPPIVAK	EIVASCDKCQ
00BW2087_2	GVRVFLDG	IDKAQEDHEK	YHSNWRAMAN	EFNLPPIVAK	EIVASCDKCQ
00BW2127_2	GIRKVLFLDG	IDKAEHEK	YHSNWRAMAN	EFNLPPVVA	EIVASCDKCQ
00BW2128_3	GIRKVLFLDG	IDKAEHEK	YHSNWRAMAS	EFNLPPIVAK	EIVASCDKCQ
00BW2276_7	GIRKVLFLDG	IDKAEHEK	YHNNWRAMAS	DFNLPPIVAK	EIVASCDKCQ
00BW3819_3	GIRKVLFLDG	IDKAQEDHEK	YHNNWRAMVS	EFNLPPIVAK	EIVASCDKCQ
00BW3842_8	GIRKVLFLDG	IDKAEHEK	YHSNWRAMAS	EFNLPPIVAK	EIVASCDKCQ
00BW3871_3	GIRKVLFLDG	IDKAEHEK	YHSNWRAMAS	EFNLPPIVAK	EIVASCDKCQ
00BW3876_9	GIRKVLFLDG	IDKAEHEK	YHSNWRAMAS	EFNLPPIVAK	EIVASCDKCQ
00BW3886_8	GIRKVLFLDG	IDKAEHEK	YHSNWRAMAS	EFNLPPIVAK	EIVASCDKCQ
00BW3891_6	GIRKVLFLDG	IDKAEHEK	YHSNWRAMAS	EFNLPPVVA	EIVASCDKCQ
00BW3970_2	GIRKVLFLDG	IDKAEHEK	YHSNWRAMAS	EFNLPPIVAK	EIVASCDKCQ
00BW5031_1	GIRKVLFLDG	IDKAEHEK	YHSNWRSMAS	DFNLPPIVAK	EIVASCDKCQ
96BW01B21	GIRKVLFLDG	IDKAEHEK	YHNNWRAMAS	EFNLPPIVAK	EIVASCDKCQ
96BW0407	GIRKVLFLDG	IDKAEHEK	YHCNWRAMAS	DFNLPPVVA	EIVASCDKCQ
96BW0502	GIRKMLFLDG	IDKAEHEK	YHNNWRAMAD	EFNLPPIVAK	EIVASCDKCQ
96BW06_J4	GIRKVLFLDG	IDKAEHEK	YHSNWRAMAS	EFNLPPIVAK	EIVASCDKCQ
96BW11_06	GIRKVLFLDG	IDKAEHEK	YHSNWRAMAS	EFNLPPIVAK	EIVASCDKCQ
96BW1210	GIRKVLFLDG	IDKAEHEK	YHNNWRAMAS	DFNLPPIVAK	EIVASCDKCQ
96BW15B03	GIRKVLFLDG	IDKAEHEK	YHSNWRAMAS	EFNLPPIVAK	EIVASCDKCQ
96BW16_26	GIRKVLFLDG	IDKAQEDHEK	YHSNWRAMAS	DFNLPPIVAK	EIVASCDKCQ
96BW17A09	GIRKVLFLDG	IDKAQEDHEK	YHGNWRAMAN	EFNLPPIVAK	EIVASCDKCQ
96BWM01_5	GIRKVLFLDG	IDKAEHEK	YHSNWRAMAS	EFNLPPIVAK	EIVASCDKCQ
96BWM03_2	GIRKILFLDG	IDKAEHEK	YHNNWRAMAS	EFNLPPIVAK	EIVASCDKCQ
98BWMC12_2	GIRKVLFLDG	IDKAQDEHEK	YHSNWRAMAS	EFNLPPIVAK	EIVASCDKCQ
98BWMC13_4	GIRKVLFLDG	IDKAQDDHER	YHSNWRAMAN	EFNLPPIVAK	EIVASCDKCQ
98BWMC14_a	GIRKVLFLDG	IDKAEHEK	YHSNWRAMAS	EFNLPPIVAK	EIVASCDKCQ
98BWM014_1	GIRKVLFLDG	IDKAEHEK	YHSNWRARAS	EFNLPPIVAK	EIVASCDKCQ
98BWM018_d	GIRKVLFLDG	IDKAEHEK	YHSNWRAMAS	EFNLPPIVAK	EIVASCDKCQ
98BWM036_a	GIRKVLFLDG	IDKAEHEK	YHNNWRAMAS	EFNLPPIVAK	EIVASCDKCQ
98BWM037_d	GIRKVLFLDG	IDKAQEDHEK	YHSNWRAMAN	EFNLPPIVAK	EIVASCDKCQ
99BW3932_1	GIRKVLFLDG	IDKAREEHEK	YHSNWRAMAS	EFNLPPIVAK	EIVASCDKCQ
99BW4642_4	GIRKVLFLDG	IDKAQDEHEK	YHSNWRAMAS	EFNLPPIVAK	EIVASCDKCQ
99BW4745_8	GIRKVLFLDG	IDKAEHEK	YHSNWRAMAS	EFNLPPVVA	EIVASCDKCQ
99BW4754_7	GIRKILFLDE	IDKAQDEHEK	YHSNWRAMAS	EFNLPPVVA	EIVACCDKCQ
99BWMC16_8	GIRKVLFLDG	IDKAEHEK	YHSNWRAMAS	EFNLPPIVAK	EIVASCDKCQ
A2_CD_97CD	GIRKVLFLDG	IDKAEHEK	YHSNWRAMAH	DFNLPPIVAK	EIVASCDKGG
A2_CY_94CY	GIRKVLFLDG	IDKAEHEK	YHSNWRAMAH	DFNLPPVVA	EIVASCDKCQ
A2D_97KR	GIRKVLFLDG	IDKAQDEHEK	YRSNWRAMAH	DFNLPPVVA	EIVACCDKCQ
A2G_CD_97C	GIRKVLFLDG	IDKAEHEK	YHSNWRAMAS	DFNLPPIVAK	EIVASCDKGG
A_BY_97BL0	XIRXVFLFX	IDKAQEXHEK	YHSN_KAMAS	DFNLPPIVAX	EIVASXDKCQ
A_KE_Q23_A	GIRKVLFLDG	IDKAEHEK	YHSNWRTMAS	DFNLPPIVAK	EIVASCDKCQ
A_SE_SE659	GIRKVLFLDG	IDKAEHEK	YHSNWRTMAS	DFNLPPVIAK	EIVASCDKCQ
A_SE_SE725	GIRKVLFLDG	IDKAEHEK	YHSNWRAMAS	DFNLPPVIAK	EIVASCDKCQ
A_SE_SE753	GIRKVLFLDG	IDKAEHEK	YHSNWRTMAS	DFNLPPIVAK	EIVASCDKCQ
A_SE_SE853	GIRKVLFLDG	IDKAEHEK	YHSNWRAMAS	DFNLPPVIAK	EIVASCNKCC
A_SE_SE889	GVRRIFLDG	IDKAEHEK	YHSNWRTMAS	DFNLPPIVAK	EIVASCDKCQ
A_SE_UGSE8	GIRKVLFLDG	IDKAEHEK	YHSNWRTMAS	DFNLPPIVAK	EIVASCDKCQ
A_UG_92UG0	GIRKVLFLDG	IDKAEHEK	YHSNWRAMAS	DFNLPPIVAK	EIVASCDKCQ

A_UG_U455_	GIRKVLFLDG	IDKAQEDHEK	YHCNWRAMAS	DFNLPPVVAK	EIVASCNKCCQ
AC_IN_2130	GIRRVFLFDG	IDKAQEEHER	YHSNWRAMAS	DFNLPPPIAK	EIVASCNQCCQ
AC_RW_92RW	GIRRVFLFDG	IDKAQEEHER	YHSNWRAMAS	DFNLPPPIVAK	EIVASCDKCCQ
AC_SE_SE94	GIRKVLFLDG	IDKAQEEHER	YHSNWRAMAS	DFNLPPPIVAK	EIVASCDKCCQ
ACD_SE_SE8	GIRKVLFLDG	IDKAQEEHER	YHSNWRAMAS	DFNLPPVIAK	EIVASCDKCCQ
ACG_BE_VI1	GIRKVLFLDG	IDKAQEEHER	YHSNWRAMAS	DFNLPPVIAK	EIVASCDKCCQ
AD_SE_SE69	GIRKILFLDG	IDKAQEEHEK	YHNNWRAMAS	DFNLPPVVAK	EIVASCDKCCQ
AD_SE_SE71	GIRKVLFLDG	IDKAQEEHER	YHSNWRAMAS	DFNLPPPIVAK	EIVASCDKCCQ
ADHK_NO_97	GIRKVLFLDG	IDKAQEAHEK	YHSNWRAMAS	DFNLPPPIVAK	EIVASCDKCCQ
ADK_CD_MAL	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAS	DFNLPPPIVAK	EIVASCDKCCQ
AG_BE_VI11	GIRKVLFLDG	IDKAQADHER	YHXNWGAMAS	DFNLPPPIVAK	EIVASCDKCCQ
AG_NG_92NG	GIRKVLFLDG	IDKAQEDHER	YHSNWRAMAS	DFNLPPPIVAK	EIVASCDKCCQ
AGHU_GA_VI	GIRKVLFLDG	IDKAQEDHER	YHSNWKAMAS	DFNLPPPIVAK	EIVASCDKCCQ
AGU_CD_Z32	GIRKVLFLDG	IDKAQEEHER	YHCNWRAMAS	DFNLPPPIVAK	EIVASCDKCCQ
AJ_BW_BW21	GIRKVLFLDG	IDKAQEEHEK	YHSKWRAMAS	DFNLPPPIVAK	EIVASCDKCCQ
B_AU_VH_AF	GIRKVLFLDG	IDKAQDDHEI	YHSNWRAMAN	DFYLPPPIVAK	DIVASCDKCCQ
B_CN_RL42_	GIRKVLFLDG	IDKAQEEHEK	YHCNWRAMAS	DFNLPPVVAK	EIVASCDKCCQ
B_DE_D31_U	GIRKVLFLDG	IDKAQDEHEK	YHSNWRAMAS	DFNLPPVVAK	EIVASCDKCCQ
B_DE_HAN_U	GIRKVLFLDG	IDKAQEDHEK	YHSNWRAMAN	DFNLPPVVAK	EIVASCDKCCQ
B_FR_HXB2_	GIRKVLFLDG	IDKAQDEHEK	YHSNWRAMAS	DFNLPPVVAK	EIVASCDKCCQ
B_GA_OYI_	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAS	DFNLPPVVAK	EIVASCDKCCQ
B_GB_CAM1_	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAS	DFNLPPVVAK	EIVASCDKCCQ
B_GB_GB8_A	GIRKILFLDG	IDKAQEDHEK	YHSNWRAMAN	DFNLPPVVAK	EIVASCDKCCQ
B_GB_MANC_	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAS	DFNLPPVVAK	EIVASCDKCCQ
B_KR_WK_AF	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAG	DFNLPPVVAK	EIVACCDKCCQ
B_NL_3202A	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAS	DFNLPPVVAK	EIVASCDKCCQ
B_TW_TWCYS	GIRKVLFLDG	IDRAQEEHEK	YHSNWRAMAS	DFNLPPVVAK	EIVASCDKCCQ
B_US_BC_L0	GVRKVLFLDG	IDKAQEEHEK	YHSNWRAMAS	DFNLPPVVAK	EIVASCDKCCQ
B_US_DH123	GIRRVFLFDG	IEKAQEEHEK	YHSNWRAMAS	EFNLPAVVAK	EIVACCDKCCQ
B_US_JRCSF	GIRKVLFLDG	IDKAQEDHEK	YHSNWRAMAS	DFNLPPPIVAK	EIVASCDKCCQ
B_US_MNCG_	GIRKVLFLDG	IDKAQEDHEK	YHSNWRAMAS	DFNLPPPIVAK	EIVASCDKCCQ
B_US_P896_	GIRKVLFLDG	IDKAQEEHEK	YHTNWRAMAS	DFNLPPVVAK	EIVASCNKCCQ
B_US_RF_M1	GIRKVLFLDG	IDKAQDEHEK	YHSNWRAMAS	DFNLPPVVAK	EIVASCDKCCQ
B_US_SF2_K	GIRKVLFLNG	IDKAQEEHEK	YHSNWRAMAS	DFNLPPVVAK	EIVASCDKCCQ
B_US_WEAU1	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAS	DFNLPPVVAK	EIVASCDKCCQ
B_US_WR27_	GIRKVLFXDG	IDXAQEDHEK	YHSNWRAMAG	EFNLPPVXAK	EIVACCDKCCQ
B_US_YU2_M	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAS	DFNLPPVVAK	EIVASCDKCCQ
BF1_BR_93B	GIRKVLFLDG	IDKAQEEHEK	YHNNWRAMAS	DFNIPPVVAK	EIVASCDKCCQ
C_BR_92BR0	GIRKVLFLDG	INKAQEEHEK	YHSNWRAMAS	EFNLPPPIVAK	EIVASCDKCCQ
C_BW_96BW0	GIRKVLFLDG	IDKAQEEHEK	YHCNWRAMAS	EFNLPPPIVAK	EIVASCDKCCQ
C_BW_96BW1	GIREVLFLDG	IDKAQEEHEK	YHSNWRAMAS	EFNLPPPIVAK	EIVASCDKCCQ
C_BW_96BW1	GIRKVLFLDG	IDKAQEEHEK	YHNNWRAMAS	DFNLPPPIVAK	EIVASCDKCCQ
C_BW_96BW1	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAS	EFNLPPPIVAK	EIVASCDKCCQ
C_ET_ETH22	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAN	EFNIPPVVPK	EIVACCDKCCQ
C_IN_93IN1	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAS	DFNLPPVVAK	EIVASCDQCCQ
C_IN_93IN9	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAS	DFNLPPVVAK	EIVASCDQCCQ
C_IN_93IN9	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAS	DFNLPPPIVAK	EIVASCGQCCQ
C_IN_94IN1	GIRRVFLFDG	IDKAQEEHEK	YHSNWRAMAS	DFNLPPVVAK	EIVASCDQCCQ
C_IN_95IN2	GIRKVLFLDG	IDKAQEEHER	YHSNWRAMAS	DFNLPPVVAK	EIVASCDQCCQ
CRF01_AE_C	GIRKVLFLDG	IDKAQEEHER	YHSNWRTMAS	DFNLPPPIVAK	EIVANCDKCCQ
CRF01_AE_C	GIRKVLFLDG	IDKAQEDHER	YHSNWRAMAS	DFNLPPPIVAK	EIVASCDKCCQ
CRF01_AE_C	GIRKVLFLDG	IDKAQEEHER	YHSNWRTMAS	DFNLPPPIVAK	EIVANCDKCCQ
CRF01_AE_T	GIRKVLFLDG	IDKAQEEHER	YHSNWRTMAS	DFNLPPPIVAK	EIVANCDKCCQ
CRF01_AE_T	GIRKVLFLDG	IDKAQEEHER	YHSNWRTMAS	DFNLPPPIVAK	EIVANCDKCCQ
CRF01_AE_T	GIRKVLFLDG	INKAQEEHER	YHSNWRTMAS	DFNLPPPIVAK	EIVANCDKCCQ
CRF01_AE_T	GIRKVLFLDG	IDKAQEEHER	YHSNWRTMAS	DFNLPPVVAK	EIVANCDKCCQ
CRF01_AE_T	GIRKVLFLDG	IDKAQEEHER	YHSNWRTMAS	DFNLPPPIVAK	EIVTNCCKCCQ
CRF01_AE_T	GIRKVLFLDG	IDKAQEEHER	YHSNWRTMAS	DFNLPPPIVAK	EIVANCDKCCQ
CRF02_AG_F	GIRKVLFLDG	IDKAQEEHGR	YHSNWRAMAS	DFNLPPPIAK	EIVACCDQCCQ
CRF02_AG_F	GIRKVLFLDG	IDKAQEEHER	YHSNWRAMAS	DFNLPPPIVAK	EIVACCDKCCQ

CRF02_AG_G	GFRKILFLDG	LDKAQEEHEK	FHSNWRAMAS	DFNLPPIVAK	EIVASCDKCQ
CRF02_AG_N	GIRKVLFLDG	IDKAQEEHER	YHSNWKAMAS	DFNLPPIVAK	EIVASCDKCQ
CRF02_AG_S	GIRKVLFLDG	IDKAQEEHER	YHSNWRAMAS	DFNLPPVVA	EIVASCDKCQ
CRF02_AG_S	GIRKVLFLDG	IDKAQEEHER	YHSNWRAMAS	EFNLPPIVAK	EIVASCDKCQ
CRF03_AB_R	GIREVLFLDG	IDKAQEEHEK	YHGNWRAMAS	DFNLPPVVA	EIVASCDKCQ
CRF03_AB_R	GIRKVLFLDG	IDKAQEAHEK	YHSNWRAMAS	DFNLPPVVA	EIVASCDKCQ
CRF04_cpx_	GIRKVLFLDG	IDKAQEEHEK	YHNNWRAMAS	DFNLPSVVA	EIVASCNKCQ
CRF04_cpx_	GIRKVLFLDG	IDKAQEDHEK	YHSNWRAMAS	DFNLPPVVA	EIVASCNKCQ
CRF04_cpx_	GIRKVLFLDG	IDKAQEEHEK	YHNNWKAMAS	DFNLPPVVA	EIVASCNKCQ
CRF05_DF_B	GIRKVLFLDG	IDKAQDEHEK	YHSNWRAMAS	DFNLPPVVA	EIVASCDKCQ
CRF05_DF_B	GIRKILFLDG	IDKAQEEHEK	YHNNWRAMAS	DFNLPPVVA	EIVASCDKCQ
CRF06_cpx_	GIRKVLFLDG	IDKAQEDHER	YHSNWRAMAN	DFNLPPIVAK	EIVASCDKCQ
CRF06_cpx_	GIRKVLFLDG	IDKAQEDHER	YHSNWRAMAS	DFNLPPIVAK	EIVASCDKCQ
CRF06_cpx_	GIRKVLFLDG	IDKAQEDHER	YHSNWRAMAS	DFNLPPILAK	EIVACCDKCQ
CRF06_cpx_	GIRKVLFLDG	IDKAQEEHER	YHSNWRAMAN	DFNLPPIVAK	EIVASCDKCQ
CRF11_cpx_	GIRKVLFLDG	IDKAQEDHDR	YHSNWRTMAS	DFNLPPIVAK	EIVASCDKCQ
CRF11_cpx_	GIRKVLFLDG	IDKAPEGHER	YHSNWRAMAS	DFNLPPVIA	EIVANCDKCQ
D_CD_84ZR0	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAS	DFNLPPVVA	EIVASCDKCQ
D_CD_ELI_K	GIRKVLFLDG	IDKAQEEHEK	YHNNWRAMAS	DFNLPPVVA	EIVASCDKCQ
D_CD_NDK_M	GIRKVLFLDG	IDKAQEEHEK	YHNNWRAMAS	DFNLPPVVA	EIVASCDKCQ
D_UG_94UG1	GIRKILFLDG	IDKAQEEHEK	YHNNWRAMAS	EFNLPPVVA	EIVASCDKCQ
F1_BE_VI85	GVRKILFLDG	IDKAQEEHEK	YHNNWRAMAS	DFNLPPIVAK	EIVASCDKCQ
F1_BR_93BR	GIRKVLFLDG	IDKAQEEHEK	YHNNWRAMAS	DFNIPAVVA	EIVASCDKCQ
F1_FI_FIN9	GIRKILFLDG	IDKAQEEHEK	YHNNWRAMAS	DFNLPPVVA	EIVASCDKCQ
F1_FR_MP41	GIRKILFLDG	IDKAQEEHEK	YHNNWRAMAS	DFNLPPVVA	EIVASCDKCQ
F2_CM_MP25	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAS	DFNLPPVVA	EIVASCDKCQ
F2KU_BE_VI	GIRKVLFLDG	IDKAQEEHEK	YHNNWRAMAS	DFNLPPIVAK	EIVASCDKCQ
G_BE_DRCBL	GIRKVLFLDG	IDKAQEEHER	YHSNWKAMAS	DFNLPPIVAK	EIVASCDKCQ
G_NG_92NG0	GIRKVLFLDG	IDKAQEEHER	YHSNWRAMAS	DFNLPPVVA	EIVASCDKCQ
G_SE_SE616	GIRKVLFLDG	IDKAQEEHER	YHNNWRAMAS	DFNLPPIVAK	EIVASCDKCQ
H_BE_VI991	GIRKVLFLDG	IDKAQVQHEK	YHSNWRAMAS	DFNLPPIVAK	EIVASCDKCQ
H_BE_VI997	GIRKVLFLDG	IDKAQEAHER	YHNNWRAMAS	EFNLPPIVAK	EIVASCDKCQ
H_CF_90CF0	GVRKVLFLDG	IDKAQEEHER	YHNNWRASVAS	DFNLPPIVAK	EIVASCDKCQ
J_SE_SE702	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAS	DFNLPPVVA	EIVASCDKCQ
J_SE_SE788	GIRKVLFLDG	IDKAQEDHEK	YHSNWRAMAS	DFNLPPVVA	EIVASCDKCQ
K_CD_EQTB1	GIRKVLFLDG	IDKAQEEHEK	YHNNWRAMAS	DFNLPPVVA	EIVASCDKCQ
K_CM_MP535	GIRKVLFLDG	IDKAQEEHEK	YHNNWRAMAS	DFNLPPIVAK	EIVASCDKCQ
N_CM_YBF30	GIRKILFLDG	IEKAQEDHDR	YHSNWKAMAS	DFNLPPIVAK	EIVASCDKCQ
O_CM_ANT70	DIRRVLFLEG	IDQAQEDHEK	YHSNWKALAS	EFGLPPVVA	EIIASCPKCH
O_CM_MVP51	DIRRVLFLEG	IDQAQEDHEK	YHSNWRALAS	DFGLPPIVAK	EIIASCPKCH
O_SN_99SE_	DIRRVLFLEG	IDQAQEDHEK	YHSNWRALAS	DFGLPPVVA	EIIANCPQCH
O_SN_99SE_	DIRRVLFLEG	IDQAQEDHEK	YHSNWRALAS	DFGLPPVVA	EIIANCPKCH
U_CD___83C	GIRKVLFLDG	IDKAQEEHER	YHSNWRAMAS	DFNLPPIVAK	EIVASCDKCQ

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00BW0762_1	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKTIL	VAVHVASGYM	EAEVIPAETG
00BW0768_2	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYM	EAEVIPAETG
00BW0874_2	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
00BW1471_2	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
00BW1616_2	LKGEATHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
00BW1686_8	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
00BW1759_3	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
00BW1773_2	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKVII	VAVHVASGYI	EAEVIPAETG
00BW1783_5	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
00BW1795_6	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKIVL	VAVHVASGYL	EAEVIPTETG
00BW1811_3	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
00BW1859_5	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYM	EAEVIPAETG
00BW1880_2	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVTPEETG
00BW1921_1	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
00BW2036_1	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKIII	VAAHVASGYI	EAEVIPAETG

850



00BW2063_6	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYV	EAEVIPAETG
00BW2087_2	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
00BW2127_2	LKGEATHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
00BW2128_3	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
00BW2276_7	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYM	EAEVIPAETG
00BW3819_3	LKGEATHGQV	DCSPGIWQLD	CTHLEGKIIL	VAIHVASGYM	EAEVTPAETG
00BW3842_8	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
00BW3871_3	LKGEATHRQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
00BW3876_9	QKGEAIHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
00BW3886_8	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKTIL	VAVHVASGYI	EAEVIPAETG
00BW3891_6	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
00BW3970_2	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
00BW5031_1	LKGEAMHGQV	DCSPGVWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
96BW01B21	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYM	EAEVIPAETG
96BW0407	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
96BW0502	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYM	EAEVIPAETG
96BW06_J4	SKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
96BW11_06	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
96BW1210	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVRVASGYI	EAEVIPAETG
96BW15B03	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
96BW16_26	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
96BW17A09	LKGEAMHGQV	DCSPGMWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
96BWM01_5	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYM	EAEVIPAETG
96BWM03_2	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYM	EAEVIPAETG
98BWMC12_2	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYM	EAEVITAETG
98BWMC13_4	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
98BWMC14_a	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVISAETG
98BWM014_1	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
98BWM018_d	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
98BWM036_a	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
98BWM037_d	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKIII	VAVHVASGYV	EAEVIPAETG
99BW3932_1	LKGEATHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
99BW4642_4	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
99BW4745_8	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
99BW4754_7	QKGEAIHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
99BWMC16_8	LKGEAIHGQV	DCSPGVWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
A2_CD_97CD	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIV	VAVHVASGYI	EAEVIPAETG
A2_CY_94CY	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
A2D_97KR	VKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
A2G_CD_97C	LKGEAMHGQV	DCSPGVWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
A_BY_97BL0	LKXEXMHXQV	DCSPXIWQLD	CTHLXXKVII	XAVXVASGYI	EAEVIPAETG
A_KE_Q23_A	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIV	VAVHVASGYI	EAEVIPAETG
A_SE_SE659	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
A_SE_SE725	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
A_SE_SE753	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
A_SE_SE853	LKGEAMHGQV	DCSPGMWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
A_SE_SE889	LKGEAMHGQV	DCSPGMWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
A_SE_UGSE8	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
A_UG_92UG0	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYV	EAEVIPAETG
A_UG_U455_	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
AC_IN_2130	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
AC_RW_92RW	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHAASGYI	EAEVIPAETG
AC_SE_SE94	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
ACD_SE_SE8	IKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
ACG_BE_VI1	LKGEAMHGQV	DCSPGIWQID	CTHLEGKVII	VAVHVASGYM	EAEVIPAETG
AD_SE_SE69	LKGEALHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
AD_SE_SE71	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
ADHK_NO_97	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
ADK_CD_MAL	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIII	VAVHVASGYI	EAEVIPAETG
AG_BE_VI11	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKIII	VAVHVASGYI	EAEVIPAETG

AG_NG_92NG	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVII	VAVHVASGYI	EAEVIPAETG
AGHU_GA_VI	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
AGU_CD_Z32	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
AJ_BW_BW21	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVII	VAVHVASGYM	EAEVIPAETG
B_AU_VH_AF	QKGEAMHGQV	DCSPGLWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
B_CN_RL42_	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
B_DE_D31_U	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
B_DE_HAN_U	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPVETG
B_FR_HXB2_	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
B_GA_OYI_	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
B_GB_CAM1_	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
B_GB_GB8_A	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
B_GB_MANC_	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
B_KR_WK_AF	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
B_NL_3202A	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
B_TW_TWCYS	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
B_US_BC_L0	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
B_US_DH123	VKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
B_US_JRCSF	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
B_US_MNCG_	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
B_US_P896_	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
B_US_RF_M1	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
B_US_SF2_K	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
B_US_WEAU1	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
B_US_WR27_	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
B_US_YU2_M	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
BF1_BR_93B	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVAGGYI	EAEVIPAETG
C_BR_92BR0	LKGEATHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
C_BW_96BW0	LKGEATHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
C_BW_96BW1	LKGEATHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
C_BW_96BW1	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVRVASGYI	EAEVIPAETG
C_BW_96BW1	LKGEATHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
C_ET_ETH22	LKGEATHGQV	NCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
C_IN_93IN1	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
C_IN_93IN9	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
C_IN_93IN9	QKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
C_IN_94IN1	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYM	EAEVIPAETG
C_IN_95IN2	LKGEATHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYM	EAEVIPAETG
CRF01_AE_C	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
CRF01_AE_C	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
CRF01_AE_C	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
CRF01_AE_T	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
CRF01_AE_T	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
CRF01_AE_T	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
CRF01_AE_T	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
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CRF01_AE_T	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
CRF02_AG_F	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
CRF02_AG_F	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
CRF02_AG_G	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
CRF02_AG_N	MKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
CRF02_AG_S	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
CRF02_AG_S	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
CRF02_AG_S	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
CRF03_AB_R	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
CRF03_AB_R	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
CRF03_AB_R	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
CRF04_cpx_	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIM	VAVHVASGYI	EAEVIPAETG
CRF04_cpx_	LKGEAMHGQX	DCSPGIWQLD	CTHLEGKIIL	VPVHVASGYI	EAEVIPAETG
CRF04_cpx_	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
CRF05_DF_B	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
CRF05_DF_B	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG

CRF06_cpx_	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
CRF06_cpx_	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
CRF06_cpx_	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
CRF06_cpx_	LKGEPMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
CRF11_cpx_	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIM	VAVHVASGYI	EAEVIPAETG
CRF11_cpx_	LKGEAMHGQV	DCSPRIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
D_CD_84ZR0	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
D_CD_ELI_K	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
D_CD_NDK_M	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
D_UG_94UG1	VKGEALHGQV	DCSPGIWQLD	CTHLEGKGIL	VAVHVASGYI	EAEVIPAETG
F1_BE_VI85	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASEYI	EAEVIPAETG
F1_BR_93BR	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYL	EAEVIPAETG
F1_FI_FIN9	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
F1_FR_MP41	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
F2_CM_MP25	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
F2KU_BE_VI	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
G_BE_DRCBL	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
G_NG_92NG0	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIII	VAVHVASGYI	EAEVIPAETG
G_SE_SE616	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIII	VAVHVASGYI	EAEVIPAETG
H_BE_VI991	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
H_BE_VI997	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	XPEVIPAETG
H_CF_90CF0	LKGEAMHGQV	DCSPGIWQLD	CTHLEGQVIL	VAVHVASGYI	EAEVIPAETG
J_SE_SE702	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
J_SE_SE788	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
K_CD_EQTB1	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
K_CM_MP535	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
N_CM_YBF30	LKGEAMHGQV	DCSPGVWQLD	CTHLEGKIIL	VAVHVASGYL	EAEVIPAETG
O_CM_ANT70	IKGEAIHGQV	DCSPEVWQID	CTHMEGKIII	VAVHVASGFI	EAEVIPAETG
O_CM_MVP51	IKGEATHGQV	DYSPEIWQMD	CTHLEGKIII	VAVHVASDFI	EAEVIPAETG
O_SN_99SE_	IKGEAIHGQV	DCSPEVWQMD	CTHLEGKIII	VAVHVASGFI	EAEVIPAETG
O_SN_99SE_	IKGEAIHGQV	DYSPEVWQID	CTHLEGKIII	VAVHVASGFI	EAEVIPAETG
U_CD___83C	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYL	EAEVIPAETG

851

900

00BW0762_1	QETAYYILKL	AGRWPVKIIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
00BW0768_2	QETAYYILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
00BW0874_2	QDTAYYILKL	AGRWPVKVIH	TDNGSNFTST	AVKAACWWAD	IQQEFGIPYN
00BW1471_2	QEAAAYFILKL	AGRWPVQIIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
00BW1616_2	QETAYYILKL	AGRWPVKIIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
00BW1686_8	QETAYYILKL	AGRWPVKIIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
00BW1759_3	QETAYLILKL	AGRWPVKIIH	TDNGSNFTST	TVKAACWWAG	IQQEFGIPYN
00BW1773_2	QETAYYILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	VQQEFGIPYN
00BW1783_5	QETAYFILKL	AGRWPVKIIH	TDNGSNFTSA	TVKAACWWAG	IQQEFGIPYN
00BW1795_6	QETAYYILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
00BW1811_3	QETAYFLLKL	AGRWPVKVIH	TDNGSNFTSN	AMKAACWWAG	IQQEFGIPYN
00BW1859_5	QETAYYILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
00BW1880_2	QETAYYILKL	AGRWPVKIIH	TDNGRNFTSA	AVKAACWWAG	IQQEFGIPYN
00BW1921_1	QETAYYILKL	AGRWPVKVIH	TDNGSNFTST	AVKAACWWAG	IQQEFGIPYN
00BW2036_1	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
00BW2063_6	QETAYFILKL	AGRWPVKIIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
00BW2087_2	QETAYYILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
00BW2127_2	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
00BW2128_3	QETAYYILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYS
00BW2276_7	QETAYFILKL	AGRWPVKVIH	TDNGSNFTST	TVKAACWWAG	IQQEFGIPYN
00BW3819_3	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSN	AVKAACWWAG	IQQEFGIPYN
00BW3842_8	QETAYYILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
00BW3871_3	QETAYYILKL	AGRWPVKVIH	TDNGSNFTST	VVKAACWWAG	IQQEFGIPYN
00BW3876_9	QETAYYILKL	AGRWPVKVIH	TDNGSNFTSS	AVKAACWWAG	TQQGFGIPYN
00BW3886_8	QETAYYILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
00BW3891_6	QETAYYILKL	AGRWPVKVIH	TDNGSNFTSN	AVKAACWWAG	IQQEFGIPYN

00BW3970_2	QETAYYILKL	AGRWPVKVIH	TDNGSNFTST	AVKAACWWAG	IKQEFGIPYN
00BW5031_1	QETVYFILKL	AGRWPVKAIH	TDNGSNFTSA	AVKAACWWAG	INQEFGIPYN
96BW01B21	QETAYYILKL	AGRWPVKVIH	TDNGTNFTSA	AVKAACWWAG	IQQEFGIPYN
96BW0407	QETAYYILKL	AGRWPVKVIH	TDNGSNFTST	AVKAACWWAG	IQQEFGIPYN
96BW0502	QETAYFILKL	AGRWPVRVIH	TDNGTNFTSA	AVKAACWWAG	IQQEFGIPYN
96BW06_J4	QDTAYYILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
96BW11_06	QETAYYILKL	AGRWPVKIIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
96BW1210	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSN	AVKAACWWAG	TQQEFGIPYN
96BW15B03	QETAYYILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
96BW16_26	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSA	TVKAACWWAG	IQQEFGIPYN
96BW17A09	QETADFILKL	AGRWPVQIIH	TDNGSNFTST	AVKAACWWAG	IQQEFGIPYN
96BWM01_5	QETAYFLLKL	AGRWPVKIIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
96BWM03_2	QDTAYFLLKL	AGRWPVKVIH	TDNGSNFTSA	AMKAACWWAG	IQQEFGIPYN
98BWMC12_2	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSG	AVKAACWWAG	IQQEFGIPYN
98BWMC13_4	QETAYYILKL	AGRWPVKIIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
98BWMC14_a	QETAYYILKL	AARWPVKVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
98BWM014_1	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
98BWM018_d	QETAYYILKL	AGRWSVKTIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
98BWM036_a	QETAYYILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
98BWM037_d	QETAYYILKL	AGRWPVKVIH	TDNGSNFTST	AVKAACWWAG	IQQEFGIPYN
99BW3932_1	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
99BW4642_4	QETAYYILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
99BW4745_8	QETAYYILKL	AGRWPVKVIH	TDNGSNFTST	AVKAACWWAG	IQQEFGIPYN
99BW4754_7	QETAYYILKL	AGRWPVKTIH	TDNGSNFTST	AVKAACWWAG	IQQEFGIPYN
99BWMC16_8	QDTAYYMLKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	VQQEFGIPYN
A2_CD_97CD	QETAYFLLKL	AGRWPVKVIH	TDNGPNFTSA	AVKAACWWAD	VKQEFGIPYN
A2_CY_94CY	QDTAYFILKL	AGRWPVKVIH	TDNGPNFISA	TVKAACWWAG	IQQEFGIPYN
A2D_97KR	QETAYFILKL	AGRWPVKVIH	TDNGPNFISA	PVKAACWWAG	VQQEFGIPYN
A2G_CD_97C	QETAYFILKL	AGGWPVKVIH	TDNGSNFTSA	AVKAACWWAN	VTQEFGIPYN
A_BY_97BL0	QETAYFLLKL	AGRWPVKVVH	TDNGPNFTSS	AVKAACWAN.	IQQEFXIPYN
A_KE_Q23_A	QETAYFLLKL	AGRWPVKIVH	TDNGSNFTSA	AVKAACWWAN	IQQEFGIPYN
A_SE_SE659	QETAYFLLKL	AGRWPVKVVH	TDNGSNFTSA	AVKAACWWAN	IQQEFGIPYN
A_SE_SE725	QETAYFLLKL	AGRWPVKIVH	TDNGSNFTSA	AFKAACWWAS	IQQEFGIPYN
A_SE_SE753	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAN	VKQEFGIPYN
A_SE_SE853	QETAYFLLKL	AGRWPVKVVH	TDNGSNFTSA	AFKAACWWAN	VQQEYGIPYN
A_SE_SE889	QETAYFLLKL	AGRWPVKVVH	TDNGSNFTSA	AFKAACWWAN	VQQEFGIPYN
A_SE_UGSE8	QEAAAYFLLKL	AGRWPVKVVH	TDNGSNFTSA	AFKAACWWAN	VQQEFGIPYN
A_UG_92UG0	QETAYFLLKL	AGRWPVKVVH	TDNGSNFTSA	AVKAACWWAN	VKQEFGIPYN
A_UG_U455_	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAVCWWAN	IQQEFGIPYN
AC_IN_2130	QETAYYILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
AC_RW_92RW	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSN	'TVKAACWWAG	IQQEFGIPYN
AC_SE_SE94	QETAYFLLKL	AGRWPVRRVH	TDNGSNFTSA	AVKAACWWAN	IQQEFGIPYN
ACD_SE_SE8	QETAYFLLKL	AGRWPVKVVH	TDNGSNFTSA	AFKAACWWAS	VQQEFGIPYN
ACG_BE_VI1	QETAYFLLKL	AGRWPVRVIH	TDNGSNFTSA	AVKAACWWAN	VTQEFGIPYN
AD_SE_SE69	QETAYFLLKL	AGRWPVRVVH	TDNGSNFTST	AVKAACWWAG	IKQEFGIPYN
AD_SE_SE71	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
ADHK_NO_97	QETAYFILKL	AGRWPVKVIH	TDNGSNFISA	AVKAACWWAD	IKQEFGIPYN
ADK_CD_MAL	QETAYFILKL	AGRWPVKVVH	TDNGSNFTSA	AVKAACWWAN	IKQEFGIPYN
AG_BE_VI11	QETAYFILKL	AGRWPVKILH	TDNGSNFISA	AVKAACWWAD	IKQEFGIPYN
AG_NG_92NG	QETAYFLLKL	AGRWPVKVIH	TDNGSNFTSA	AMKAACWWAN	IQQEFGIPYN
AGHU_GA_VI	QETAYFILKL	AGRWPVKVIH	TDNGTNFTSA	AVKAACWWAN	VTQEFGIPYN
AGU_CD_Z32	QETAYFILKL	AGRWPVKVVH	TDNGSNFTSA	AVKAACWWAN	ITQEFGIPYN
AJ_BW_BW21	QETAYFLLKL	AGRWPVTVIH	TDNGSNFTSA	AVKAACWWAG	VRQEFGIPYN
B_AU_VH_AF	QETAYFLLKL	AGRWPVKTVH	TDNGPIFIST	AVKAACWWAG	IKQEFGIPYN
B_CN_RL42_	QETAYFLLKL	AGRWPVKTIH	TDNGRNFTSN	SVKAACWWAG	IKQEFGIPYN
B_DE_D31_U	QETAYFILKL	AGRWPVKTIH	TDNGSNFTST	TVKAACWWAG	VKQEFGIPYN
B_DE_HAN_U	QETAYFLLKL	AGRWPVKTVH	TDNGPNFTST	TVKAACWWAG	IKQEFGIPYN
B_FR_HXB2_	QETAYFLLKL	AGRWPVKTIH	TDNGSNFTGA	TVRAACWWAG	IKQEFGIPYN
B_GA_OYI_	QETAYFILKL	AGRWPVKTIH	TDNGSNFTST	TVKAACWWAG	IKQEFGIPYN
B_GB_CAM1_	QETAYFLLKL	AGRWPVKTIH	TDNGGNFIST	TVKAACWWAG	IKQEFGIPYN

B_GB_GB8_A	QDTAYFILKL	AGRWPVKTIH	TDNGRNFTST	TVKAACWWAG	IKQEFGIPYN
B_GB_MANC_	QETAYFLLKL	AGRWPVTTIH	TDNGSNFTST	TVKAACWWAG	IKQEFGIPYN
B_KR_WK_AF	QETAYFLLKL	AGRWPVKTIH	TDNGSNFTSN	TVKAACWAR.	IKQEFGIPYN
B_NL_3202A	QETAYFILKL	AGRWPVTTIH	TDNGSNFTSA	TVKAACWWAG	IKQEFGIPYN
B_TW_TWCYS	QETAYFLLKL	AGRWPVKTIH	TDNGSNFTSA	AVKAACWWAG	IKQKFGIPYN
B_US_BC_L0	QETAYFLLKL	AGRWPVKTIH	TDNGSNFTST	TVKAACWWAG	IKQEFGIPYN
B_US_DH123	QETAYFILKL	AGRWPVKTIH	TDNGSNFTST	TVKAACWWAG	IKQEFGIPYN
B_US_JRCSF	QETAYFLLKL	AGRWPVTTIH	TDNGSNFTST	TVKAACWWAG	IKQEFGIPYN
B_US_MNCG_	QETAYFLLKL	AGRWPVKTIH	TDNGPNFTST	TVKAACWWTG	IKQEFGIPYN
B_US_P896_	QETAYFLLKL	AGRWPVKTIH	TDNGSNFTST	TVKAACWWAG	IKQEFGIPYN
B_US_RF_M1	QETAYFILKL	AGRWPVKVIH	TDNGSNFTST	TVKAACWWAG	IKQEFGIPYN
B_US_SF2_K	QETAYFLLKL	AGRWPVKTIH	TDNGSNFTST	TVKAACWWAG	IKQEFGIPYN
B_US_WEAU1	QETAYFILKL	AGRWPVKTIH	TDNGSNFTST	TVKAACWWAG	IKQEFGIPYN
B_US_WR27_	QETAYFILKL	AXRWPVXTIH	TDNGSNFIST	TVXAAXWWAG	IXQEFGIPYN
B_US_YU2_M	QETAYFLLKL	AGRWPVTTIH	TDNGSNFTSA	TVKAACWWAG	IKQEFGIPYN
BF1_BR_93B	QETAYFLLKL	AGRWPVKTIH	TDNGSNFTST	TVKAACWWAG	IKQEFGIPYN
C_BR_92BR0	QETAYFILKL	AGRWPVKVIH	TDNGSNFISN	TVKAACWWAG	IQQEFGIPYN
C_BW_96BW0	QETAYYILKL	AGRWPVKVIH	TDNGSNFTST	AVKAACWWAG	IQQEFGIPYN
C_BW_96BW1	QETAYYILKL	AGRWPVKI IH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
C_BW_96BW1	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSN	AVKAACWWAG	TQQEFGIPYN
C_BW_96BW1	QETAYYILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
C_ET_ETH22	QETAYFLLKL	AGRWPVRVIH	TDNGSNFTSN	AVKAACWWAG	IQQEFGIPYN
C_IN_93IN1	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
C_IN_93IN9	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAS	IQQEFGIPYN
C_IN_93IN9	QETAYYILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
C_IN_94IN1	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
C_IN_95IN2	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
CRF01_AE_C	QETAYFLLKL	AG.RPVKVIH	TDNGSNFTSA	AMKAACWWAN	VQQEFGIPYN
CRF01_AE_C	QETAYFLLKL	AGRWPVRVIH	TDNGSNFTSA	AVKAACWWAN	VQQEFGIPYN
CRF01_AE_C	QETAYFLLKL	AGRWPVKVIH	TDNGSNFTSA	TVKAACWWAN	VQQEFGIPYN
CRF01_AE_T	QETAYFLLKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAN	VRQEFGIPYN
CRF01_AE_T	QETAYFLLKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAN	VRQEFGIPYN
CRF01_AE_T	QETAYFLLKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAN	VRQEFGIPYN
CRF01_AE_T	QETAYFLLKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAN	VQQEFGIPYN
CRF01_AE_T	QETAYFLLKL	AGRWPVKVVH	TDNGSNFTSA	AVKAACWWAN	VRQEFGIPYN
CRF02_AG_F	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAN	VTQEFGIPYN
CRF02_AG_F	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAN	VTQEFGIPYN
CRF02_AG_G	QETAYFILKL	AGRWPVKI IH	TDNGSNFTSA	AVRAACWWAN	VTQEFGIPYN
CRF02_AG_N	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAN	VTQEFGIPYN
CRF02_AG_S	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAN	VTQEFGIPYN
CRF02_AG_S	QETAYFILKL	AGRWP.VKVH	TDNGSNFTSA	AVKAACWWPK	LHQELGIYN.
CRF03_AB_R	QETAYFVLKL	AGRWPVKI IH	TDNGSNFTST	AVKAACWWAG	IKQEFGIPYN
CRF03_AB_R	QETAYFVLKL	AGRWPVKVIH	TDNGSNFIST	AVKAACWWAG	IKQEFGIPYN
CRF04_cpx_	QETAYFILKL	AGRWPVKMIH	ADNGPNFTSA	AVKAACWWAD	INQEFGIPYN
CRF04_cpx_	QETAYFILKL	AGRWPVKI IH	TDNGPNFTSA	AVKAACWWAD	VQQEFGIPYN
CRF04_cpx_	QETAYFILKL	AGRWPVKI IH	TDNGSNFTSA	AVKAACWWAN	IQQEFGVPYN
CRF05_DF_B	QDTAYFILKL	AGRWPVKMIH	TDNGPNFTSG	AVKAACWWAG	IQQEFGIPYN
CRF05_DF_B	QETAYFILKL	AGRWPVKMVH	TDNGSNFTSA	AVKAACWWAG	IKQEFGIPYN
CRF06_cpx_	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAN	ITQEFGIPYN
CRF06_cpx_	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAN	ITQEFGIPYN
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CRF06_cpx_	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAN	VTQEFGIPYN
CRF11_cpx_	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSS	TVKAACWWAN	IQQEFGIPYN
CRF11_cpx_	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSN	AVKAACWWAG	IQQEFGIPYN
D_CD_84ZR0	QEAAAYFLLKL	AGRWPVKVVH	TDNGSNFTSA	TVKAACWWAG	IKQEFGIPYN
D_CD_ELI_K	QETAYFLLKL	AGRWPVKVVH	TDNGSNFTSA	AVKAACWWAG	IKQEFGIPYN
D_CD_NDK_M	QETAYFLLKL	AGRWPVKVVH	TDNGSNFTSA	TVKAACWWAG	IKQEFGIPYN
D_UG_94UG1	QETAYFLLKL	AGRWPVKVVH	TDNGSNFTSA	AVKAACWWAG	IKQEFGIPYN
F1_BE_VI85	QETAYFILKL	AGRWPVKI IH	TDNGSNFTSA	AVKASCWWAG	IQQEFGIPYN

F1_BR_93BR	QETAYFLLKL	AGRWPVKTIH	TDNGTNFTSA	TVKAACWWAG	IQQEFGIPYN
F1_FI_FIN9	QDTAYFILKL	AGRWPVKMIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
F1_FR_MP41	QETAYFILKL	AGRWPVKIIH	TDNGSNFTSS	AVKAACWWAG	IQQEFGIPYN
F2_CM_MP25	QEAAFFILKL	AGRWPVKIIH	TDNGSNFTSA	VVKAACWWAG	IQQEFGIPYN
F2KU_BE_VI	QETAFFILKL	AGRWPVKIIH	TDNGSNFISA	TVKAACWWAG	IQQEFGISYN
G_BE_DRCBL	QETAYFILKL	AGRWPVKIIH	TDNGSNFTSA	AVKAACWWAS	ITQEFGIPYN
G_NG_92NG0	QETAYFILKL	AGRWPVKVIH	TDNGPNFISA	AVKAACWWAN	ITQEFGIPYN
G_SE_SE616	QETAYFILKL	AGRWPVTVIH	TDNGSNFTSA	AVKAACWWAN	ITQEFGIPYN
H_BE_VI991	QETAYFILKL	AGRWPVKMIH	TDNGSNFTSA	AVKAACWWAD	IQQEFGIPYN
H_BE_VI997	QETAYFILKL	AGRWPVKMIH	TDNGTNFTST	AVKAACWWAD	IQQDFGIPYN
H_CF_90CF0	KETAYFLLKL	ASRWPVKVIH	TDNGSNFTSA	AVKAACWWAD	IQQEFGIPYN
J_SE_SE702	QEAAFFILKL	AGGWPVKAIH	TDNGSNFTSG	AVKAACWWAD	IKQEFGIPYN
J_SE_SE788	QEAAFFILKL	AGRWPVKVIH	TDNGSNFTSG	AVKAACWWAD	IKQEFGIPYN
K_CD_EQTB1	QETAYFILKL	AGRWPVVRVIH	TDNGSNFTSA	VVKAACWWAD	IKQEFGIPYN
K_CM_MP535	QETAYFILKL	AGRWPVKVIH	TDNGTNFTST	VVKAACWWAG	VKQEFGIPYN
N_CM_YBF30	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSA	TVKAACWWAN	IKQEFGIPYN
O_CM_ANT70	QETAYFLLKL	AARWPVKVIH	TDNGPNFTST	TMKAACWWAN	IQHEFGIPYN
O_CM_MVP51	QETAYFLLKL	AARWPVKVIH	TDNGPNFTSA	AMKAACWWTG	IQHEFGIPYN
O_SN_99SE_	QETAYFLLKL	AARWPVKVIH	TDNGPNFTSA	AMKAACWWAN	IKHEFGIPYN
O_SN_99SE_	QETAYFLLKL	AARWPVKIIH	TDNGPNFTSA	TMKAACWWTG	IKHEFGIPYN
U_CD___83C	QETAYFVLKL	AGRWPVTVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN

901			950		
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96BW06_J4	PQSQGVVESM	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGGIGGY
96BW11_06	PQSQGVVESM	NKELKKIIGQ	VRDQAEYLKT	AVQMAVFIHN	FKRKGGIGGY
96BW1210	PQSQGVVESM	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGGIGGY
96BW15B03	PQSQGVVESM	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGGIGGY
96BW16_26	PQSQGVVESM	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGGIGGY
96BW17A09	PQSQGVVESM	NKELKKIIGQ	VRDQAEHLKT	AVLMAVFIHN	FKRKGGIGGY

96BWM01_5	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
96BWM03_2	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
98BWM012_2	PQSQGVVESH	NKELKKIIGQ	IRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
98BWM013_4	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
98BWM014_a	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
98BWM014_1	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
98BWM018_d	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
98BWM036_a	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
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99BW4745_8	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
99BW4754_7	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
99BWM016_8	PQSQGVVEST	NKELKKIIGQ	VREQAEHLKT	AVQMAVFIHN	FKRKGIGGY
A2_CD_97CD	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
A2_CY_94CY	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
A2D_97KR	PQSQGVVESH	NKELKKIIGQ	IRDQAEHLKT	AVQMAVFIHN	SKRKGIGGY
A2G_CD_97C	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
A_BY_97BL0	XQSQGVVESH	NKELKKIIRQ	VREQAEHLKT	AVQMAVFIHN	FKRKGIGGY
A_KE_Q23_A	PQSQGVVESH	NKELKKIIGQ	VREQAEHLKT	AVQMAVFIHN	FKRKGIGGY
A_SE_SE659	PQSQGVVESH	NKELKKIIGQ	VREQAEHLKT	AVQMAVFIHN	FKRKGIGGY
A_SE_SE725	PQSQGVVESH	NKELKKIIGQ	VREQAEHLKT	AVQMAVFIHN	FKRKGIGGY
A_SE_SE753	PQSQGVVESH	NKELKKIIGQ	VREQAEHLKT	AVQMAVFIHN	FKRKGIGGY
A_SE_SE853	PQSQGVVESH	NKELKKIIGQ	VREQAEHLKT	AVQMAVFIHN	FKRKGIGGY
A_SE_SE889	PQSQGVVESH	NKELKKIIGQ	VREQAEHLKT	AVQMAVFIHN	FKRKGIGGY
A_SE_UGSE8	PQSQGVVESH	NKELKKIIGQ	VREQAEHLKT	AVQMAVFIHN	FKRKGIGGY
A_UG_92UG0	PQSQGVVESH	NKELKKIIGQ	VREQAEHLKT	AVQMAVFIHN	FKRKGIGGY
A_UG_U455_	PQSQGVVESH	NKELKKIIGQ	VREQAEHLKT	AVQMAVFIHN	FKRKGIGGY
AC_IN_2130	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
AC_RW_92RW	PQSQGVIESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
AC_SE_SE94	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
ACD_SE_SE8	PQSQGVVESH	NKELKKIIGQ	VREQAEHLKT	AVQMAVFIHN	FKRKGIGGY
ACG_BE_VI1	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
AD_SE_SE69	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
AD_SE_SE71	PQSQGVVESH	NKELKKIIGQ	VREQAEHLKT	AVQMAVFIHN	FKRKGIGGY
ADHK_NO_97	PQSQGVVESH	NKELKKIIGQ	VREQAEHLKT	AVQMAVFIHN	FKRKGIGGY
ADK_CD_MAL	PQSQGVVESH	NKELKKIIGQ	VREQAEHLKT	AVQMAVFIHN	FKRKGIGGY
AG_BE_VI11	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
AG_NG_92NG	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
AGHU_GA_VI	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
AGU_CD_Z32	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
AJ_BW_BW21	PQSQGVVESH	NKELKKIIGQ	VREQAEHLKT	AVQMAVFIHN	FKRKGIGGY
B_AU_VH_AF	PQRQGVVDSH	NNDLTTIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
B_CN_RL42_	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
B_DE_D31_U	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
B_DE_HAN_U	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
B_FR_HXB2_	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
B_GA_OYI_	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
B_GB_CAM1_	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
B_GB_GB8_A	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
B_GB_MANC	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
B_KR_WK_AF	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
B_NL_3202A	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
B_TW_TWCYS	PQSQGVIESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
B_US_BC_L0	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
B_US_DH123	PQSQGVVESH	NKELKKIIEQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
B_US_JRCSF	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
B_US_MNCG_	PQSQGVIESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
B_US_P896_	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
B_US_RF_M1	PQSQGVVESH	NKQLKQIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY

B_US_SF2_K	PQSQGVVESH	NNELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGGIGGY
B_US_WEAU1	PQSQGVIESM	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGGIGGY
B_US_WR27	PQSQGVVESX	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGGIGGY
B_US_YU2_M	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGGIGGY
BF1_BR_93B	PQSQGVIESM	NKELKKIIGQ	VRDQAEHLKT	AVQTAVFIHN	FKRKGGIGGY
C_BR_92BR0	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKR.GGIGGY
C_BW_96BW0	PQSQGVVESH	NKELKKIIGQ	VREQAEHLKT	AVQMAVFIHN	FKRKGGIGGY
C_BW_96BW1	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGGIGGY
C_BW_96BW1	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGGIGGY
C_BW_96BW1	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGGIGGY
C_ET_ETH22	PQSQGVVESH	NKELKKIIGQ	VREQAEHLKT	AVQMAVFIHN	FKRRGGIGGY
C_IN_93IN1	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGGIGGY
C_IN_93IN9	PQSQGVVEAM	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGGIGGY
C_IN_93IN9	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQVAVFIHN	FKRKGGIGGY
C_IN_94IN1	PQSQGVVEAM	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGGIGGY
C_IN_95IN2	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGGIGGY
CRF01_AE_C	PQSQGVVESH	NKELKKVIGQ	VREQAEHLKT	AVQMAVFIHN	FKRKGGIGGY
CRF01_AE_C	PQSQGVVESH	NKELKKIIGQ	VREQAEHLKT	AVQMAVFIHN	FKRKGGIGEY
CRF01_AE_C	PQSQGVVESH	NKELKKIIGQ	VREQAEHLKT	AVQMAVFIHN	FKRKGGIGGY
CRF01_AE_T	PQGGGVVESH	NKELKEIIGQ	VREQAEHLKT	AVQMAVFIHN	FKRKGGIGGY
CRF01_AE_T	PQSQGVVESH	NKELKKIIGQ	VREQAEHLKT	AF.MAVFIHN	FKRKGGIG.Y
CRF01_AE_T	PQSQGVVESH	NKELKKIIGQ	VREQAEHLKT	AVQMAVFIHN	FKRKGGIGGY
CRF01_AE_T	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGGIGGY
CRF01_AE_T	PQSQGVVESH	NKELKKIIGQ	VREQAEHLKT	AVQMAVFIHN	FKRKGGIGGY
CRF01_AE_T	PQSQGVVESH	NKELKKIIGQ	VREQAEHLKT	AVQMAVFIHN	FKRKGGIGGY
CRF02_AG_F	PQSQGVVEAM	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGGIGGY
CRF02_AG_F	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGGIGGY
CRF02_AG_G	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGGIGGY
CRF02_AG_N	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGGIGGY
CRF02_AG_S	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVLIHN	FKRRGGIGGY
CRF02_AG_S	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRRGGIGGY
CRF03_AB_R	PQSQGVVESH	NKQLKQTIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGGIGGY
CRF03_AB_R	PQSQGVVESH	NKQLKQIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGGIGGY
CRF04_cpx_	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGGIGGY
CRF04_cpx_	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGGIGGY
CRF04_cpx_	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGGIEGY
CRF05_DF_B	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMTVFIHN	FKRKGGIGGY
CRF05_DF_B	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGGIGGY
CRF06_cpx_	PQSQGVVESH	NKELKKIIGQ	VREQAEHLKT	AVQMAVFIHN	FKRKGGIGGY
CRF06_cpx_	PQSQGVVESH	NKELKKIIGQ	VREQAEHLKT	AVQMAVFIHN	FKRKGGIGGY
CRF06_cpx_	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGGIGGY
CRF06_cpx_	PQSQGVVKSM	NKELKKIIGQ	IRDQAEHLKT	AVQMAVYIHN	FKRKGGIGGY
CRF11_cpx_	PQSQGVVESH	NKELKKIIGQ	IRDQAEHLKT	AVQMAVFIHN	FKRKGGIGGY
CRF11_cpx_	PQSQGVVESH	NKGLKEIIGQ	VREQAEHLKT	AVQMAVFIHN	FKGKGGIGGY
D_CD_84ZR0	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGGIGGY
D_CD_ELI_K	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRRRGIGGY
D_CD_NDK_M	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGGIGGY
D_UG_94UG1	PQSQGVVESH	NKELKKIIGQ	VREQAEHLKT	AVQMAVFIHN	FKRKGGIGGY
F1_BE_VI85	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGGIGGY
F1_BR_93BR	PQSQGVVESH	NKELKKIIGQ	IRDQAEHLKT	AVQMAVFIHN	FKRKGGIGGY
F1_FI_FIN9	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGGIGGY
F1_FR_MP41	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGGIGGY
F2_CM_MP25	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGGIGGY
F2KU_BE_VI	PQSQGVVESH	NKELKKIIGQ	IRDQAEHLKT	AVQMAVFIHN	FKRKGGIGGY
G_BE_DRCBL	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGGIGGY
G_NG_92NG0	PQSQGVVESH	NKELKKIIGQ	VGDQAEHLKT	AVQMAVFIHN	FKRKGGIGGY
G_SE_SE616	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGGIGGY
H_BE_VI991	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLRT	AVQMAVFIHN	FKRKGGIGGY
H_BE_VI997	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLRT	AVQMAVFIHN	FKRKGGIGGY
H_CF_90CF0	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGGIGGY



J_SE_SE702	PQSQGVVESM	NKELKKIIGQ	VREQAHLKT	AVQMAVFIHN	FKRKGIGGY
J_SE_SE788	PQSQGVVESM	NKELKKIIGQ	VREQAHLKT	AVQMAVFIHN	FKRKGIGGY
K_CD_EQTB1	PQSQGVVESM	NKELKKIIGQ	VREQAHLKT	AVQMAVFIHN	FKRKGIGGY
K_CM_MP535	PQSQGVVESM	NKELKKIIGQ	VRDQAHLKT	AVQMAVFIHN	FKRKGIGGY
N_CM_YBF30	PQSQGVVESM	NKELKKIIGQ	IRDQAHLKT	AVQMAVFIHN	FKRKGIGGY
O_CM_ANT70	PQSQGVVEAM	NKELKSIIQ	VRDQAHLRT	AVQMAVFIHN	FKRKGIGGY
O_CM_MVP51	PQSQGVVEAM	NKELKSIIQ	VRDQAHLKT	AVQMAVFIHN	FKRKGIGGY
O_SN_99SE_	PQSQGVVEAM	NKELKSIIQ	VRDQAHLKT	AVQMAVFIHN	YKRKGIGGY
O_SN_99SE_	PQSQGVVEAM	NKELKSIIQ	VRDQAHLKT	AVQMAVFIHN	YKRKGIGGY
U_CD___83C	PQSQGVVESM	NKELKKIIGQ	VRDQAHLKT	AVQMAVFIHN	FKRKGIGGY

	951				1000
00BW0762_1	SAGERIIDII	ATDIQTRELQ	KRIIQIQNFR	VYYRDSRDPI	WKGPAKLLWK
00BW0768_2	SAGERIIDII	ATDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
00BW0874_2	SAGERIIDII	ATDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
00BW1471_2	SAGERIVDII	ASDIQTKELQ	KQITKIQNFR	VYYRDSREP	WKGPAKLLWK
00BW1616_2	SAGERIVDII	ATDIQTRELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
00BW1686_8	SAGERIIDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
00BW1759_3	SAGERIIDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
00BW1773_2	SAGERIIDII	ATDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
00BW1783_5	SAGERIIDII	ATDIQTRELQ	KQIIKIQNFR	VYYGDSRDPI	WKGPAKLLWK
00BW1795_6	SAGERIIDII	ATDIQTRELQ	KQIIKIQNFR	VYYRDNRPDI	WKGPAKLLWK
00BW1811_3	SAGERIIDII	ATDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
00BW1859_5	SAGERIIDII	ATDIQTRELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
00BW1880_2	SAGERIIDII	ATDIQTRELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
00BW1921_1	SAGERIIDII	ATDIQTKELQ	KQITNIQKFR	VYYRDSRDPI	WKGPAKLLWK
00BW2036_1	SAGERIIDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
00BW2063_6	SAGERIIDII	ATDIQTRELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
00BW2087_2	SAGERIIDII	ATDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
00BW2127_2	SAGERIIDII	ATDIQTKELQ	KRIIQIQNFR	VYYRDSRDPI	WKGPAKLLWK
00BW2128_3	SAGERIIDII	ATDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
00BW2276_7	SAGERIIDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
00BW3819_3	SAGERIIDII	ATDIQTRELQ	KQIIQIQNFR	VYYRDSRDPI	WKGPAKLLWK
00BW3842_8	SAGERIIDII	ATDIQTKELQ	NQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
00BW3871_3	SAGERIIDII	ATDIQTKELQ	KQITKIQNFR	AYYRDSRDPI	WKGPAKLLWK
00BW3876_9	SAGERIIDII	ATDIQTKELQ	NQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
00BW3886_8	SAGERIIDII	ATDIQTKELQ	NQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
00BW3891_6	SAGGRIIDII	ATDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
00BW3970_2	SAGERIIDII	ATDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
00BW5031_1	SAGERIIDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
96BW01B21	SAGERIIDII	ATDIRTKELQ	KQIMKIRNFR	VYYRDSRDPI	WRGPAKLLWK
96BW0407	SAGERIIDII	ATDIQTKELQ	KQIIKIQNFR	VYYRDSRDPV	WKGPAKLLWK
96BW0502	SAGERIIDII	ATDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
96BW06_J4	SAGERIIDII	ATDIQTKELQ	KQITNIQKFR	VYYRDSRDPI	WKGPAKLLWK
96BW11_06	SAGERIIDMI	ATDIQTRELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
96BW1210	SAGERIIDII	ATDIQTTELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
96BW15B03	SAGERIIDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLIWK
96BW16_26	TAGERIIDII	ATDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
96BW17A09	SAGERIVDII	ATDIQTKELQ	KQIIKIQNFR	VYYRDSREP	WKGPAKLLWK
96BWM01_5	SAGERIIDII	ATDIQTRELQ	KQIIKIQNFR	VYYRDNRPDI	WKGPAKLLWK
96BWM03_2	SAGERIIDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
98BWMC12_2	SAGERIIDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPV	WKGPAKLLWK
98BWMC13_4	SAGERIIDII	ATDIQTRELQ	KQIIKIQNFR	VYYRDNRPDI	WKGPAKLLWK
98BWMC14_a	SAGERIIDII	ATDIQTRELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWR
98BWM014_1	SAGERIIDII	ATDIQTKELQ	KQILNIQKFR	VYYRDSRDPI	WKGPAKLLWK
98BWM018_d	SAGERIIDII	ATDIQTRELQ	RQIIKIQIFR	VYYRDSRDPI	WKGPAKLLWK
98BWM036_a	SAGERIIDII	ATDIQTKELQ	RQILKIQNFR	VYYRDSRDPI	WKGPAKLLWK
98BWM037_d	SAGERIIDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSGDPI	WKGPAKLLWK
99BW3932_1	SAGERIIDII	ATDIQTRELQ	KQIIQIQNFR	VYYRDSRDPI	WKGPAKLLWK
99BW4642_4	SAGERIIDII	ATDIQTRELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK

99BW4745_8	SAGERIIDII	ATDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
99BW4754_7	SAGERIIDII	ASDIQTRELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
99BWMC16_8	SAGERIIDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
A2_CD_97CD	SAGERIIDII	ATDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
A2_CY_94CY	SAGERIIDII	ATDIQTKELQ	RQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
A2D_97KR	SAGERIIDII	ATDIQTKELQ	RQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
A2G_CD_97C	SAGERIIDII	ASDIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
A_BY_97BL0	SAXERIIDII	ATDIQTKELQ	KXITKIQNFX	VYYRDSRDPI	WKGPAKLLXK
A_KE_Q23_A	SAGERIIDII	ATDIQTKELQ	KHITKIQNFR	VYYRDSRDPL	WKGPAKLFWK
A_SE_SE659	SAGERIIDII	ATDIQTRELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
A_SE_SE725	SAGERIIDII	ATDIQTKELQ	KQITKIQKFR	VYYRDSRDPI	WKGPAKLLWK
A_SE_SE753	SAGERIIDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
A_SE_SE853	SAGERIIDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
A_SE_SE889	SAGERIIDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPL	WKGPAKLLWK
A_SE_UGSE8	SAGERIIDII	ATDIQTKELQ	KQIT. IQNFR	VYYRDSRDPI	WKGPAKLLWK
A_UG_92UG0	SAGERIIDII	ASDLQTKELQ	KQITKIQKFR	VCYRDSRDPI	WKGPAKLLWK
A_UG_U455_	SAGERIIDII	ATDIQTKELQ	KQISKIQNFR	VYYRDSRDPI	WKGPAKLLWK
AC_IN_2130	SAGERIIDII	ATDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
AC_RW_92RW	SAGERIIDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
AC_SE_SE94	SPGERIIDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
ACD_SE_SE8	SVGERIIDII	ATDIQTKELQ	KQITKIQKFR	VYYRDSRNPI	WKGPAKLLWK
ACG_BE_VI1	SARERIIDII	ASDIQTKELQ	KPITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
AD_SE_SE69	SAGERIIDII	ATDIQTKELQ	RQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
AD_SE_SE71	SAGERIIDII	ATDIQTKELQ	KHITKIQNFR	VYYRDSRDPL	WKGPAKLLWK
ADHK_NO_97	SAGERIIDXI	ATDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
ADK_CD_MAL	SAGERIIDMI	ATDIQTKELQ	KQITKIQNFR	VYYRDNRDPI	WKGPAKLLWK
AG_BE_VI11	SAGERIIDII	ASDIQTKELQ	KXITKIXNFR	VYYRDSRDPI	WKGPAKLLWK
AG_NG_92NG	SAGERIIDII	ASDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
AGHU_GA_VI	SAGERIIDII	ASDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
AGU_CD_Z32	SAGERIVDII	ASDIQTKELQ	NQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
AJ_BW_BW21	SAGERIIDMI	ATDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
B_AU_VH_AF	SAGERIIDII	ASDIQTKELQ	KQITKVQNFR	VYYRDSRDPL	WKGPAKLLWK
B_CN_RL42_	SAGERIVDII	ATDIQTRELQ	KQITKIQNFR	VYYRGSRDPL	WKGPAKLLWK
B_DE_D31_U	SAGERIVDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPL	WKGPAKLLWK
B_DE_HAN_U	SAGERIVDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSREPF	WKGPAKLLWK
B_FR_HXB2_	SAGERIVDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRNPL	WKGPAKLLWK
B_GA_OYI_	SAGERIVDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSREPL	WKGPAKLLWK
B_GB_CAM1_	SAGERIIDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPL	WKGPAKLLWK
B_GB_GB8_A	SAGERIVDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPL	WKGPAKLLWK
B_GB_MANC_	SAGGRIVDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRNPL	WKGPAKLLWK
B_KR_WK_AF	SAGERIIDII	ATDIQTKELQ	KQVTKIQNFR	VYYRDSRDPL	WKGPAKLLWK
B_NL_3202A	SAGERIVDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPL	WKGPAKLLWK
B_TW_TWCYS	SAGERIVDII	ATDIQTKELQ	KQITKIQNFR	VYYRDNRDPL	WKGPAKLLWK
B_US_BC_L0	SAGERIVDII	ATDIQTKELQ	KQITKIQNFR	VYYRDNKDPL	WKGPAKLLWK
B_US_DH123	SAGERIVDII	ASDIQTKELQ	KQITKIQNFR	VYYRDSRDPL	WKGPAKLLWK
B_US_JRCSF	SAGERIIDII	ATDIQTKELQ	KQITKIQNFR	VYYRDNRDPI	WKGPAKLLWK
B_US_MNCG_	SAGERIVGII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPL	WKGPAKLLWK
B_US_P896_	SAGERIVDII	ASDIQTKELQ	KQITKIQNFR	VYYRDSRDPL	WKGPAKLLWK
B_US_RF_M1	SAGERIVDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPL	WKGHAKLLWK
B_US_SF2_K	SAGERIVDII	ATDIQTKELQ	KQITKIQNFR	VYYRDNKDPL	WKGPAKLLWK
B_US_WEAU1	SAGERIIDII	ATDIQTQOLQ	KQITKIQNFR	VYYRDSRDPL	WKGPAKLLWK
B_US_WR27_	SAGERIIDII	ATDIQXKXLQ	XQXTIXQNXR	VYYRDSRDPL	WKGPAKLLWK
B_US_YU2_M	SAGERIVDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPL	WKGPAKLLWK
BF1_BR_93B	SAGERIVDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPL	WKGPAKLLWK
C_BR_92BR0	SAGERIIDII	ATDIQTKELQ	KQIMKIQNFR	VYYRDSRDPI	WKGPAKLLWK
C_BW_96BW0	SAGERIIDII	ATDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
C_BW_96BW1	SAGERIIDMI	ATDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
C_BW_96BW1	SAGERIIDII	ATDIQTTELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
C_BW_96BW1	SAGERIIDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLIWK
C_ET_ETH22	SAGERIIDII	ASDIQTKELQ	NQILKIQNFR	VYYRDSRDPI	WKGPAKLLWK

C_IN_93IN1	SAGERIIDII	ATDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
C_IN_93IN9	SAGERIIDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
C_IN_93IN9	SAGERIIDII	ATDIQTKELQ	KQIIKIHNFR	VYYRDSRDPI	WKGPAKLLWK
C_IN_94IN1	SAGERIIDII	STDIQTRELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
C_IN_95IN2	SAGERIIDII	ATDIQTKELQ	KQITKVQNFR	VYYRDSRDPI	WKGPAKLLWK
CRF01_AE_C	SAGERIIDII	ATEIQTKEXQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
CRF01_AE_C	SAGERIIDII	ATDIQTKALQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
CRF01_AE_C	SAGERIIDII	ATDIQTKELQ	KHITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
CRF01_AE_T	SAGERIIDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
CRF01_AE_T	SVGERIIDII	AADIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
CRF01_AE_T	SAGERIIDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
CRF01_AE_T	SAGERIIDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
CRF01_AE_T	SAGERIIDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
CRF01_AE_T	SAGERIIDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
CRF02_AG_F	SAGERIIDII	ASDIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
CRF02_AG_F	SAGERIIDII	ASDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
CRF02_AG_G	SAGERIIDII	ASDIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
CRF02_AG_N	SAGERIIDII	ASDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
CRF02_AG_S	SAGERIIDII	ASDIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
CRF02_AG_S	SAGERIIDII	ASDIQTKELQ	KQITNIQKFR	VYYRDSRDPI	WKGPAKLLWK
CRF03_AB_R	SAGERIIDII	ATDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
CRF03_AB_R	SAGERIIDII	ATDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
CRF04_cpx_	SAGERIIDII	ASDIQTKELQ	KQITKIQNFR	VYYRDSREPI	WKGPAKLLWK
CRF04_cpx_	SAGERIIDII	ASDIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
CRF04_cpx_	SAGERIIDII	ASDIQTKELQ	KQIIKIQNFR	VYYRDSKDPI	WKGPAKLLWK
CRF05_DF_B	GAGERIIDII	TTDIQTKELQ	KQIIKIQNFR	VYYRDSRDPV	WKGPAKLLWK
CRF05_DF_B	SAGEGIIDII	STDIQTKELQ	KQITKIQNFR	VYYRDSRDPV	WKGPAKLLWK
CRF06_cpx_	SAGERIIDII	ASDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
CRF06_cpx_	SAGERIIDII	ASDIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
CRF06_cpx_	SAGERIIDII	ASDIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
CRF06_cpx_	SAGERIIDII	ASDIQTKELQ	KQITKIRNFR	VYYRDSRDPI	WKGPAKLLWK
CRF11_cpx_	SAGERIVDII	ATDLQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
CRF11_cpx_	SAGERIIDII	ATDLQTKELQ	KQITKIQKFR	VYYRDSRDPI	WKGPAKLLWK
D_CD_84ZR0	SAGERIIDII	ASDIQTKRELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
D_CD_ELI_K	SAGERIIDII	ATDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
D_CD_NDK_M	SAGERIIDII	ATDIQTRELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
D_UG_94UG1	SAGERIIDII	ATDIQTKELQ	KQIIKIQNFR	VYYRDSRDPV	WKGPAKLLWK
F1_BE_VI85	SAGERIIDII	STDIQTRELQ	KQITKIQNFR	VYYRDSRNPV	WKGPAKLLWK
F1_BR_93BR	SAGERTIDII	ATDIQTRELQ	KQIIKIQNFR	VYYRDSRDPV	WKGPAKLLWK
F1_FI_FIN9	SAGERIIDII	ATDIQTKELQ	KQVTKIQNFR	VYYRDSRDPV	WKGPAKLLWK
F1_FR_MP41	SAGERIIDII	STDIQTRELQ	KQIIKIQNFR	VYYRDSRDPV	WKGPAKLLWK
F2_CM_MP25	SAGERIIDII	ATDIQTKELQ	KQISKIQNFR	VYFRDSRDPV	WKGPAKLLWK
F2KU_BE_VI	SAGERIVDII	ASDIQTRALQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
G_BE_DRCBL	SAGERIIDII	ASDIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
G_NG_92NG0	SAGERIIDII	ASDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
G_SE_SE616	SAGERIIDII	ASDIQTKELQ	KQITKIQNFR	VYYRDSRDPV	WKGPAKLLWK
H_BE_VI991	SARERIIDII	ATDIPTKELQ	KQISQIQKFR	VYYRDSRDPI	WKGPAKLLWK
H_BE_VI997	SAGERIIDII	ATDIQTKELQ	KQISNIQKFR	VYYRDSRDPI	WKGPAKLLWK
H_CF_90CF0	SAGERIIDII	ATDIQTKELQ	KQISNIQKFR	VYYRDSRDPI	WKGPAKLLWK
J_SE_SE702	SAGERIIDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
J_SE_SE788	SAGERIIDII	ATDIQTRELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLPWK
K_CD_EQTB1	SAGERIIDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSREPI	WKGPAKLLWK
K_CM_MP535	SAGERIVDII	ATDIQTKELQ	KQILNIQKFR	VYYRDSREPI	WKGPAKLLWK
N_CM_YBF30	TAGERIIDII	ATDIQTTNLQ	TQILKVQNFR	VYYRDSRDPI	WKGPAKLLWK
O_CM_ANT70	TAGERIIDIL	ASQIQTTTELQ	KQILKXHKFR	VYYRDSRDPI	WKGPAQLLWK
O_CM_MVP51	TAGERIIDIL	ASQIQTTTELQ	KQILKINNFR	VYYRDSRDPI	WKGPAQLLWK
O_SN_99SE_	TAGERIIDIL	ASQIQTTTELQ	KQIFKIQKFQ	VYYRDSRDPI	WKGPAQLLWK
O_SN_99SE_	TAGERIIDIL	ASQIQTTTELQ	KQIFKIQKFQ	VYYRDSRDPI	WKGPAQLLWK
U_CD___83C	SAGERIIDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK

	1001				1046
00BW0762_1	GE.GAVVIQD	NSDIKVIPRR	KAKI IKDYGK	QMAGADCVAG	RQDED.
00BW0768_2	GE.GAVVIQD	NSDIKVVPRR	KVKI IKDYGK	QMAGADCVAG	RQDED.
00BW0874_2	GE.GAVVIQD	NGDIKVVPRR	KVKI IKDYGK	QMAGADCVAG	RQDED.
00BW1471_2	GE.GAVVIQD	NSDIKVVPRR	KAKI IRDYGK	QMAGADCVAG	RQDED.
00BW1616_2	GE.GAVVIQD	NSDIKVVPRR	KVKI IRDYGK	QMAGADCVAG	RQDED.
00BW1686_8	GE.GAVVIQD	NSDIKVVPRR	KAKI IRDYGK	QMAGADCVAG	RQDEDQ
00BW1759_3	GE.GAVVIQD	NSDIKVVPRR	KVKI IKDYGK	QMAGADCVAG	RQDEDQ
00BW1773_2	GE.GAVVIQD	NNDIKVVPRR	KVKI IKGYGK	QMAGADCVAG	GQDEN.
00BW1783_5	GE.GAVVIQD	NSDIKVVPRR	KVKI IKDYGK	QMAGADCMAG	RQDEDQ
00BW1795_6	GE.GAVVLQD	NSEIKVVPRR	KVKI IRDYGK	QMAGADCVAG	RQDEDQ
00BW1811_3	GE.GAVVIQD	NSDIKVVPRR	KVKI IRDYGK	QMAGADCVAG	GQDEN.
00BW1859_5	GE.GAVVIQD	NSDIKVVPRR	KAKI IRDYGK	QMAGADCVAS	RQDED.
00BW1880_2	GE.GAVVIQD	KSDIKVVPRR	KVKI IRDYGK	QMAGADCVAD	RQDED.
00BW1921_1	GE.GAVVIQD	NSDVKVVPRR	KAKI IRDYGK	QMAGADCVAD	RQDED.
00BW2036_1	GE.GAVVIQD	NSDIKVVPRR	KVKI IKDYGK	QMAGADCVAG	RQDED.
00BW2063_6	GE.GAVVIQD	NSDIKVVPRR	KVKI IKDYGK	QMAGADCVAG	RQDED.
00BW2087_2	GE.GAVVIQD	NSDIKVVPRR	KVKI IKDYGK	QMAGADCVAG	RQDED.
00BW2127_2	GE.GAVVIQD	NSDIKVVPRR	KAKI IKDYGK	QMAGADCVAS	RQDED.
00BW2128_3	GE.GAVVLQD	NSDIKVVPRR	KVKI IKDYGK	QMAGADCVAG	GQDEN.
00BW2276_7	GE.GAVVIQD	NSDIKVVPRR	KVKI IKDYGK	QMAGADCVAG	RQDED.
00BW3819_3	GE.GAVVIQD	NGDIKVVPRR	KAKI IKDYGK	QMAGADCVAS	RQDEN.
00BW3842_8	GE.GAVVIQD	NSDIKVVPRR	KVKI IKDYGK	QMAGADCVAG	RQDED.
00BW3871_3	GE.GAVVIQD	NSDIKVVPRR	KAKI IKDYGK	QMAGADCVAG	RQDED.
00BW3876_9	GE.GAVVIQD	NSDIKVVPRR	KAKI IKNYGK	QMAGADCVAG	RQDED.
00BW3886_8	GE.GAVVIQD	KGDIKVVPRR	KAKI IKDYGK	QMAGADCVAG	RQDED.
00BW3891_6	GE.GAVVIQD	NSDIKVVPRR	KVKI IRDYGK	QMAGDDCVAG	RQDED.
00BW3970_2	GE.GAVVIQD	NSDIKVVPRR	RAKI IRDYGK	QMAGADCVAD	RQDED.
00BW5031_1	GE.GAVVIQD	NSDIKAVPRR	KAKI IKDYGQ	QMAGADCVAG	RQDEN.
96BW01B21	GE.GAVVIQD	NSDIKVVPRR	KVKI IKDYGK	QMAGADCVAG	RQDED.
96BW0407	GE.GAVVIQD	NSDIKVVPRR	KVKI IRDYGK	QMAGDDCVAG	RQDED.
96BW0502	GE.GAVVIQD	NSDIKVVPRR	KAKI IKDYGK	QMAGADCVAG	GQDEN.
96BW06_J4	GE.GAVVIQD	NSDIKVVPRR	KVKI IKDYGK	QMAGADCVAS	RQDED.
96BW11_06	GE.GAVVIQD	NSDIKVVPRR	KVKI IRDYGK	QMAGADCVAG	RQDED.
96BW1210	GE.GAVVIQD	NSDIKVVPRR	KVKI IKDYGK	QMAGADCVAG	RQDED.
96BW15B03	GEGAVVIQD	NSDIKVVPRR	KVKI IRDYGK	QMAGADCVAG	RQDED.
96BW16_26	GE.GAVVLQD	NSDIKVVPRR	KVKI IKDYGK	QMAGADCVAG	GQDEN.
96BW17A09	GE.GAVVIQD	NSDIKVVPRR	KAKI IRDYGK	QMAGADCVAG	RQDED.
96BWM01_5	GE.GAVVIQD	NSEIKVVPRR	KAKI IRDYGK	QMAGADCVAG	RQDEDQ
96BWM03_2	GE.GAVVIQD	NSDIKVVPRR	KAKI IRDYGK	QMAGADCVAG	RQDEDQ
98BWMC12_2	GD.GAVVIQD	NSDIKVVPRR	KAKI IRDYGK	QMAGADCVAG	RQDED.
98BWMC13_4	GE.GAVVIQD	NSEIKVVPRR	KVKI IRDYGK	QMAGADCVAG	RQDEDQ
98BWMC14_a	GE.GAVVIQD	SSDIKVVPRR	KAKI IKDYGK	QMAGADCVAG	RQDED.
98BWM014_1	GE.GAVVIQD	NSDIKVVPRR	KAKI IKDYGK	QMAGADCVAG	RQDED.
98BWM018_d	GE.GAVVIQD	NSDIKVVPRR	KVKI IKDYGK	QMAGADCVAG	RQDEDQ
98BWM036_a	GE.GAVVIQD	NSDIKVVPRR	KAKI IKDYGK	QMAGADCVAG	GQDED.
98BWM037_d	GE.GAVVIQD	NSDIKVVPRR	KAKI IRDYGK	QMAGADCVAG	RQDEDQ
99BW3932_1	GE.GAVVIQD	NSDIKVVPRR	KAKI IKDYGK	QMAGADCVAS	RQDED.
99BW4642_4	GE.GAVVIQD	NSDIKVVPRR	KAKI IKDYGK	QMAGADCVAD	RQDED.
99BW4745_8	GE.GAVVIQD	NSDIKVVPRR	KVKI IKDYGK	QMAGADCVAG	RQDED.
99BW4754_7	GE.GAVVIQD	KSDIKVVPRR	KAKI IKDYGK	QMAGDDCVAG	RQDED.
99BWMC16_8	GE.GAVVIQD	NSDIKVVPRR	KAKI IKDYGK	QMAGADCVAG	RQDED.
A2_CD_97CD	GE.GAVVIQD	NGDIKVVPRR	KAKI IRDYGK	QMAGDDCVAG	RQDED.
A2_CY_94CY	GE.GAVVIQD	NSDIKVVPRR	KAKI IRDYGK	QMAGDDCVAG	RQDED.
A2D_97KR	GE.GAVVIQD	NSDIKVVPRR	RAKI IRDYGK	QMAGDDCVAG	RQDED.
A2G_CD_97C	GE.GAVVIQD	NNEIKVVPRR	GTKILRDYGK	QMAGDDCVAG	RQDED.
A_BY_97BL0	GE.GAVVIQD	NXDIKVVPRR	KAKI IXDXXK	QMAGXDCVAS	RQDED.
A_KE_Q23_A	GE.GAVVIQD	NSDIKVVPRR	KAKI IRDYGK	QMAGDDCVAG	RQDED.
A_SE_SE659	GE.GAVVIQD	NSDIKVVPRR	KAKI IRDYGK	QMAGDDCVAG	RQDED.
A_SE_SE725	GE.GAVVIQD	NNDIKVVPRR	KAKI LRDYGK	QMAGDDCVAG	RQDED.

A_SE_SE753	GE.GAVVIQD	NSDIKVVPRR	KVKIIRDYGK	QMAGDDCVAG	RQDED.
A_SE_SE853	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
A_SE_SE889	GE.GAVLIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDGCVAG	RQDED.
A_SE_UGSE8	GE.GAVVIQD	QSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAS	RQDED.
A_UG_92UG0	GE.GAVVIQD	NSDIKVVPRR	KVKIIRDYGK	QMAGDDCVAG	RQDED.
A_UG_U455_	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCMAG	RQDED.
AC_IN_2130	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGADCVAG	RQDED.
AC_RW_92RW	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
AC_SE_SE94	GE.GAVVIQD	NSDIKVVPRR	KVKIIRDYGK	QMAGDDCVAG	RQDED.
ACD_SE_SE8	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDEDW
ACG_BE_VI1	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDGCVAG	RQDED.
AD_SE_SE69	GE.GAVVIQD	NSEIKVVPRR	KVKIIRDYGK	QMAGDDCVAS	RQDED.
AD_SE_SE71	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
ADHK_NO_97	GE.GAVVIQD	NGDIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
ADK_CD_MAL	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	GQDED.
AG_BE_VI11	GE.GAVAIQD	NNEIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
AG_NG_92NG	GE.GAVVIQD	NSEIKVVPRR	KVKIIRDYGK	QMAGGDCVAG	RQDED.
AGHU_GA_VI	GE.GAVVIQD	NSEIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
AGU_CD_Z32	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
AJ_BW_BW21	GE.GAVVIQD	NSEIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
B_AU_VH_AF	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAS	RQDED.
B_CN_RL42_	GE.GAVVIQD	NSDIKVVPRR	KVKIIRDYGK	QMAGDDCVAS	RQDED.
B_DE_D31_U	GE.GAVVIQD	NSEIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
B_DE_HAN_U	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMGSDDCVAS	RQDED.
B_FR_HXB2_	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAS	RQDED.
B_GA_OYI_	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAS	RQDED.
B_GB_CAM1_	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAS	RQDED.
B_GB_GB8_A	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAS	RQDED.
B_GB_MANC_	GE.GAVVIQD	NSEIKVVPRR	KVKIIRDYGK	QMAGDDCVAG	RQDED.
B_KR_WK_AF	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAS	RQDED.
B_NL_3202A	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAS	RQDED.
B_TW_TWCYS	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
B_US_BC_L0	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAS	RQDED.
B_US_DH123	GE.GAVVIQD	KSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAS	RQDED.
B_US_JRCSF	GE.GAVVIQD	NSDIKVVPRR	KVKIIRDYGK	QMAGDDCVAS	RQDED.
B_US_MNCG_	GE.GAVVIQD	NNDIKVVPRR	KAKVIRDYGK	QTAGDDCVAS	RQDED.
B_US_P896_	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAS	RQDED.
B_US_RF_M1	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAS	RQDED.
B_US_SF2_K	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAS	RQDED.
B_US_WEAU1	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAS	RQDED.
B_US_WR27_	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAS	RQDED.
B_US_YU2_M	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
BF1_BR_93B	GE.GAVVIQD	NSDIKVVPRR	KVKIIRDYGK	QMAGGDCVAG	RQDED.
C_BR_92BR0	GE.GAVVLQD	NSDIKVVPRR	KVKIIRDYGK	QMAGADCMAS	RQDED.
C_BW_96BW0	GE.GAVVIQD	NSDIKVVPRR	KVKIIRDYGK	QMAGADCVAG	RQDED.
C_BW_96BW1	GE.GAVVIQD	NSDIKVVPRR	KVKIIRDYGK	QMAGADCVAG	RQDED.
C_BW_96BW1	GE.GAVVIQD	NSDIKVVPRR	KVKIIRDYGK	QMAGADCVAG	RQDED.
C_BW_96BW1	GEGAVVIQD	NSDIKVVPRR	KVKIIRDYGK	QMAGADCVAG	RQDED.
C_ET_ETH22	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGADCVAG	RQDED.
C_IN_93IN1	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGADCVAG	RQDED.
C_IN_93IN9	GE.GAVVLQD	NSDIKVVPRR	KAKIIRDYGK	QMAGADCVAG	RQDED.
C_IN_93IN9	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGADCVAG	RQDED.
C_IN_94IN1	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGADCVAG	RQDED.
C_IN_95IN2	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGADCVAG	RQDED.
CRF01_AE_C	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDEN.
CRF01_AE_C	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDEN.
CRF01_AE_C	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
CRF01_AE_T	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
CRF01_AE_T	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAS	RQDED.
CRF01_AE_T	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.

CRF01_AE_T	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
CRF01_AE_T	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
CRF01_AE_T	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
CRF02_AG_F	GE.GAVVIQD	KSDIKVVPRR	KAKI IKDYGK	QMAGDDCVAG	RQDED.
CRF02_AG_F	GE.GAVVIQD	KSDIKVVPRR	KAKI IKDYGK	QMAGDDCVAG	RQDED.
CRF02_AG_G	GE.GAVVIQD	NSDIKVVPRR	KAKILRDYGK	QMAGDDCVAG	RQDED.
CRF02_AG_N	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
CRF02_AG_S	GE.GAVVIQD	NSDIKVVPRR	KVKIVRDYGK	QMAGDDCVAG	RQDED.
CRF02_AG_S	GE.GAVVIQD	NSDIKVVPRR	KTKILRDYGK	QMAGDDCVAG	GQDED.
CRF03_AB_R	GE.GAVVIQD	NNDIKVVPRR	KAKIIRDYGK	QMAGDDCVAS	RQDED.
CRF03_AB_R	GE.GAVVIQD	NNDIKVVPRR	KAKIIRDYGK	QMAGDDCVAS	RQDED.
CRF04_cpx_	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGNDCVAG	RQDED.
CRF04_cpx_	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
CRF04_cpx_	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
CRF05_DF_B	GE.GAVVIQD	NSEIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
CRF05_DF_B	GE.GAVVIQD	NSEIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
CRF06_cpx_	GE.GAVVIQD	NSEIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
CRF06_cpx_	GE.GAVVIQD	NSEIKVVPRR	KAKI IKDYGK	QMAGDDCVAG	RQDED.
CRF06_cpx_	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
CRF06_cpx_	GE.GAVVIQD	NSEIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
CRF11_cpx_	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
CRF11_cpx_	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	SQDED.
D_CD_84ZR0	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAS	RQDED.
D_CD_ELI_K	GE.GAVVIQD	KSDIKVVPRR	KVKIIRDYGK	QMAGDDCVAS	RQDED.
D_CD_NDK_M	GE.GAVVIQD	NSDIKVVPRR	KVKIIRDYGK	QMAGDDCVAS	RQDED.
D_UG_94UG1	GE.GAVVIQD	NSEIKVVPRR	KAKIIRDYGK	QMAGDDCVAS	RQDED.
F1_BE_VI85	GE.GAVVIQD	NSEIKIVPRR	KAKIIRDYGK	QMAVDDCVAG	RQDED.
F1_BR_93BR	GE.GAVVIQD	NSEIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
F1_FI_FIN9	GE.GAVVIQD	NSEIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
F1_FR_MP41	GE.GAVVIQD	NSEIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
F2_CM_MP25	GE.GAVVIQD	NNEIKVIPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
F2KU_BE_VI	GE.GAVVIQD	NSEIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
G_BE_DRCBL	GE.GAVVIQD	NNEIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
G_NG_92NG0	GE.GAVVIQD	NNEIKVVPRR	KAKILKDYGK	QMAGGDCVAG	RQDED.
G_SE_SE616	GE.GAVVIQD	NNEIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
H_BE_VI991	GE.GAVVIQD	NSEIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
H_BE_VI997	GE.GAVVIQD	NSEIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
H_CF_90CF0	GE.GAVVIQD	NSEIKVVPRR	EAKIIRDYGK	QMAGDDCVAS	RQDED.
J_SE_SE702	GE.GAVVIQD	NSEIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
J_SE_SE788	GE.GAVVIQD	NSEIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
K_CD_EQTB1	GE.GAVVIN.	.SEIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
K_CM_MP535	GE.GAVVIQD	NSEIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
N_CM_YBF30	GE.GAVVIQD	NGDIKVVPRR	KAKIIRDYGK	QMAGDGCVAS	GQDENQ
O_CM_ANT70	GE.GAVVIQD	KGDIKVVPRR	KAKI IREYK	QMAGTDSMAS	GQTESE
O_CM_MVP51	GE.GAVVIQD	KGDIKVVPRR	KAKIIRDYGK	QMAGTDSMAN	RQTESE
O_SN_99SE_	GE.GAVVIQD	KGDIKVVPRR	KAKIIRHYGK	QMAGTDSMAS	GQTESE
O_SN_99SE_	GE.GAVVIQD	KGDIKVVPRR	KAKIIRHYGK	QMAGTDSMAS	GQTESE
U_CD___83C	GE.GAVVIQD	NSEIKVVPRR	KAKIIRDYGK	QMAGDDCVAS	RQDEN.

Table 15. HIV Rev Sequence Alignment

GCG Multiple Sequence File.

Written by Omega 1.1

Name: 00BW0762_1	<u>SEQ ID NO: 970</u>	Len: 129	Check: 4903	Weight: 1.00
Name: 00BW0768_2	<u>SEQ ID NO: 971</u>	Len: 129	Check: 5102	Weight: 1.00
Name: 00BW0874_2	<u>SEQ ID NO: 972</u>	Len: 129	Check: 5815	Weight: 1.00
Name: 00BW1471_2	<u>SEQ ID NO: 973</u>	Len: 129	Check: 4144	Weight: 1.00
Name: 00BW1616_2	<u>SEQ ID NO: 974</u>	Len: 129	Check: 5298	Weight: 1.00
Name: 00BW1686_8	<u>SEQ ID NO: 975</u>	Len: 129	Check: 3871	Weight: 1.00
Name: 00BW1759_3	<u>SEQ ID NO: 976</u>	Len: 129	Check: 4976	Weight: 1.00
Name: 00BW1773_2	<u>SEQ ID NO: 977</u>	Len: 129	Check: 5775	Weight: 1.00
Name: 00BW1783_5	<u>SEQ ID NO: 978</u>	Len: 129	Check: 6142	Weight: 1.00
Name: 00BW1795_6	<u>SEQ ID NO: 979</u>	Len: 129	Check: 5055	Weight: 1.00
Name: 00BW1811_3	<u>SEQ ID NO: 980</u>	Len: 129	Check: 5804	Weight: 1.00
Name: 00BW1859_5	<u>SEQ ID NO: 981</u>	Len: 129	Check: 5252	Weight: 1.00
Name: 00BW1880_2	<u>SEQ ID NO: 982</u>	Len: 129	Check: 4995	Weight: 1.00
Name: 00BW1921_1	<u>SEQ ID NO: 983</u>	Len: 129	Check: 6482	Weight: 1.00
Name: 00BW2036_1	<u>SEQ ID NO: 984</u>	Len: 129	Check: 4770	Weight: 1.00
Name: 00BW2063_6	<u>SEQ ID NO: 985</u>	Len: 129	Check: 5384	Weight: 1.00
Name: 00BW2087_2	<u>SEQ ID NO: 986</u>	Len: 129	Check: 4848	Weight: 1.00
Name: 00BW2127_2	<u>SEQ ID NO: 987</u>	Len: 129	Check: 5783	Weight: 1.00
Name: 00BW2276_7	<u>SEQ ID NO: 988</u>	Len: 129	Check: 5364	Weight: 1.00
Name: 00BW3819_3	<u>SEQ ID NO: 989</u>	Len: 129	Check: 5712	Weight: 1.00
Name: 00BW3842_8	<u>SEQ ID NO: 990</u>	Len: 129	Check: 5586	Weight: 1.00
Name: 00BW3871_3	<u>SEQ ID NO: 991</u>	Len: 129	Check: 5299	Weight: 1.00
Name: 00BW3876_9	<u>SEQ ID NO: 992</u>	Len: 129	Check: 4423	Weight: 1.00
Name: 00BW3886_8	<u>SEQ ID NO: 993</u>	Len: 129	Check: 5415	Weight: 1.00
Name: 00BW3891_6	<u>SEQ ID NO: 994</u>	Len: 129	Check: 5426	Weight: 1.00
Name: 00BW3970_2	<u>SEQ ID NO: 995</u>	Len: 129	Check: 2613	Weight: 1.00
Name: 00BW5031_1	<u>SEQ ID NO: 996</u>	Len: 129	Check: 4597	Weight: 1.00
Name: 96BW01B21	<u>SEQ ID NO: 997</u>	Len: 129	Check: 5653	Weight: 1.00
Name: 96BW0407	<u>SEQ ID NO: 998</u>	Len: 129	Check: 4310	Weight: 1.00
Name: 96BW0502	<u>SEQ ID NO: 999</u>	Len: 129	Check: 4675	Weight: 1.00
Name: 96BW06_J4	<u>SEQ ID NO: 1000</u>	Len: 129	Check: 5079	Weight: 1.00
Name: 96BW11_06	<u>SEQ ID NO: 1001</u>	Len: 129	Check: 5939	Weight: 1.00
Name: 96BW1210	<u>SEQ ID NO: 1002</u>	Len: 129	Check: 5666	Weight: 1.00
Name: 96BW15B03	<u>SEQ ID NO: 1003</u>	Len: 129	Check: 5102	Weight: 1.00
Name: 96BW16_26	<u>SEQ ID NO: 1004</u>	Len: 129	Check: 5675	Weight: 1.00
Name: 96BW17A09	<u>SEQ ID NO: 1005</u>	Len: 129	Check: 2825	Weight: 1.00
Name: 96BWMO1_5	<u>SEQ ID NO: 1006</u>	Len: 129	Check: 5636	Weight: 1.00
Name: 96BWMO3_2	<u>SEQ ID NO: 1007</u>	Len: 129	Check: 6552	Weight: 1.00
Name: 98BWMC12_2	<u>SEQ ID NO: 1008</u>	Len: 129	Check: 3043	Weight: 1.00
Name: 98BWMC13_4	<u>SEQ ID NO: 1009</u>	Len: 129	Check: 5518	Weight: 1.00
Name: 98BWMC14_a	<u>SEQ ID NO: 1010</u>	Len: 129	Check: 4358	Weight: 1.00
Name: 98BWMO14_1	<u>SEQ ID NO: 1011</u>	Len: 129	Check: 7531	Weight: 1.00
Name: 98BWMO18_d	<u>SEQ ID NO: 1012</u>	Len: 129	Check: 5291	Weight: 1.00
Name: 98BWMO36_a	<u>SEQ ID NO: 1013</u>	Len: 129	Check: 6801	Weight: 1.00
Name: 98BWMO37_d	<u>SEQ ID NO: 1014</u>	Len: 129	Check: 4790	Weight: 1.00
Name: 99BW3932_1	<u>SEQ ID NO: 1015</u>	Len: 129	Check: 5736	Weight: 1.00
Name: 99BW4642_4	<u>SEQ ID NO: 1016</u>	Len: 129	Check: 6464	Weight: 1.00
Name: 99BW4745_8	<u>SEQ ID NO: 1017</u>	Len: 129	Check: 6181	Weight: 1.00
Name: 99BW4754_7	<u>SEQ ID NO: 1018</u>	Len: 129	Check: 5182	Weight: 1.00
Name: 99BWMC16_8	<u>SEQ ID NO: 1019</u>	Len: 129	Check: 4245	Weight: 1.00
Name: A2_CD_97CD	<u>SEQ ID NO: 1020</u>	Len: 129	Check: 2625	Weight: 1.00
Name: A2_CY_94CY	<u>SEQ ID NO: 1021</u>	Len: 129	Check: 4125	Weight: 1.00
Name: A2D_97KR	<u>SEQ ID NO: 1022</u>	Len: 129	Check: 4114	Weight: 1.00
Name: A2G_CD_97C	<u>SEQ ID NO: 1023</u>	Len: 129	Check: 1115	Weight: 1.00
Name: A_BY_97BL0	<u>SEQ ID NO: 1024</u>	Len: 129	Check: 9470	Weight: 1.00
Name: A_KE_Q23_A	<u>SEQ ID NO: 1025</u>	Len: 129	Check: 2684	Weight: 1.00

Name: A_SE_SE659	SEQ ID NO: 1026	Len:129	Check: 4659	Weight: 1.00
Name: A_SE_SE725	SEQ ID NO: 1027	Len:129	Check: 4491	Weight: 1.00
Name: A_SE_SE753	SEQ ID NO: 1028	Len:129	Check: 3636	Weight: 1.00
Name: A_SE_SE853	SEQ ID NO: 1029	Len:129	Check: 1862	Weight: 1.00
Name: A_SE_SE889	SEQ ID NO: 1030	Len:129	Check: 2798	Weight: 1.00
Name: A_SE_UGSE8	SEQ ID NO: 1031	Len:129	Check: 6865	Weight: 1.00
Name: A_UG_92UG0	SEQ ID NO: 1032	Len:129	Check: 4427	Weight: 1.00
Name: A_UG_U455_	SEQ ID NO: 1033	Len:129	Check: 3229	Weight: 1.00
Name: AC_IN_2130	SEQ ID NO: 1034	Len:129	Check: 5110	Weight: 1.00
Name: AC_RW_92RW	SEQ ID NO: 1035	Len:129	Check: 5015	Weight: 1.00
Name: AC_SE_SE94	SEQ ID NO: 1036	Len:129	Check: 7976	Weight: 1.00
Name: ACD_SE_SE8	SEQ ID NO: 1037	Len:129	Check: 2296	Weight: 1.00
Name: ACG_BE_VI1	SEQ ID NO: 1038	Len:129	Check: 3968	Weight: 1.00
Name: AD_SE_SE69	SEQ ID NO: 1039	Len:129	Check: 4558	Weight: 1.00
Name: AD_SE_SE71	SEQ ID NO: 1040	Len:129	Check: 2678	Weight: 1.00
Name: ADHK_NO_97	SEQ ID NO: 1041	Len:129	Check: 1890	Weight: 1.00
Name: ADK_CD_MAL	SEQ ID NO: 1042	Len:129	Check: 5260	Weight: 1.00
Name: AG_BE_VI11	SEQ ID NO: 1043	Len:129	Check: 4003	Weight: 1.00
Name: AG_NG_92NG	SEQ ID NO: 1044	Len:129	Check: 5027	Weight: 1.00
Name: AGHU_GA_VI	SEQ ID NO: 1045	Len:129	Check: 1978	Weight: 1.00
Name: AGU_CD_Z32	SEQ ID NO: 1046	Len:129	Check: 1958	Weight: 1.00
Name: AJ_BW_BW21	SEQ ID NO: 1047	Len:129	Check: 2263	Weight: 1.00
Name: B_AU_VH_AF	SEQ ID NO: 1048	Len:129	Check: 4074	Weight: 1.00
Name: B_CN_RL42	SEQ ID NO: 1049	Len:129	Check: 4483	Weight: 1.00
Name: B_DE_D31_U	SEQ ID NO: 1050	Len:129	Check: 5079	Weight: 1.00
Name: B_DE_HAN_U	SEQ ID NO: 1051	Len:129	Check: 4550	Weight: 1.00
Name: B_FR_HXB2	SEQ ID NO: 1052	Len:129	Check: 3649	Weight: 1.00
Name: B_GA_OYI_M	SEQ ID NO: 1053	Len:129	Check: 3334	Weight: 1.00
Name: B_GB_CAM1	SEQ ID NO: 1054	Len:129	Check: 3865	Weight: 1.00
Name: B_GB_GB8_A	SEQ ID NO: 1055	Len:129	Check: 3083	Weight: 1.00
Name: B_GB_MANC	SEQ ID NO: 1056	Len:129	Check: 5502	Weight: 1.00
Name: B_KR_WK_AF	SEQ ID NO: 1057	Len:129	Check: 4156	Weight: 1.00
Name: B_NL_3202A	SEQ ID NO: 1058	Len:129	Check: 3826	Weight: 1.00
Name: B_TW_TWCYS	SEQ ID NO: 1059	Len:129	Check: 3546	Weight: 1.00
Name: B_US_BC_L0	SEQ ID NO: 1060	Len:129	Check: 4674	Weight: 1.00
Name: B_US_DH123	SEQ ID NO: 1061	Len:129	Check: 4202	Weight: 1.00
Name: B_US_JRCFS	SEQ ID NO: 1062	Len:129	Check: 3217	Weight: 1.00
Name: B_US_MNCG	SEQ ID NO: 1063	Len:129	Check: 3512	Weight: 1.00
Name: B_US_P896	SEQ ID NO: 1064	Len:129	Check: 3297	Weight: 1.00
Name: B_US_RF_M1	SEQ ID NO: 1065	Len:129	Check: 5527	Weight: 1.00
Name: B_US_SF2_K	SEQ ID NO: 1066	Len:129	Check: 3616	Weight: 1.00
Name: B_US_WEAU1	SEQ ID NO: 1067	Len:129	Check: 4435	Weight: 1.00
Name: B_US_WR27	SEQ ID NO: 1068	Len:129	Check: 812	Weight: 1.00
Name: B_US_YU2_M	SEQ ID NO: 1069	Len:129	Check: 4948	Weight: 1.00
Name: BF1_BR_93B	SEQ ID NO: 1070	Len:129	Check: 3645	Weight: 1.00
Name: C_BR_92BR0	SEQ ID NO: 1071	Len:129	Check: 4262	Weight: 1.00
Name: C_BW_96BW0	SEQ ID NO: 1072	Len:129	Check: 4323	Weight: 1.00
Name: C_BW_96BW1	SEQ ID NO: 1073	Len:129	Check: 3054	Weight: 1.00
Name: C_BW_96BW1	SEQ ID NO: 1074	Len:129	Check: 3900	Weight: 1.00
Name: C_BW_96BW1	SEQ ID NO: 1075	Len:129	Check: 4051	Weight: 1.00
Name: C_ET_ETH22	SEQ ID NO: 1076	Len:129	Check: 3843	Weight: 1.00
Name: C_IN_93IN1	SEQ ID NO: 1077	Len:129	Check: 2878	Weight: 1.00
Name: C_IN_93IN9	SEQ ID NO: 1078	Len:129	Check: 4499	Weight: 1.00
Name: C_IN_93IN9	SEQ ID NO: 1079	Len:129	Check: 3994	Weight: 1.00
Name: C_IN_94IN1	SEQ ID NO: 1080	Len:129	Check: 4362	Weight: 1.00
Name: C_IN_95IN2	SEQ ID NO: 1081	Len:129	Check: 3765	Weight: 1.00
Name: CRF01_AE_C	SEQ ID NO: 1082	Len:129	Check: 4444	Weight: 1.00
Name: CRF01_AE_C	SEQ ID NO: 1083	Len:129	Check: 3760	Weight: 1.00
Name: CRF01_AE_C	SEQ ID NO: 1084	Len:129	Check: 3562	Weight: 1.00
Name: CRF01_AE_T	SEQ ID NO: 1085	Len:129	Check: 5676	Weight: 1.00



Name:	CRF01_AE_T	SEQ ID NO: 1086	Len:129	Check: 6090	Weight: 1.00
Name:	CRF01_AE_T	SEQ ID NO: 1087	Len:129	Check: 6846	Weight: 1.00
Name:	CRF01_AE_T	SEQ ID NO: 1088	Len:129	Check: 5393	Weight: 1.00
Name:	CRF01_AE_T	SEQ ID NO: 1089	Len:129	Check: 6189	Weight: 1.00
Name:	CRF01_AE_T	SEQ ID NO: 1090	Len:129	Check: 5202	Weight: 1.00
Name:	CRF02_AG_F	SEQ ID NO: 1091	Len:129	Check: 5063	Weight: 1.00
Name:	CRF02_AG_F	SEQ ID NO: 1092	Len:129	Check: 3731	Weight: 1.00
Name:	CRF02_AG_G	SEQ ID NO: 1093	Len:129	Check: 2202	Weight: 1.00
Name:	CRF02_AG_N	SEQ ID NO: 1094	Len:129	Check: 4873	Weight: 1.00
Name:	CRF02_AG_S	SEQ ID NO: 1095	Len:129	Check: 3995	Weight: 1.00
Name:	CRF02_AG_S	SEQ ID NO: 1096	Len:129	Check: 6502	Weight: 1.00
Name:	CRF03_AB_R	SEQ ID NO: 1097	Len:129	Check: 2858	Weight: 1.00
Name:	CRF03_AB_R	SEQ ID NO: 1098	Len:129	Check: 2808	Weight: 1.00
Name:	CRF04_cpx	SEQ ID NO: 1099	Len:129	Check: 3912	Weight: 1.00
Name:	CRF04_cpx	SEQ ID NO: 1100	Len:129	Check: 3700	Weight: 1.00
Name:	CRF04_cpx	SEQ ID NO: 1101	Len:129	Check: 3297	Weight: 1.00
Name:	CRF05_DF_B	SEQ ID NO: 1102	Len:129	Check: 3974	Weight: 1.00
Name:	CRF05_DF_B	SEQ ID NO: 1103	Len:129	Check: 4062	Weight: 1.00
Name:	CRF06_cpx	SEQ ID NO: 1104	Len:129	Check: 2954	Weight: 1.00
Name:	CRF06_cpx	SEQ ID NO: 1105	Len:129	Check: 1655	Weight: 1.00
Name:	CRF06_cpx	SEQ ID NO: 1106	Len:129	Check: 2327	Weight: 1.00
Name:	CRF06_cpx	SEQ ID NO: 1107	Len:129	Check: 2706	Weight: 1.00
Name:	CRF11_cpx	SEQ ID NO: 1108	Len:129	Check: 2064	Weight: 1.00
Name:	CRF11_cpx	SEQ ID NO: 1109	Len:129	Check: 1685	Weight: 1.00
Name:	D_CD_84ZR0	SEQ ID NO: 1110	Len:129	Check: 4305	Weight: 1.00
Name:	D_CD_ELI_K	SEQ ID NO: 1111	Len:129	Check: 4483	Weight: 1.00
Name:	D_CD_NDK_M	SEQ ID NO: 1112	Len:129	Check: 3024	Weight: 1.00
Name:	D_UG_94UG1	SEQ ID NO: 1113	Len:129	Check: 3298	Weight: 1.00
Name:	F1_BE_VI85	SEQ ID NO: 1114	Len:129	Check: 2602	Weight: 1.00
Name:	F1_BR_93BR	SEQ ID NO: 1115	Len:129	Check: 2572	Weight: 1.00
Name:	F1_FI_FIN9	SEQ ID NO: 1116	Len:129	Check: 3253	Weight: 1.00
Name:	F1_FR_MP41	SEQ ID NO: 1117	Len:129	Check: 2465	Weight: 1.00
Name:	F2_CM_MP25	SEQ ID NO: 1118	Len:129	Check: 2231	Weight: 1.00
Name:	F2KU_BE_VI	SEQ ID NO: 1119	Len:129	Check: 461	Weight: 1.00
Name:	G_BE_DRCBL	SEQ ID NO: 1120	Len:129	Check: 3194	Weight: 1.00
Name:	G_NG_92NG0	SEQ ID NO: 1121	Len:129	Check: 4325	Weight: 1.00
Name:	G_SE_SE616	SEQ ID NO: 1122	Len:129	Check: 2614	Weight: 1.00
Name:	H_BE_VI991	SEQ ID NO: 1123	Len:129	Check: 2347	Weight: 1.00
Name:	H_BE_VI997	SEQ ID NO: 1124	Len:129	Check: 1680	Weight: 1.00
Name:	H_CF_90CF0	SEQ ID NO: 1125	Len:129	Check: 2751	Weight: 1.00
Name:	J_SE_SE702	SEQ ID NO: 1126	Len:129	Check: 2099	Weight: 1.00
Name:	J_SE_SE788	SEQ ID NO: 1127	Len:129	Check: 2149	Weight: 1.00
Name:	K_CD_EQTB1	SEQ ID NO: 1128	Len:129	Check: 3510	Weight: 1.00
Name:	K_CM_MP535	SEQ ID NO: 1129	Len:129	Check: 2798	Weight: 1.00
Name:	N_CM_YBF30	SEQ ID NO: 1130	Len:129	Check: 3973	Weight: 1.00
Name:	O_CM_ANT70	SEQ ID NO: 1131	Len:129	Check: 9677	Weight: 1.00
Name:	O_CM_MVP51	SEQ ID NO: 1132	Len:129	Check: 8852	Weight: 1.00
Name:	O_SN_MP129	SEQ ID NO: 1133	Len:129	Check: 1678	Weight: 1.00
Name:	O_SN_MP130	SEQ ID NO: 1134	Len:129	Check: 2242	Weight: 1.00
Name:	U_CD__83C	SEQ ID NO: 1135	Len:129	Check: 9312	Weight: 1.00

SEQ ID NO	1					50
970	00BW0762_1	MAGRSGD...	NDDTLLQAVR	IIKILYQSNP	YPK.PEGTRQ	ARRNRRRRRWR
971	00BW0768_2	MAGRSEDS..	.DATLLQAVR	IIKILYQSNP	YPK.PEGTRQ	ARKNRRRRRRR
972	00BW0874_2	MAGRSGD...	SDEALLQAVR	IIKVLQSNP	YPK.PEGTRQ	ARKNRRRRRWR
973	00BW1471_2	MAGRSGD...	SDEALLQAVR	IIRILYQSNP	YPKPEG.TRQ	ARKNRRRRRWR
974	00BW1616_2	MAGRSGDS..	.DEALLQAVR	TIKILYQSNP	YPE.PKGTRQ	ARKNRRRRRWR
975	00BW1686_8	MAGRSGDS..	.DEALLQAIK	SIKILYQSNP	YPE.PQGTRQ	AQRNRRRRRWR

<u>976</u>	00BW1759_3	MAGRSGD...	NDEAVLQAIR	IIKILYQSNP	YPK.PRGTRO	AQKNRRRRWR
<u>977</u>	00BW1773_2	MAGRSGDS..	.DEALLQAVK	IIKILYQSNP	YPE.PKGTRQ	ARKNRRRRWR
<u>978</u>	00BW1783_5	MAGRSGD...	SDEAVLQAVR	IIKILYQSNP	YPK.PEGTRQ	ARKNRRRRWR
<u>979</u>	00BW1795_6	MAGRSGD...	GDAALLQAVR	IIKILYQSNP	YPK.PEGTRQ	ARKNRRRRWR
<u>980</u>	00BW1811_3	MAGRSGD...	SDEELLQVAR	IIKILYQSNP	YPE.PRGTRO	ARKNRRRRWR
<u>981</u>	00BW1859_5	MAGRSEDS..	.DAALLQAAK	IIKIIYQSNP	YPE.PKGTRQ	ARRNRRRRWR
<u>982</u>	00BW1880_2	MAGRSGD...	NDEALLQAVR	IIKILYQSNP	FPK.PEGTRQ	ARKNRRRRWR
<u>983</u>	00BW1921_1	MAGRSGD...	NDEALLQAVR	IIKILYQSNP	YPE.PQGTRQ	ARKNRRRRWR
<u>984</u>	00BW2036_1	MAGRSEDS..	.DEALLQAIR	LIKILYQSNP	YPE.PKGTRQ	ARKNRRRRWR
<u>985</u>	00BW2063_6	MAGRSGDN.D	ADAALLQAVK	IIKILYQSNP	YPK.PEGTRQ	ARKNRRRRWR
<u>986</u>	00BW2087_2	MAGRSGD...	SDEALLQAVR	IIKILYQSNP	YPK.PEGTRQ	ARKNRRRRWR
<u>987</u>	00BW2127_2	MAGRSGD...	NDEARLQVVK	IIKILYQSNP	YPK.PEGTRQ	ARKNRRRRWR
<u>988</u>	00BW2276_7	MAGRSGD...	SDEALLQAVR	IIKIIYQSNP	YPK.PEGTRQ	ARRNRRRRWK
<u>989</u>	00BW3819_3	MAGRSGD...	SDEDLLKAVR	LIKILYQSNP	YPK.PEGTRR	AQRNRRRRWR
<u>990</u>	00BW3842_8	MAGRSEDS..	.DEALLRVVR	IIKILYQSNP	YPE.PKGTRQ	ARKNRRRRWR
<u>991</u>	00BW3871_3	MAGRSGDS..	.DEALLQAIR	TIKILYQSNP	YPE.PKGTRQ	ARKNRRRRWR
<u>992</u>	00BW3876_9	MAGRSGDS..	.DEALLHAVR	TIKILYXSNP	YPE.PKGTRQ	ARKNRKRRWR
<u>993</u>	00BW3886_8	MAGRSGDS..	.DEALLQAVR	IIKILYQSNP	YPE.HQGTRQ	ARKNRRRRWG
<u>994</u>	00BW3891_6	MAGRSGDS..	.DEALLQAVR	IIKILYQSNP	YPK.PEGTRQ	ARKNRRRRWR
<u>995</u>	00BW3970_2	MAGRSGDS..	.DEALLQAVK	IIKILYQSDP	YPK.PEGTRQ	ARKNRRRRWR
<u>996</u>	00BW5031_1	MAGRSGDN..	.DEALLQAVR	IIKILYQSNP	YPK.PEGTRQ	ARKNRRRRWR
<u>997</u>	96BW01B21	MAGRSGD...	SDEALLQAVR	IIRILYQSNP	YPE.PRGTTR	ARKNRRRRWR
<u>998</u>	96BW0407	MAGRSGD...	SDEALLQAVK	IIKILYQSNP	YPK.PEEIRQ	ARKNRRRRWR
<u>999</u>	96BW0502	MAGRSGDS..	.DEALLQAVK	AIKILYQSNP	YPE.PKGTRQ	ARKNRRRRWR
<u>1000</u>	96BW06_J4	MAGRSGDS..	.DEALLQAVR	IIKILYQSNP	SPE.PKGNRQ	ARKNRRRRWR
<u>1001</u>	96BW11_06	MAGRSGD...	NDEALLQAVR	IIKILYQSNP	YPK.PEGTRQ	ARKNRRGRWR
<u>1002</u>	96BW1210	MAGRSGD...	SDEALLQAVR	IIKILYQNNP	YPK.PEGTRQ	ARKNRRRRWR
<u>1003</u>	96BW15B03	MAGRSEDS..	.DEALLHAVR	IIKILYQSNP	YPE.PKGTRQ	ARKNRRRRWR
<u>1004</u>	96BW16_26	MAGRSGDS..	.DAALLQAVR	IIKILYQSNP	YPK.PKGTRQ	ARKNRRRRWR
<u>1005</u>	96BW17A09	MAGRSGD...	NDEALLQAMG	IIKILYQSNP	YPKPEG.TRR	ARKNRRRRWR
<u>1006</u>	96BWM01_5	MAGRSGD...	SDEALLQAVR	IIKILYQSNP	YPK.PEGTRQ	ARRNRRRRWR
<u>1007</u>	96BWM03_2	MAGRSGD...	SDEALLQAVR	TIKILYQSNP	YPK.PEGTRQ	ARKNRRRRWR
<u>1008</u>	98BWMC12_2	MAGRSGDS..	.DEALLQAVR	IIKILYQSNP	QPK.PEGTRQ	ARKNRRRRWR
<u>1009</u>	98BWMC13_4	MAGRSGD...	SDEALLQAVR	IIKILYQSNS	YPK.PEGTRQ	ARKNRRRRWR
<u>1010</u>	98BWMC14_a	MAGRSGDS..	.DEALLQAVR	IIKILYQSNP	PPE.RRGIGQ	ARXNRRRRWR
<u>1011</u>	98BWM014_1	MAGRSGD...	DDERLLQAVR	IIKILYQSNP	YPS.PEGTRQ	ARRNRRRRWR
<u>1012</u>	98BWM018_d	MAGRSGD...	SDEALLQAVR	IIKILYQSNP	YPK.PEGTRQ	ARKNRRRRWR
<u>1013</u>	98BWM036_a	MAGRSGV...	SDEALLQAVK	IIKILYQSNP	YPNNPEGSQ	AQRNRRRRWR
<u>1014</u>	98BWM037_d	MAGRSGD...	SDEALLQAVR	IIKILYQSNR	YPK.PEGTRQ	AQRNRRRRWR
<u>1015</u>	99BW3932_1	MAGRSGD...	PDEALLQAIR	IIKILYQSNP	YPK.PEGTRQ	ARRNRRRRWR
<u>1016</u>	99BW4642_4	MAGRSEDSG.	.DAALLQAVR	IIKILYQSNP	YPE.PKGTRQ	ARKNRRRRWR
<u>1017</u>	99BW4745_8	MAGRSGDS..	.DEALLQAVR	IIKILYQSNP	YPK.PKETRO	ARRNRRRRWR
<u>1018</u>	99BW4754_7	MAGRSGD...	NDAALLLAVQ	TIKILLYQSNP	YPK.PEGTRQ	ARRNRRRRWR
<u>1019</u>	99BWMC16_8	MAGRSGDS..	.DEALLQAVR	IIKILYQSNP	CPE.PRGTRO	ARKNRRRRWR
<u>1020</u>	A2_CD_97CD	MAGRSGD...	PDEDLIRAIR	IIKILYQSNP	YPKPRG.TRQ	ARKNRRRRWR
<u>1021</u>	A2_CY_94CY	TAGRSD...	PDESLLQAIR	TIKILYQSNP	YPKPRG.SRQ	AQRNRRRRWR
<u>1022</u>	A2D___97KR	MAGRSGD...	PDEDLLRAVR	AIRILYQSNP	SPDPRG.SRQ	ARKNRRRRWR

<u>1023</u>	A2G_CD_97C	MAGRSGS...	TDEELLQAAR	IIKILYQSNP	YPPPEG.TRQ	ARKNRRRRWR
<u>1024</u>	A_BY_97BL0	MAGRSGG...	TDAELLTAVR	IIIXFLYQSNP	YPTPRK.TRQ	AXKNQRRRXR
<u>1025</u>	A_KE_Q23_A	MAGRSGD...	SDEELLRAVR	IIKILYKSNP	YPKPKG.SRQ	ARKNRRRRWR
<u>1026</u>	A_SE_SE659	MAGRSGP...	GDEELLKAIR	IIKILYQSNP	YPKPRG.TRQ	ARKNRRRRWR
<u>1027</u>	A_SE_SE725	MAGRSGD...	SDEELLRAVR	IIKILYQSNP	YPRPKG.SRQ	AQKNRRRRWR
<u>1028</u>	A_SE_SE753	MAGRSGN...	SDEELLRAIR	IIKILYNSNP	YPKPKG.SRQ	ARKNRRRRWR
<u>1029</u>	A_SE_SE853	MAGRSGN...	SDEELLRAIR	IIKILYQSNP	HPKPRG.SRQ	ARKNRRRRWR
<u>1030</u>	A_SE_SE889	MAGRSGD...	SDEELLKAVR	IIKILYQSNP	YPKPRG.TRQ	ARKNRRRRWR
<u>1031</u>	A_SE_UGSE8	MAGRSGD...	SDEELLKAVR	TIKILYQSNP	YPQPKG.SRQ	ARKNRRRRWR
<u>1032</u>	A_UG_92UG0	MAGRSGN...	PDEELLRAIR	IIKILYQSNP	YPEPKG.TRQ	ARKNRRRRWR
<u>1033</u>	A_UG_U455_	MARRSGN...	PDEDLLKAVR	IIKLLYQSNP	CPNPRG.SRQ	ARKNRRRRWR
<u>1034</u>	AC_IN_2130	MAGRSGD...	SDEELLQVVR	IIKILYRSNP	YPKPRG.TRQ	ARKNRRRRWR
<u>1035</u>	AC_RW_92RW	MAGRSGD...	SDETLLQAVK	IIKILYQSNP	YPK.PEGTRQ	ARRNRRRRWR
<u>1036</u>	AC_SE_SE94	MAGRSGD...	SDEALLQAVR	IIKILYQSNP	YPKPRG.TRQ	ARKNRRRRWR
<u>1037</u>	ACD_SE_SE8	MAGRSGD...	SDEDLLRAIR	IIKILYKSNP	YPKPRG.SRQ	ARKNRRRRWR
<u>1038</u>	ACG_BE_VI1	MAGRSGA...	SDEELLRAVR	IVKILYQSNP	YKPPEG.TRQ	ARRNRRRRWR
<u>1039</u>	AD_SE_SE69	MAGRSGD...	SDEXLLKAVR	LIKTLYQSNP	PPSPEG.TRQ	ARRNRRRRWR
<u>1040</u>	AD_SE_SE71	MAGRSGN...	SDEELLQAAR	IIKILYQSNP	YPKPKG.SRQ	ARKNRRRRWR
<u>1041</u>	ADHK_NO_97	MAGRSGD...	RDADLLKAVR	IIKILYQSNP	YPE.PTGSRQ	ARRNRRRRWR
<u>1042</u>	ADK_CD_MAL	MAGRSGD...	SDEDLLRAIR	LIKILYQSNP	PPNTEGTTRQ	ARRNRRRRWR
<u>1043</u>	AG_BE_VI11	MAGRTGS...	TDEELLKAVR	TIKILYQSNP	YPSSEG.SRQ	ARKNRRRRWR
<u>1044</u>	AG_NG_92NG	MAGRSGD...	ADEELLRVTR	IIKILYQSNP	YPPPEG.TRQ	ARKNRRRRWR
<u>1045</u>	AGHU_GA_VI	MAGRSGA...	SDEELLKAVR	IIKILYQSNP	FPE.PTGTRQ	ARRNRRRRWR
<u>1046</u>	AGU_CD_Z32	MAGRSGD...	SDEELLKIVR	IIKILYQGNP	YPPPEG.TRQ	ARRNRRRRWR
<u>1047</u>	AJ_BW_BW21	MAGRSGD...	NDEQLLLRAIR	IIKILYKSNP	YPKPNG.SRQ	ARRNRRRRWR
<u>1048</u>	B_AU_VH_AF	MAGRSGD...	SDEELLKTVR	LIKFLYQSNP	PPSPEG.TRQ	ARRNRRRRWR
<u>1049</u>	B_CN_RL42_	MAGRSED...	SDEELLKTVR	LIKLLYQSNP	LPSPEG.TRQ	ARRNRRRRWR
<u>1050</u>	B_DE_D31_U	MAGRSGD...	SDEELLKTVR	LIKFLYQSNP	PPSPEG.TRQ	ARRNRRRRWR
<u>1051</u>	B_DE_HAN_U	MAGRSGD...	SDEELLKTVR	LIKFLYQSNP	PPSNEG.TPT	ARRNRRRRWR
<u>1052</u>	B_FR_HXB2_	MAGRSGD...	SDEELIRTVR	LIKLLYQSNP	PPNPEG.TRQ	ARRNRRRRWR
<u>1053</u>	B_GA_OYI_M	MAGRSGD...	SDEELLKTVR	LIKFLYQSNP	PPNPEG.TRQ	ARRNRRRRWR
<u>1054</u>	B_GB_CAM1_	MAGRSGD...	SDEELLKAVR	LIKLLYQSNP	LPSSKG.TRQ	ARRNRRRRWR
<u>1055</u>	B_GB_GB8_A	MAGRSGD...	SDEDFLKTVR	FIKFLYQSNP	PPNPKG.TRQ	ARRNRRRRWR
<u>1056</u>	B_GB_MANC_	MAGRSGD...	SDEELLQTVK	LVKFLYQSNP	PPSPEG.TRQ	ARRNRRRRWR
<u>1057</u>	B_KR_WK_AF	MAGRSGD...	SDEELLRTIR	IIKFLYQSNP	LPEPEG.TRQ	ARRNRRRRWR
<u>1058</u>	B_NL_3202A	MAGRSGD...	SDEDLLKTVR	LIKFLYQSNP	PPSPEG.TRQ	ARRNRRRRWR
<u>1059</u>	B_TW_TWCYS	MAGRSGD...	SDEELLRTVR	LIKLIYQSNP	PPNPEG.TRQ	ARRNRRRRWR
<u>1060</u>	B_US_BC_L0	MAGRSGD...	SDEELLKTVR	LIKLLYQSNP	PPNPEG.TRQ	ARRNRRRRWR
<u>1061</u>	B_US_DH123	MAGRSGE...	SDEDLLNTVR	LIKLLYQSNP	LPSLEG.TRQ	ARRNRRRRWR
<u>1062</u>	B_US_JRCSF	MAGRSGD...	SDEDLLKTVR	LIKFLYQSNP	PPSNEG.TRQ	ARRNRRRRWR
<u>1063</u>	B_US_MNCG_	MAGRSGD...	SDEELLKTVR	LIKFLYQSNP	PPSSEG.TRQ	ARRNRRRRWR
<u>1064</u>	B_US_P896_	MAGRSGD...	SDEDLLKTVR	LIKFLYQSNP	PPSLEG.TRQ	ARRNRRRRWR
<u>1065</u>	B_US_RF_M1	MAGRSGD...	SDEDLLKAVR	LIKSLYQSNP	PPSPEG.TRQ	ARRNRRRRWR
<u>1066</u>	B_US_SF2_K	MAGRSGD...	SDEELLRTVR	LIKLLYQSNP	PPSPEG.TRQ	ARRNRRRRWR
<u>1067</u>	B_US_WEAU1	MAGRSGD...	SDEDLLKTVR	LIKILYQSNP	PPSPEG.TRQ	ARRNRRRRWR
<u>1068</u>	B_US_WR27_	MAGRSGD...	SDEELLQKV.	LIRFLYQSNP	PPSSEG.TRQ	ARRNRRRRWE
<u>1069</u>	B_US_YU2_M	MAGRSGD...	SDEDLLRTVR	LIKVLQYQSNP	PPSSEG.TRQ	ARRNRRRRWR

<u>1070</u>	BF1_BR_93B	MAGRSGD...	SDTELLKAVS	YIKILYQSNP	LPKPKG.TRQ	ARRNRRRRWR
<u>1071</u>	C_BR_92BR0	MAGRSGD...	SDEALLQAVR	IIKILYQSNP	YPK.PEGTRQ	ARRNRRRRWR
<u>1072</u>	C_BW_96BW0	MAGRSGD...	SDEALLQAVR	IIKILYQSNP	YPK.PEGTRQ	AWNRRRRWR
<u>1073</u>	C_BW_96BW1	MAGRSGD...	NDEALLQAVR	IIKILYQSNP	YPK.PEGTRQ	ARKNRRRRWR
<u>1074</u>	C_BW_96BW1	MAGRSGD...	SDEALLQAVR	IIKILYQNNP	YPK.PEGTRQ	ARKNRRRRWR
<u>1075</u>	C_BW_96BW1	MAGRSEDS..	.DEALLHAVR	IIKILYQSNP	YPE.PKGTRQ	ARKNRRRRWR
<u>1076</u>	C_ET_ETH22	MAGRSGD...	SDEELLKAVR	IIKILYQSNP	YPT.PEGTRQ	ARRNRRRRWR
<u>1077</u>	C_IN_93IN1	MAGRSGDS..	.DEALLQAVR	IIKILYQSNP	YPE.PKGTRQ	ARKNRRRRWR
<u>1078</u>	C_IN_93IN9	MAGRSGDS..	.DEELLKAVR	IIKILYQSNP	YPE.PRGTRQ	ARKNRRRRWR
<u>1079</u>	C_IN_93IN9	MAGRSGDS..	.DEALLRAVR	IIKILYQSNP	YPE.PRGTRQ	ARKNRRRRWR
<u>1080</u>	C_IN_94IN1	MAGRSGDS..	.DEALLKAVR	IIKILYQSNP	YPE.PRGTRQ	ARKNRRRRWR
<u>1081</u>	C_IN_95IN2	MAGRSGDS..	.DEALLKAVR	IIKILYQSNP	YPE.PRGTRQ	ARKNRRRRWR
<u>1082</u>	CRF01_AE_C	MAGRSGN...	TDEDLLQAVR	IIKILYQSNP	YPPPEG.TRQ	ARKNRRRRWR
<u>1083</u>	CRF01_AE_C	MAGRSGS...	TDEDLLRTVR	IIKILYQSNP	YPPAEG.TRQ	ARKNRRRKWR
<u>1084</u>	CRF01_AE_C	MAGRSGS...	TDEELLRAAR	AIKILFQSNP	YPSSEG.TRQ	ARKNRRRRWR
<u>1085</u>	CRF01_AE_T	MAGRSGS...	TDEELLRAVR	IINILYQSNP	YPSSEG.TRQ	TRKNRRRRWR
<u>1086</u>	CRF01_AE_T	MAGRSGS...	TDEELLRAVR	IIKILYQSNP	YPSSEG.TRQ	TRKNRRRRWR
<u>1087</u>	CRF01_AE_T	MAGRSGS...	TDEELLRAVR	IINILYQSNP	YPSSEGTRQ	TRKNRRRRWR
<u>1088</u>	CRF01_AE_T	MAGRSGS...	TDEELLRAVR	IIKLLYESNP	PPSSEG.TRQ	TRKNRRRRWR
<u>1089</u>	CRF01_AE_T	MAGRSGS...	TDEELLRAVR	IIKILYQSNP	FPSSEG.TRQ	TRNRRRRWR
<u>1090</u>	CRF01_AE_T	MAGRSGS...	TDEELLRAVK	IINILYQSNP	LPSSEG.SRQ	TRKNRRRRWR
<u>1091</u>	CRF02_AG_F	MAGRSGD...	ADEELLRVVR	IIKILYQSNP	YPPPEG.TRQ	TRKNRRRRWR
<u>1092</u>	CRF02_AG_F	MAGRSGD...	ADEELLRVVR	IVKILYQSNP	YPPPEG.TRQ	ARKNRRGRWR
<u>1093</u>	CRF02_AG_G	MAGRSGD...	ADEELLRVIR	IIKILYQSNP	YPKPEG.TRQ	ARRNRRRRWR
<u>1094</u>	CRF02_AG_N	MAGRSGD...	ADEELLRAVR	IIKILYQSNP	YPPPEG.TRQ	TRKNRRRRWR
<u>1095</u>	CRF02_AG_S	MAGRSGN...	ADEELLRAVR	TIKILYQSNP	YPPPEG.TRQ	ARKNRRRRWR
<u>1096</u>	CRF02_AG_S	MAGRSGD...	ADEGLLRAVR	IIRILYQSNP	YPPPEG.SRQ	ARRNRRRRWR
<u>1097</u>	CRF03_AB_R	MAGRSGD...	SDEELLKTIR	LIKFLYQSNP	PPSPEG.TRQ	ARRNRRRRWR
<u>1098</u>	CRF03_AB_R	MAGRSGD...	SDEDLLKTIR	LIKFLYQSNP	PPNPEG.TRQ	ARRNRRRRWR
<u>1099</u>	CRF04_cpx_	MAGRSGN...	IDEDLFKAAR	AIKILYQSNP	YPNNPTGTRQ	ARRNRRRRWR
<u>1100</u>	CRF04_cpx_	MAGRSG....	SNEDLLGSVG	IVKILYQSNP	YPN.PTGTRK	ARRNRRRRWR
<u>1101</u>	CRF04_cpx_	MAGRSGS...	TDEDLLKAVG	IVKILYQSNP	YPNNTAGTRQ	ARRNRRRRWR
<u>1102</u>	CRF05_DF_B	MAGRSGD...	RDEDLLKAVR	LIKILYQSNP	LPSPEG.TRQ	ARRNRRRRWR
<u>1103</u>	CRF05_DF_B	MAGRSGD...	RDEDLLKAVR	LIKFLYQSNP	PPRPEG.TRQ	ARRNRRRRWR
<u>1104</u>	CRF06_cpx_	MAGRSGD...	SDDRLLLA VR	IIKILYQSNP	YPKPNG.SRQ	ARRNRRRRWR
<u>1105</u>	CRF06_cpx_	MAGRSGD...	NDEQLLLAVR	IIKILYQNNP	YPKPNG.GRQ	ARRNRRRRWR
<u>1106</u>	CRF06_cpx_	MAGRSGD...	NDEQLLLAVR	TIKILYQSNP	YPKPSG.SRQ	ARRNRRRRWR
<u>1107</u>	CRF06_cpx_	MAGRSGD...	SDEQLLWAVR	VIKILYQSNP	YPKLSG.SRQ	ARRNRRRRWR
<u>1108</u>	CRF11_cpx_	MAGRSGD...	NDEQLLTAVK	IIKILYQSNP	QPNPTG.SRQ	ARRNRRRRWR
<u>1109</u>	CRF11_cpx_	MAGRSGD...	SDAQLLAAAR	IIKILYQSSP	YPKPAG.TRQ	ARRNQRRWR
<u>1110</u>	D_CD_84ZR0	MAGRSGD...	SDEDLLTAVR	LIKILYQSNP	PPSPEG.TRQ	ARRNRRRRWR
<u>1111</u>	D_CD_ELI_K	MAGRSGD...	SDEDLLKAVR	LIKFLYQSNP	PPSPEG.TRQ	ARRNRRRRWR
<u>1112</u>	D_CD_NDK_M	MAGRSGD...	SDENLLKAIR	LIKFLYQSNP	PPSPEG.TRQ	ARRNRRRRWR
<u>1113</u>	D_UG_94UG1	MAGRSGD...	RDEELLQAVR	LIKILYQSNP	PPSPEG.TRQ	ARRNRRRRWR
<u>1114</u>	F1_BE_VI85	MAGRSGD...	SDTELLKAVK	CIKILYQSNP	YPKPEG.TRQ	ARRNRRRRWR
<u>1115</u>	F1_BR_93BR	MAGRSGD...	SDQELLKAVR	YIKILYQSNP	YPKPEG.TRQ	ARRNRRRRWR
<u>1116</u>	F1_FI_FIN9	MAGRSGD...	SDTELLKAVK	YIKILYQSNP	YSPDG.TRQ	ARRNRRRRWR

1117	F1_FR_MP41	MAGRSGD...	NDEELLRAVR	AIKILYQSNP	YPKPEG.TRQ	ARRNRRRRWR
1118	F2_CM_MP25	MAGRSGD...	RDEELLKAVR	YIKILYQSNP	YPKLEG.TRK	ARRNRRRRWR
1119	F2KU_BE_VI	MAGRSGD...	SDEELLKAVR	LIKILYQSNP	YPKPEG.TRQ	ARRNRRKRWR
1120	G_BE_DRCBL	MAGRSGS...	TDEELLTAVR	IIKLLYQSNP	SPPPEG.TRQ	ARRNRRRRWR
1121	G_NG_92NG0	MAGRSGD...	PDEELLRAVR	IIKTLYQSNP	YPSPEG.TRQ	ARKNRRRRWR
1122	G_SE_SE616	MAGRSGS...	TDEELLRAVK	AIKILYQSNP	YPPPEG.TRQ	ARRNRRRRWR
1123	H_BE_VI991	MAGRSGD...	NDEGLLRACR	IIRLLYQSNP	YPE.PAGTRQ	AQRNRRRRWR
1124	H_BE_VI997	MAGRSGA...	GDEQLPQVCK	IIKIIYQSNP	YPE.PAGTRQ	ARRNRRRRWR
1125	H_CF_90CF0	MAGRSGA...	SDTELLQVCK	IIKILYQSNP	CPE.PTGTRQ	ARRNRRRRWR
1126	J_SE_SE702	MAGRSGD...	NDDQLLLA VR	IIKILYQSNP	YSKPNG.SRQ	ARRNRRRRWR
1127	J_SE_SE788	MAGRSGD...	SDDQLLLA VR	LIKILYQSNP	YPKPNG.SRQ	ARRNRRRRWR
1128	K_CD_EQTB1	MAGRSGD...	SEQQLLTPVR	IIKILYQSNP	YPKPEG.TRQ	ARRNRRRRWR
1129	K_CM_MP535	MAGRSGD...	PDEQLLTTVR	TIKILYESNP	YPNLEG.SRQ	TRRNRRRRWR
1130	N_CM_YBF30	MAGRSGVN..	.DEELLRAVR	VIKILYQSNP	YPNSKG.TRQ	ARRNRRRRWR
1131	O_CM_ANT70	MAGRSED...	.DQ.LLQAIQ	IIKILYQSNP	QPSPRG.SRN	ARKNRRRRWR
1132	O_CM_MVP51	MAGRSEE...	.DQQLLQAIQ	IIKILYQSNP	CPTPAG.SRN	ARKNRRRRWR
1133	O_SN_MP129	MAGRSDG...	.DQPLLRAIQ	IIKILYQSNP	HTSPTG.SRS	ARRNRRRRWR
1134	O_SN_MP130	MAGRSDG...	.DQPLLRAIQ	IIKILYQSNP	HPSPTTGSTS	ARRNRRRRWR
1135	U_CD___83C	MAGRSGE...	SDEELLRAVR	IIKILYQSNP	PPNPEG.TRQ	ARKNRRRRWR

	51				100
00BW0762_1	ARQRQIHSIS	ERILSTVLGR	PAEPVPFQLP	PIERLHIGCS	ESGGTSGTQQ
00BW0768_2	ARQRQINSIS	ERILSTCLGR	PAEAVPLQLP	PIERLHIGCN	ESGGTSGTQQ
00BW0874_2	ARQRQINSIS	GRILSACLGR	PTEPVPFQLP	PIERLHINCS	ENGGTSGTQQ
00BW1471_2	ARQRQIRAI	ERILDTCLGR	LTEPVHLPLP	PLERLHLDCS	EDCEPTGTEQ
00BW1616_2	ARQRQIHSIS	ERILSACLGR	SAEPVPFQLP	PIERLHIDCS	ESSGNSG...
00BW1686_8	ARQRQIHSIS	ERILSTCLGR	SAEPVPLQLP	PIERLHIDCS	ESGGTFTGTQQ
00BW1759_3	ARQRQIDSIS	ERVLSTVLGR	PTEPVPFQLP	PIERLDIGDS	ESGGTSGTER
00BW1773_2	ARQRQIREIS	QRILSTYLGR	PAEPVPLLLP	PIERLHIDCS	ESGGTSGTQQ
00BW1783_5	ARQRQIHSIS	ERILSTCLGR	STEPVPFQLP	PIERLHIGDS	KSSGTSGTQQ
00BW1795_6	ARQRQIHSIS	ERILSTCLGR	PAEPVPFLLP	PLERLHIGDS	ESSGTSGTQQ
00BW1811_3	ARQRQIREIS	ERILCTCLGR	STEPVPFLLP	PIERLHIGDS	EGSGTSGTQQ
00BW1859_5	ARQRQIHTIS	ERILSTCLGR	PAEPVPLQLP	PIERLHIDCS	ESSGTSGTQQ
00BW1880_2	ARQRQIHSIS	ERILSTCLGR	STEPVPFQLP	PIERLHIGDS	ESSGTSGTQR
00BW1921_1	ARQRQINSIS	ERILTTCLGR	SEEPVPLQLP	PIERLNIGGS	ESSGTSGTQQ
00BW2036_1	ARQRQIDSIS	ARILSTCLGR	PAEPVPFQLP	PIERLNIGDN	ESGGTSGTQQ
00BW2063_6	ARQKQIHSIS	ERILSTCLGR	SEEPVPLLLP	PIERLRIGDS	ESSGTSGTQQ
00BW2087_2	ARQREIHSIS	ERILTTVLGR	SAEPVPFQLP	PIERLNINCS	EGSGTSGTQQ
00BW2127_2	ARQRQIHSIS	ERILSTCLGR	STEPVPFQLP	PIERLNIGDS	EGSGTSGTQR
00BW2276_7	ARQRQIHTIS	ERILSTCLGR	PAEPVPLQLP	PIERLYIGDS	EGGGTSGTQQ
00BW3819_3	ARQRQIHSIS	ERILSACLGR	PAEPVPFQLP	PIERLNIGDS	EGDRTYGTQQ
00BW3842_8	ARQRQIDSIS	GRLLSTCLGR	SAEPVPLQLP	PIERLNIGDS	ESGGTSGTQQ
00BW3871_3	ARQRQINSIS	ERILSTCLGR	SAEPVPLQLP	PIERLHIDCS	ESGGTSGTQQ
00BW3876_9	ARQKQIHSIS	ERILSACLGR	SAEPVPLQLP	PIERLHIGGS	ESGGTSGTQQ
00BW3886_8	ARQRQINSIT	ERILSDCLGR	SAEPVPLQLP	PIERLHIVDS	ESGGTSGTQQ
00BW3891_6	ARQRQIHSL	ERILSTCLGR	SAEPVPLQLP	PLERLHIGDS	ESGGTSGTQQ
00BW3970_2	ARQKEIHSLS	ERILSTCLGR	PAEPVPLQLP	PLERLHIDCS	ESGGTSGTQ.
00BW5031_1	ARQRQIHSIG	ERILSTCLGR	SAEPVPLQLP	PLERLHIDCS	ESSGTPGTQQ
96BW01B21	ARQRQIHSIS	ERILTTCLGR	FTEPVPFQLP	PIERLHIGDS	ESGGTSGTQQ
96BW0407	ARQRQIHSIS	ERILSTCLGR	PTEPVPFQLP	PIERLHIDCS	ESSGASGTQR
96BW0502	ARQRQIHSL	ERILSACLGR	PAEPVPFQLP	PIERLHIDCS	KSVGTSG...
96BW06_J4	ARQRQINSIS	ERILSTCLGR	SAEPVPFQLP	PIERLHIGGS	ESGGTSGTQQ
96BW11_06	TRQKQINSIS	ERILSTCLGR	SAEPVPFLLP	PIERLHISDS	ESSGTSGTQQ
96BW1210	ARQRQIHSIS	ERILSTCLGR	PAEPVPLQLP	PIERLHIGGS	ENSGTTGTQQ
96BW15B03	ARQRQIDSIS	TRILSTCLGR	PEEPVPFQLP	PIERLNIGDS	ESGGTSGTQQ

96BW16_26	ARQRQIRAI	ARIFSACLGR	PAEPVPLQLP	PIERLHIGSS	ESGGTSGTQ.
96BW17A09	ARQRQIHSIS	ERILSTCLGR	PTEPVHLPLP	PLERLHLD	EDCEPTGTEQ
96BWM01_5	ARQRQINSIS	ERILSACLGR	PAEPVPFLLP	PIERLHIGDS	ESSGTSGTQQ
96BWM03_2	ARQRQIHSIS	ERILSACLGR	PTEPVPFQLP	PIERLSIGDS	ESSGTSGTQQ
98BWMC12_2	ARQKHIHSIS	ERILSDCLGR	SAEPVPLQLP	PIERLHIDCS	ESGGTSGTQQ
98BWMC13_4	ARQRQINSIS	ERILSTCLGR	STEPVPFLLP	PIERLHIGDS	ESSGTSGTQQ
98BWMC14_a	ARQTQINSLS	ERIVSTCLGR	PAERAPFQLP	PIEKLHIDCS	ESGGTPG...
98BWM014_1	ARQRQIRALS	ERILSTVLGR	PTEPVPFQLP	PIERLNINCS	ESSGTSGTQQ
98BWM018_d	ARQRQINSIS	ERILSTCLGR	PAEPVPFQLP	PIERLHIDCS	ESSGTSGTQH
98BWM036_a	ARQRQIHSIS	ERILSSCLGR	PTEPVPFQLP	PIERLHIGDS	ESGGTYGTQQ
98BWM037_d	ARQRQIHSIS	ERILSTCLGR	SAEPVPLQLP	PIERLHIADS	KGGGTSGIQQ
99BW3932_1	ARQRQIHSIS	ERILFTCLGR	STEPVPFQLP	PIERLNIGDS	ESGGTYGTLQ
99BW4642_4	ARQRQISSLS	ERILSTCLGR	SAEPVPLQLP	PIERLHIDCS	ESSGTSGTQQ
99BW4745_8	ARQNQIRAI	KRILSTCLGR	PAEPVPLQLP	PLERLHIGDS	ESGGTSGTQQ
99BW4754_7	ARQRQIHSIS	ERILSNCLGR	PAEPVPFQLP	PIEGLHIDCN	ESSGTSGTQQ
99BWMC16_8	ARQRQIDSIS	QRILSDCLGG	PAEPVSFQLP	PIERLNIDCN	ESGGTSGTQQ
A2_CD_97CD	ARQRQIDSIS	ERILSTCLGR	PTEPVPLQLP	PLERLHLD	EDCGTCGTQQ
A2_CY_94CY	ARQRQIDSIS	ERVLRTCLGR	PTEPVPLQLP	PLERLHIDCS	EDCGTSGTLQ
A2D_97KR	ARQRQIRAI	ERILSACLGR	PTEPVPLQLP	PLERLHLD	EDCGTSGTQQ
A2G_CD_97C	ARQRQIREIS	ERILSTCLGR	PTEPVPLLLP	PLERLHLD	EDGGTAETQQ
A_BY_97BL0	ARQRQINSIS	KRIFSTCXGR	SXEPVSLQLP	PIERLHLD	EDCXTSETQQ
A_KE_Q23_A	ARQRQIDSIS	ERILSTCLGR	PTEPVPLQLP	PLERLHLD	EDCGTSGTQQ
A_SE_SE659	ARQRQIDSIS	ERILSACLGR	STEPVPLQLP	PLERLNLD	EDCGTSGTQQ
A_SE_SE725	ARQRQIDSIS	ERILSTCLGR	SEEPVPLQLP	SLETLHLD	DDCGTSGTQQ
A_SE_SE753	ARQRQIDSIS	ERILNACLGG	STEPVPLQLP	PLERLNLD	EDCGTSGTQQ
A_SE_SE853	ARQRQIDSIS	ERILSTCLGR	SAEPVPLQLP	PLEGLHLD	EDCGTSGTEG
A_SE_SE889	ARQKQIDSL	ERILSTCLGR	PQEPVPLLLP	PIERLHLD	EDCGTSGTQQ
A_SE_UGSE8	ARQRQIDSL	QRILSACLGR	SEEPVPLQLP	PLERLHLD	EDCGTSGTG.
A_UG_92UG0	ARQRQIDTSL	ERVLSTCLGR	PAEPVPLQLP	PIERLHLD	EDCGTSGTQQ
A_UG_U455_	ARQRQIDSL	ERILSDCLGR	PAEPVPLQLP	PIERLRLD	ESCGTSGTQQ
AC_IN_2130	ARQRQIDSIS	ERILSTFLGR	SAEPVPLQLP	PLERLHLD	EDCGTSGTQQ
AC_RW_92RW	ARQRQIHSIS	ERILSTCLGR	PTEPVPFQLP	PIERLTIDCS	EDGGTSGTQQ
AC_SE_SE94	ARQRQIDSIS	ERILSTCLGR	SAEPVPLQLP	PLERLHLD..	.....SGTQQ
ACD_SE_SE8	ARQRQIDSIS	QRILSTCLGR	SEEPVPLQLP	PLERLNLD	EDCGTSGTQQ
ACG_BE_VI1	ARQRHIHSL	ERILCTCLGR	SEEPVHLPLP	PLEGLTLDCN	ESSGTSGTEG
AD_SE_SE69	ARQRQINSIG	ERILSTYLGR	SQEPVPLQLP	PLERLTLNCI	EDCGTSGTQQ
AD_SE_SE71	ARQNQIDSIS	KRILSNCLGR	PAEPVPLQLP	PLERLNLD	KDCGTSGTQQ
ADHK_NO_97	ARQXQIHSIG	ERVLATCMGR	PAEPVPLQLP	PLERLTLDS	EDCDIAGKQG
ADK_CD_MAL	ARQRQINSIG	ERILSTYLGR	PEEPVPLQLP	PLERLTLNCN	EDCGTSGTQQ
AG_BE_VI11	ARQRHIQAI	RRILDACLGR	PAEPVPLQLP	PLERLSLD	KDIGTSGTQR
AG_NG_92NG	ARQRQISALS	ERILSTCLGR	PAEPVPLQLP	PIERLSLD	EDSRTPETQQ
AGHU_GA_VI	ARQKQIHSIG	ERVLATYLGR	PAEPVPLQLP	PLERLTLDCS	EDCGTSGEKG
AGU_CD_Z32	ARQRQIHSIG	ERILTTCLGR	STEPVPFLLP	PIERLRIDCS	EDRGDSDPQG
AJ_BW_BW21	ARQNQIDSIS	ERILSTCLGR	PTEPVPFQLP	PIERLRIDCS	EDCGHSGTQQ
B_AU_VH_AF	ARQRQIRQIS	GWILSTYLGR	PAEPVPLQLP	PLERLTLDCS	KDCGTSGTQQ
B_CN_RL42_	ARQRQIREIS	DRILVTYLGG	STEPVPLQLP	PLERLTLDCS	KDCGTSGTQQ
B_DE_D31_U	QRQRQIQSIS	ERILSTYLGR	PEQPVPLPLP	PLERLTLDCS	EDCGTSGTQQ
B_DE_HAN_U	ERQRQIRSIS	ERILSTFLGR	PAEPVPLQLP	PLERLTLDCS	EDCGNSGTQQ
B_FR_HXB2_	ERQRQIHSIS	ERILGTYLGR	SAEPVPLQLP	PLERLTLDCN	EDCGTSGTQQ
B_GA_OYI_M	ERQRQIRKIS	GWILSTYLGR	SAEPVPLQLP	PLERLNLD	EDCGTSGTQQ
B_GB_CAM1_	ERQRHIRAIS	NWILSTHLGR	PAEPVPLQLP	PLERLTLDCS	KDCGTSGTQQ
B_GB_GB8_A	ARQRQIHQIG	EWILSAFLGR	PAEPVPLQLP	PIERLTLDCD	EDCGTSGTQQ
B_GB_MANC_	GRQRQIQSLS	AWILSTRLGR	STQPVPLQLP	PLERLTLDCS	EDCGTSGTQQ
B_KR_WK_AF	RRQWWIQSLS	GWILNTHLGR	PAEPVPLQLP	PLERLTLDCN	EBCGTSGTQQ
B_NL_3202A	ERQRQIRSIS	ERILSTYLGR	SAEPVPLQLP	PLERLTLDCD	EDCGTSGTQQ
B_TW_TWCYS	ERQRQIRTIS	GWILSNYLGR	PAEPVPLQLP	PLERLTLDCD	EDCGTSGTQQ
B_US_BC_L0	ERQRQIRSIS	ERILSTFLGR	SAEPVPLQLP	PLERLNLD	EDCGTSGTQQ
B_US_DH123	QRQRQIQSIS	GWILSNHLGR	PADAVPLQLP	PLERLTLDCN	EDCGTSGTQQ
B_US_JRCSF	ERQRQIRTIS	ERILSTYLGR	PAEPVPLQLP	PLERLTLDCN	EDCGTSGTQQ
B_US_MNCG_	ERQRHIRSIS	AWILSNYLGR	PAEPVPLQLP	P.QRLTLDCS	EDCGTSGTQQ

B_US_P896_	ERQRQIRSIS	ERILGTFLGR	FEEPVPPLPLP	PLEKLTLDNC	EDCGTSGTQG
B_US_RF_M1	ERQRQIRRC	EWILDTYLGR	SVDPVQLQLP	PLERLTLDSS	EDCGTSGTQG
B_US_SF2_K	ERQRQIRSIS	GWILSTYLGR	SAEPVPLQLP	PLERLTLDSC	EDCGNSGAQG
B_US_WEAU1	ERQRQIRKIS	GWILNTYLGR	PTEPVPLPLP	PLDRLTLDCK	EDCGTSGTQG
B_US_WR27_	.RQRQIQSL	AWIISTHLGR	PAEPVPLQLP	PLERLTLDSC	EDCGTSGTQG
B_US_YU2_M	ERQRQIRSIS	GWLLSNYLGR	PTEPVPFQLP	PLERLTLDNC	EDCGTSGTQG
BF1_BR_93B	ARQRQIREIS	ERILSSCLGR	PEEPVPLQLP	PLERLHINCS	EDCGQGTEEG
C_BR_92BR0	ARQRQIHSIS	ERILSTCVGR	PAEPVPFQLP	PIERLNINCS	ESGGTSGTQG
C_BW_96BW0	ARQRQIHSIS	ERILSTCLGR	PTEPVPLQLP	PIERLHIDCS	ESSGASGTQG
C_BW_96BW1	ARQKQINSIS	ERILSTCLGR	SAEPVPFLLP	PIERLHISDS	ESGGTSGTQG
C_BW_96BW1	ARQRQIHSIS	ERILSTCLGR	PAEPVPLQLP	PIERLHIGGS	ENSGTTGTQG
C_BW_96BW1	ARQRQIDSIS	TRILSTCLGR	PEEPVPFQLP	PIERLNIGDS	ESGGTSGTQG
C_ET_ETH22	ARQRQIHTLS	ERILSNFLGR	PAEPVPLQLP	PLERLNLDSC	EDSGTSGTQG
C_IN_93IN1	ARQRQIHSIS	ERILSTCLGR	STEPVPLQLP	PIERLHIGGS	ESGGTSGTQG
C_IN_93IN9	ARQRQIHSIS	ERILSACLGR	PAEPVPLQLP	PLERLHISGS	ESGGTSGTQG
C_IN_93IN9	ARQKQIHSLS	ERILSTCLGR	SAEPVPLQLP	PLERLHISGS	ESGGTSGTQG
C_IN_94IN1	ARQRQIHSIS	ERILSACLGR	PAEPVPLQLP	PIERLHISGS	ESGGTSGTQG
C_IN_95IN2	ARQRQIHSIS	ERILSTFLGR	PAEPVPLQLP	PIERLHISGS	ESAGTSGTPQ
CRF01_AE_C	RRQRQIHSLS	ERILVACVGR	STEPVPLQLP	PLERLHIDCS	EDCGTSGTQG
CRF01_AE_C	ARQRQIHKIG	ERILSTCLGR	SPEPVPLQLP	PLERLHLDSC	EDCGTSGTQG
CRF01_AE_C	ARQRQIRALS	ERILSACLGR	SAEPVPLQLP	PLERLHLDSC	EDCGTSGTQG
CRF01_AE_T	ARQRQIRAIS	ERILITCLGR	STEPVPLQLP	PLERLHLDNC	EDCGTSGTQG
CRF01_AE_T	ARQRQIRAIS	ERILNACVGR	STEPVPLQLP	PLERLHLDSC	EDCGTSGTQG
CRF01_AE_T	ARQRQIRAIS	ERILSTCLGR	STEPVPLQLP	PLERLHLDSC	EDCGTSGTQG
CRF01_AE_T	ARQRQIREIS	ERILSSCVGR	STEPVPLPLP	PLERLHLDSC	EDCGTSGTQG
CRF01_AE_T	ARQRQISALS	ERILSTCLGR	STEPVPLQLP	PVERLNLDSC	EDGGTSGTQG
CRF01_AE_T	ARQRQISALS	ERILSACLGR	STEPVSLPLP	PLERLHLDSC	EDCGTSGTQG
CRF02_AG_F	ARQRQIRALS	ERFLSTCLGR	SAEPVPLQLP	PIERLCLDSC	EGCGTSGTQG
CRF02_AG_F	ARQRQIRALS	QRILSTCLGR	SAEPVPLQLP	PLERLCLDSC	EGCGTSGTQG
CRF02_AG_G	ARQRQIHSLS	ERILSTCLGR	PEEPVSFQLP	PLERLNLDSC	EDCGNSGTQS
CRF02_AG_N	ARQRQIRALS	ERILSTCLGR	SAEPVPLQLP	PIERLNLDSC	EDCGTSGTQL
CRF02_AG_S	ARQRQIRALS	ERILSTCLGR	SAEPVPLQLP	PIERLRLDSC	EDCGTSGTQG
CRF02_AG_S	ARQRQVRAIS	ERILSTCLGR	PAEPVPLPLP	PIERLCLDSC	EDSGTSGTQG
CRF03_AB_R	ERQRHIHSIS	EQILSTYLGR	PEEPVLLHLP	PLERLTLDSC	EDCGTSGTQG
CRF03_AB_R	ERQRHIHSIS	QRILSTYLGR	PEEPVPLHLP	PLERLTLDSC	EDCGTSGTQG
CRF04_cpx_	ARQKQIHSLS	ERILATYLGR	PAEPVPLQLP	PLEKLTLNCS	EDCGTSGDKG
CRF04_cpx_	ARQKQIHSIS	ERVLATYLGR	PAEPVPLQLP	PLEKLTLNCS	EDCGTSGEKG
CRF04_cpx_	ARQNRIHSIS	ERILAACLGR	PAEPVPLQLP	PIEKLTLDSC	EDCGTSGDKG
CRF05_DF_B	ARQRQINSIG	ERLLSTYLGR	SEEPVPLQLP	PLERLNLNCS	EDCGTSGTQG
CRF05_DF_B	ARQRQIRSIA	DRIVDTYLGR	PEEPVPLQLP	PLERLNLNCS	EDCGTSGTQG
CRF06_cpx_	ARQNQIDSIS	ERVLTCLGR	SAEPVPLQLP	PIERLRLDSC	EDCGNSGTQG
CRF06_cpx_	ARQNQIDSIS	ERILSTCLGR	PTEPVPFQLP	PIERLRLDSC	EDCGNSGTQG
CRF06_cpx_	ARQKQIDSIS	ERILSTCLGR	SAEPVPLQLP	PIERLRLDSC	EDCGNSGTQG
CRF06_cpx_	ARQNQIDSIS	ERILSSCLGR	SEEPVPLQLP	PIERLRLDCT	EDCGNSGTQG
CRF11_cpx_	ARQNQIDSIS	QRILSDCLGR	SEEPVPLQLP	PIERLHLDSC	EDCGNPGTQG
CRF11_cpx_	ARQNQLHSIS	QRILSTCLGR	SEEPVPLPLP	PIERLHLDSC	EDCGNSGTQG
D_CD_84ZR0	ARQRYIHSIG	ERILSTYLGR	SEEPVPLQLP	PLERINLNCS	EDCGTSGTQG
D_CD_ELI_K	ARQRQIREIA	ERILGTYLGR	PAEPVPLQLP	PLERLNLNCS	EDCRTSGTQG
D_CD_NDK_M	ARQRQIHSIG	ERIICTFLGR	PEEPVPLQLP	PLERLNLNCS	EDCGTSGTQG
D_UG_94UG1	ARQRQIHSIG	ERIISTYLGR	FEEPVPLQLP	PLERLNLNCS	EDCGTSGTQG
F1_BE_VI85	ARQRQIRALS	DRILSSCLGR	SEEPVPLQLP	PLERLHINCS	EDCGQGPEEG
F1_BR_93BR	ARQRQIREIS	DRILSSCLGR	PAEPVPLQLP	PLERLHINCS	EDCGQGAEEG
F1_FI_FIN9	ARQRQIRALS	ERILSSCLGR	LEEPVPLQLP	PLERLHINCS	EDCGQGTEEG
F1_FR_MP41	ARQKQIRSIS	ERILVACLGR	PEEPVPLQLP	PLERLHINCS	KDCGQGTNEG
F2_CM_MP25	ARQRQIHQIS	ERILSTCLGR	LQEPVRLQLP	LLEKLHINCS	EDCGQGTEKG
F2KU_BE_VI	ARQRQIHSIS	QRILSTCLGR	PAEPVPFQLP	PLERLNLDSC	EDSREGAEEG
G_BE_DRCBL	ARQRQIHSIS	ERILSTCLGR	PEEPVPLQLP	PLERLHLDSC	EDGGTSGTQG
G_NG_92NG0	ARQRQIHSIS	ERILSACLGR	PAEPVPFQLP	PLEGLSLDSC	KDGGTSGTQG
G_SE_SE616	ARQRQISALS	ERILTAYLGR	PAEPVPLQLP	PLERLHLDSC	EDSGTSGTQG
H_BE_VI991	ARQRQIHSIG	ERVLATCLGG	PAEPVPLQLP	PLERLTLDSC	EDCGTSGEKG

H_BE_VI997	ARQRQIRAI	ERILTDCLGR	PPEPVPLQLP	PLERLTLDN	KDCGTSGEKG
H_CF_90CF0	ARQRQIREIS	ERILTSCLGR	PPEPVTQLP	PLERLTNCS	EDCGTSGEKG
J_SE_SE702	ARQNQIDSI	ERILSSCLGR	PAEPVPLQLP	PIERLRLDCS	EDCGNSGTQG
J_SE_SE788	ARQNQIDSI	ERIPSSCLGR	PAEPVPLQLP	PIERLRLDCS	EDCGNSGTQG
K_CD_EQTB1	ARQRQIREIS	QRLSSCLGR	STEPVPLQLP	PLERLSLNC	EDSGQGTEGE
K_CM_MP535	ARQKQISSIS	ERLLSACLGR	SAEPVPLQLP	PIEKLNLNC	EDPGKGTEGG
N_CM_YBF30	ARQRQIRAI	ERILSSCLGG	PPEPVDLPLP	PLDRLTLDT	EDSGTPGTES
O_CM_ANT70	RRQAQVDTLA	ARVLATVVHG	PQNNNIVDLP	PLEQLSIRDP	EGDQLSEAWT
O_CM_MVP51	RRQAQVDSL	TRILATVVHG	SQDNNLVDLP	PLEQLNIRDP	EADRLPGTGT
O_SN_MP129	TRHAHVDTLA	ARILATVVHG	PQDNNLVELP	PLEQLSIRDP	DGDQPSGTWT
O_SN_MP130	KRQAQIDTLA	ARILATVVHG	PQDNNLVELP	PLEQLSIRDP	DGDQPSGTWT
U_CD___83C	RRQQQIRSI	ERILSTCLGR	PAEPVHLQLP	PLERLNLDCS	....KGTATG

	101		129
00BW0762_1	PQGTPEGMG	P.....	.....
00BW0768_2	SQGTSEGVGS	P.....	.....
00BW0874_2	SQGTTEGVGN	P.....	.....
00BW1471_2	SQGITEGVGS	P.....	.....
00BW1616_2	....TQGVGS	P.....	.....
00BW1686_8	SQGATEGVGN	P.....	.....
00BW1759_3	.....VGS	P.....	.....
00BW1773_2	SQGTTEGVGS	P.....	.....
00BW1783_5	SQGTTEGVGN	P.....	.....
00BW1795_6	SQGTPEGVGN	P.....	.....
00BW1811_3	SQGTPEGVGN	P.....	.....
00BW1859_5	SQGTTEGVGS	P.....	.....
00BW1880_2	SQGTPEGVGN	P.....	.....
00BW1921_1	SQGTTEGVGN	P.....	.....
00BW2036_1	SQGTTEGVGS	P.....	.....
00BW2063_6	SQGTPEGVGN	P.....	.....
00BW2087_2	PQGTTEGVGN	P.....	.....
00BW2127_2	.....VGS	P.....	.....
00BW2276_7	SQGTTEGVGS	P.....	.....
00BW3819_3	SQGTTEGVGS	P.....	.....
00BW3842_8	PQGTTEGVGS	P.....	.....
00BW3871_3	SQGTTEGVGN	P.....	.....
00BW3876_9	SQGTKEGVGS	P.....	.....
00BW3886_8	SQGTTEGVGS	P.....	.....
00BW3891_6	SQGTTEGVGS	P.....	.....
00BW3970_2	.....GVGH	P.....	.....
00BW5031_1	PQGDTEGVGR	P.....	.....
96BW01B21	SQGTTEGVGN	P.....	.....
96BW0407	SQGTTEGVGN	P.....	.....
96BW0502	....TEGVGS	P.....	.....
96BW06_J4	SQGPTEGVGS	P.....	.....
96BW11_06	SQGTPEGVGN	P.....	.....
96BW1210	SQGTTEGVGS	P.....	.....
96BW15B03	SQGTTEGVGS	P.....	.....
96BW16_26	.....GVGS	P.....	.....
96BW17A09	SQGATEGVGS	P.....	.....
96BWM01_5	SQGTPEGVGN	P.....	.....
96BWM03_2	SQGTTEGVGS	S.....	.....
98BWMC12_2	SQGTAEGVGS	P.....	.....
98BWMC13_4	SHGTPEGVGN	P.....	.....
98BWMC14_a	....TQGVGN	P.....	.....
98BWM014_1	SLGTTEGVGS	P.....	.....
98BWM018_d	SQGTTEGVGN	P.....	.....
98BWM036_a	PQGTTEGVGN	P.....	.....
98BWM037_d	PQGTTEGVGS	P.....	.....
99BW3932_1	SQGTTEGVGS	P.....	.....



99BW4642_4	SQGTTEGVGS	P.....	.....
99BW4745_8	SQGTTEGVGS	P.....	.....
99BW4754_7	SQGTPEGVGN	S.....	.....
99BWMC16_8	SQGTTEGVGS	P.....	.....
A2_CD_97CD	SQGAETGVGR	PQTSVESSGI	LGSGIEDX.
A2_CY_94CY	SQGTETGVGR	SQESVESSVI	LGSGTEEX.
A2D_97KR	PQGTETGVGR	PQISVEPSVV	LGSGTEEX.
A2G_CD_97C	PQGTETGVGG	.TIFVESSVI	LGSRTKEQX
A_BY_97BL0	SQXTETXVXX	PQISXESSXI	XXSGTKEX.
A_KE_Q23_A	SQGAETGVGR	HQVSVESPVI	LGSGTKNX.
A_SE_SE659	SQGVETGVGR	PQVSGESPVI	LGSGTKNX.
A_SE_SE725	SQGVETGVGR	PQVPGEPTV	LGSGTKTX.
A_SE_SE753	SQGIETGVGR	PQVSVESPVI	LGSGTKEX.
A_SE_SE853	.....VGR	PQVSVESPGV	LDSGTKNX.
A_SE_SE889	SQGAETGVGG	PQVSEESSII	LGSGTKTX.
A_SE_UGSE8	.....	TQVSGESSVV	LDSGTKDX.
A_UG_92UG0	SQGVETGVGR	TQVSGESPVV	LGSGTKNX.
A_UG_U455_	PQGTETGVGG	PQISVESSAV	LGSGTKNX.
AC_IN_2130	SQGVETGVGR	PQVSVESPGI	LGSGTKNX.
AC_RW_92RW	SQGTTEGVGN	PVSRKSCAVL	GSSTKKEX.
AC_SE_SE94	SQGTETGVGR	PQVSVESSAI	LGPSTKNX.
ACD_SE_SE8	.....VGS	NQISVESPAV	LDSGTKEX.
ACG_BE_VI1	.....VGS	SQTSGEHPVI	LESGTKEX.
AD_SE_SE69	.....VGS	PQIPVEPPAV	LDSGTKEX.
AD_SE_SE71	.....VGS	PQIPVESPAI	LDSGTENX.
ADHK_NO_97	.....VGD	PQIPGESSAV	LGTGTKEK.
ADK_CD_MAL	.....VGS	PQISVESPAI	LGSGTEEX.
AG_BE_VI11	SQGTETGVGR	PQIFVESSGV	LGSGTKEX.
AG_NG_92NG	SPGTETGVGG	PQISVESPVV	LGSGTKEX.
AGHU_GA_VI	.....VGS	PQISVESPTV	LGTGAKEX.
AGU_CD_Z32	.....VGD	SQIPGESCDL	LGSGTKEX.
AJ_BW_BW21	.....VGD	PQVSGESCPI	LGEGTKEX.
B_AU_VH_AF	.....VGG	PQVLVESPAV	LESGAAEX.
B_CN_RL42_	.....VGS	PQILVESPAV	LDSGTKEX.
B_DE_D31_U	.....VGS	PQILVESPAV	LESGTKEX.
B_DE_HAN_U	.....VGS	PQVLVESPAV	LEPGTKEX.
B_FR_HXB2_	.....VGS	PQILVESPTV	LESGTKEX.
B_GA_OYI_M	.....VGS	PEILVESPAV	LEPGTKEX.
B_GB_CAM1_	.....VGS	PQILVESPAV	LESGTKEX.
B_GB_GB8_A	.....VGS	PQVLVESPAV	LDPSTKEK.
B_GB_MANC_	.....VGN	PQVLVESPAV	LESGSKEK.
B_KR_WK_AF	.....VGN	PQILVESPAV	LESGTKEX.
B_NL_3202A	.....VGS	PQILVESPAV	LESGTKEX.
B_TW_TWCYS	.....VGS	PQIFVESPTV	LDSTKEK.
B_US_BC_L0	.....VGS	PQVLVESPTV	LEPGTKEX.
B_US_DH123	.....VGT	PQILVESPAV	LESGTKEX.
B_US_JRCSF	.....VGN	PEILVESPTV	LESGTKEX.
B_US_MNCG_	.....VGS	PQILVESPTV	LESGTKEX.
B_US_P896_	.....VGS	PQILVESPAI	LEPGTKEX.
B_US_RF_M1	.....VGS	PQVLVESPAV	LESGAKEX.
B_US_SF2_K	.....VGS	PQILVESPAV	LDSTKEK.
B_US_WEAU1	.....VGS	SQILLESAPV	LEPGTKEX.
B_US_WR27_	.....VGD	PQILGESPTV	LGSGAKEX.
B_US_YU2_M	.....VGS	PQILVESPPV	LDSTKEK.
BF1_BR_93B	.....VGS	PQTSGESRAV	LESGTKEX.
C_BR_92BR0	PQGNTERVGN	PVFGRPCAVL	ESRVKKEX.
C_BW_96BW0	SQGTTEGVGN	PVSGKSCAIL	GSRAKKEX.
C_BW_96BW1	SQGTPEGVGN	PISGKSCAVL	GARAKKEX.
C_BW_96BW1	SQGTTEGVGS	PISGKSCAVL	GSSTKKEX.
C_BW_96BW1	SQGTTEGVGS	PVSGKSCAVL	GSSTKKEX.

C_ET_ETH22	SQGTTEGVGN	PISGKPCAVL	GSGAKKEX.
C_IN_93IN1	.....L..GS	PISGKSCAVL	GSGAKKEX.
C_IN_93IN9	SQGTTERVGS	PISGKSCAVL	GSGAKKEX.
C_IN_93IN9	SQGTTEGVGS	PISGKSCAVL	GYRAKKEX.
C_IN_94IN1	SQGTTERVGS	PISGKSCAVL	GSGAKKEX.
C_IN_95IN2	SQGTTEGVGS	PISGKSCTVL	GSGAEKEX.
CRF01_AE_C	SQGTETGVGG	PQISGESESVI	LGSGETKNX.
CRF01_AE_C	STGTETEVR	PQISGESESVI	LGSGETKNX.
CRF01_AE_C	SRGTETGVGR	PQISGESESVI	LGSGETENX.
CRF01_AE_T	SQGTETGVGR	PQISGESESVI	LGPGETKNX.
CRF01_AE_T	SQGTETGVGR	PQISGESESVI	LGSGETKNX.
CRF01_AE_T	SQGTETGVGR	PQISGESESVI	LGPGETKNX.
CRF01_AE_T	SQGTETGVGR	PQISGESPIVI	LGPGETKNX.
CRF01_AE_T	SQGTETGVGR	PQISGESESVI	LGPGETKNX.
CRF01_AE_T	SQGTETGVGR	PQISVESEGI	LGPGETKNX.
CRF02_AG_F	PQGTETGVGS	PPISGESSTI	LGSGETKEX.
CRF02_AG_F	SQGTETGLGS	PQISGESESDI	LGAGTKEX.
CRF02_AG_G	.....VAD	PQIPGESRAI	LGSGETKEX.
CRF02_AG_N	SQGTETGVGS	PQISVESYII	LGSGETKEX.
CRF02_AG_S	.....VGS	PQISVESEIV	LGSGETKEX.
CRF02_AG_S	SQGTETGVGS	SQTSVESESVI	LGSGETKEX.
CRF03_AB_R	.....VGS	PQILVESPTV	LDSEGETKEX.
CRF03_AB_R	.....VGS	PQILVESPTV	LDSEGETKEX.
CRF04_cpx_	.....VGS	PQVSVELPAV	LGTGAKEX.
CRF04_cpx_	.....VGS	PQVSVEPPAV	LGTGAKEX.
CRF04_cpx_	.....VGN	PQVPVEPPAV	LGTGDKEX.
CRF05_DF_B	.....VGS	PQISVEPPAI	LESEGETKEX.
CRF05_DF_B	.....VGS	PQISVESPTV	LESEGAKEX.
CRF06_cpx_	.....VGN	PQISGEPMDL	LGTGTTEX.
CRF06_cpx_	.....VGD	PQIPGEPGVV	LGTGTTEX.
CRF06_cpx_	.....VGD	PQIPVEPGVL	LGTGTTEX.
CRF06_cpx_	.....VGD	PQIPGEPGVV	LGTGTTEX.
CRF11_cpx_	.....VGD	SQISGESDTV	LGPRTEEX.
CRF11_cpx_	.....VGE	SQIPGESSTV	LGPRTEEX.
D_CD_84ZR0	.....VGS	PQISVESPAI	LESRTTEEX.
D_CD_ELI_K	.....VGH	PQISVESPTV	LESGTEEQX
D_CD_NDK_M	.....VGS	PQIPVEPPAV	LESGTEEX.
D_UG_94UG1	.....VGS	HQISVESPAV	LDSEGETKEX.
F1_BE_VI85	.....VGS	SQISGESHAV	LESEGETKEX.
F1_BR_93BR	.....VGS	SQISGESHTV	LGSGETKEX.
F1_FI_FIN9	.....VGS	PQISGEHHTV	LESEGETKEX.
F1_FR_MP41	.....VGN	PQISMEPRTV	LESEGETKEX.
F2_CM_MP25	.....VGS	PQISVESRAV	LGSGETKEX.
F2KU_BE_VI	.....LGN	PQIPVEPCAV	LGSGETKEX.
G_BE_DRCBL	SQGTTEIGVGS	PQIFVESESVV	LGSGETKEX.
G_NG_92NG0	PQGTETGVGR	PQVLVEPPVV	LGSGETKEX.
G_SE_SE616	PQGTETGVGR	.SIFVESESVV	LGQGTTEX.
H_BE_VI991	.....VGS	PQTSGESPAV	LGTGAKEX.
H_BE_VI997	.....KGG	PQIPVESSTV	LGTGTTEX.
H_CF_90CF0	.....EGS	PQISLESSTI	LGTGTTEX.
J_SE_SE702	.....VGD	PQISGEPCMV	LGAGTKEX.
J_SE_SE788	.....VGD	PQISGEPCMV	LGAGTKEX.
K_CD_EQTB1	.....LGS	PQIPVEPDTV	LGSGDKEX.
K_CM_MP535	.....LGS	PQISVEPCTV	LESEGETKEX.
N_CM_YBF30	QQG.TATTET	QNTLVGNTCI	LGKRVKGX.
O_CM_ANT70	VDPR.AEDNC	LQNLCSNTI	LATRIAEX.
O_CM_MVP51	VDPG.TKDNS	LT.LWSCNAI	LATRIEEX.
O_SN_MP129	VDSE.TEDNC	LQTLHSCNTI	LATRVAEX.
O_SN_MP130	VDPG.TEDNC	LQNLHSCNTI	LATRVAEX.
U_CD___83C	.....VGS	TQIPGESCAV	LGSGETKE..

Table 16. HIV Tat Alignment

GCG Multiple Sequence File.

Written by Omega 1.1

Name: 00BW0762_1	<u>SEQ ID NO: 1136</u>	Len: 108	Check: 5728	Weight: 1.00
Name: 00BW0768_2	<u>SEQ ID NO: 1137</u>	Len: 108	Check: 4583	Weight: 1.00
Name: 00BW0874_2	<u>SEQ ID NO: 1138</u>	Len: 108	Check: 5462	Weight: 1.00
Name: 00BW1471_2	<u>SEQ ID NO: 1139</u>	Len: 108	Check: 4359	Weight: 1.00
Name: 00BW1616_2	<u>SEQ ID NO: 1140</u>	Len: 108	Check: 5389	Weight: 1.00
Name: 00BW1686_8	<u>SEQ ID NO: 1141</u>	Len: 108	Check: 6742	Weight: 1.00
Name: 00BW1759_3	<u>SEQ ID NO: 1142</u>	Len: 108	Check: 6187	Weight: 1.00
Name: 00BW1773_2	<u>SEQ ID NO: 1143</u>	Len: 108	Check: 5566	Weight: 1.00
Name: 00BW1783_5	<u>SEQ ID NO: 1144</u>	Len: 108	Check: 6579	Weight: 1.00
Name: 00BW1795_6	<u>SEQ ID NO: 1145</u>	Len: 108	Check: 6027	Weight: 1.00
Name: 00BW1811_3	<u>SEQ ID NO: 1146</u>	Len: 108	Check: 4928	Weight: 1.00
Name: 00BW1859_5	<u>SEQ ID NO: 1147</u>	Len: 108	Check: 6153	Weight: 1.00
Name: 00BW1880_2	<u>SEQ ID NO: 1148</u>	Len: 108	Check: 6898	Weight: 1.00
Name: 00BW1921_1	<u>SEQ ID NO: 1149</u>	Len: 108	Check: 6286	Weight: 1.00
Name: 00BW2036_1	<u>SEQ ID NO: 1150</u>	Len: 108	Check: 4808	Weight: 1.00
Name: 00BW2063_6	<u>SEQ ID NO: 1151</u>	Len: 108	Check: 7492	Weight: 1.00
Name: 00BW2087_2	<u>SEQ ID NO: 1152</u>	Len: 108	Check: 4005	Weight: 1.00
Name: 00BW2127_2	<u>SEQ ID NO: 1153</u>	Len: 108	Check: 6532	Weight: 1.00
Name: 00BW2276_7	<u>SEQ ID NO: 1154</u>	Len: 108	Check: 7138	Weight: 1.00
Name: 00BW3819_3	<u>SEQ ID NO: 1155</u>	Len: 108	Check: 4977	Weight: 1.00
Name: 00BW3842_8	<u>SEQ ID NO: 1156</u>	Len: 108	Check: 5730	Weight: 1.00
Name: 00BW3871_3	<u>SEQ ID NO: 1157</u>	Len: 108	Check: 7576	Weight: 1.00
Name: 00BW3876_9	<u>SEQ ID NO: 1158</u>	Len: 108	Check: 4797	Weight: 1.00
Name: 00BW3886_8	<u>SEQ ID NO: 1159</u>	Len: 108	Check: 7443	Weight: 1.00
Name: 00BW3891_6	<u>SEQ ID NO: 1160</u>	Len: 108	Check: 5634	Weight: 1.00
Name: 00BW3970_2	<u>SEQ ID NO: 1161</u>	Len: 108	Check: 5984	Weight: 1.00
Name: 00BW5031_1	<u>SEQ ID NO: 1162</u>	Len: 108	Check: 8884	Weight: 1.00
Name: 96BW01B21	<u>SEQ ID NO: 1163</u>	Len: 108	Check: 6237	Weight: 1.00
Name: 96BW0407	<u>SEQ ID NO: 1164</u>	Len: 108	Check: 5097	Weight: 1.00
Name: 96BW0502	<u>SEQ ID NO: 1165</u>	Len: 108	Check: 5303	Weight: 1.00
Name: 96BW06_J4	<u>SEQ ID NO: 1166</u>	Len: 108	Check: 5679	Weight: 1.00
Name: 96BW11_06	<u>SEQ ID NO: 1167</u>	Len: 108	Check: 7244	Weight: 1.00
Name: 96BW1210	<u>SEQ ID NO: 1168</u>	Len: 108	Check: 5043	Weight: 1.00
Name: 96BW15B03	<u>SEQ ID NO: 1169</u>	Len: 108	Check: 5056	Weight: 1.00
Name: 96BW16_26	<u>SEQ ID NO: 1170</u>	Len: 108	Check: 5774	Weight: 1.00
Name: 96BW17A09	<u>SEQ ID NO: 1171</u>	Len: 108	Check: 4288	Weight: 1.00
Name: 96BWM01_5	<u>SEQ ID NO: 1172</u>	Len: 108	Check: 6335	Weight: 1.00
Name: 96BWM03_2	<u>SEQ ID NO: 1173</u>	Len: 108	Check: 5085	Weight: 1.00
Name: 98BWMC12_2	<u>SEQ ID NO: 1174</u>	Len: 108	Check: 5048	Weight: 1.00
Name: 98BWMC13_4	<u>SEQ ID NO: 1175</u>	Len: 108	Check: 5714	Weight: 1.00
Name: 98BWMC14_a	<u>SEQ ID NO: 1176</u>	Len: 108	Check: 6475	Weight: 1.00
Name: 98BWM014_1	<u>SEQ ID NO: 1177</u>	Len: 108	Check: 5085	Weight: 1.00
Name: 98BWM018_d	<u>SEQ ID NO: 1178</u>	Len: 108	Check: 4268	Weight: 1.00
Name: 98BWM036_a	<u>SEQ ID NO: 1179</u>	Len: 108	Check: 6665	Weight: 1.00
Name: 98BWM037_d	<u>SEQ ID NO: 1180</u>	Len: 108	Check: 5564	Weight: 1.00
Name: 99BW3932_1	<u>SEQ ID NO: 1181</u>	Len: 108	Check: 5875	Weight: 1.00
Name: 99BW4642_4	<u>SEQ ID NO: 1182</u>	Len: 108	Check: 6405	Weight: 1.00
Name: 99BW4745_8	<u>SEQ ID NO: 1183</u>	Len: 108	Check: 4857	Weight: 1.00
Name: 99BW4754_7	<u>SEQ ID NO: 1184</u>	Len: 108	Check: 5219	Weight: 1.00
Name: 99BWMC16_8	<u>SEQ ID NO: 1185</u>	Len: 108	Check: 4870	Weight: 1.00
Name: A2_CD_97	<u>SEQ ID NO: 1186</u>	Len: 108	Check: 4523	Weight: 1.00
Name: A2_CY_94	<u>SEQ ID NO: 1187</u>	Len: 108	Check: 3933	Weight: 1.00
Name: A2D_97_9	<u>SEQ ID NO: 1188</u>	Len: 108	Check: 4676	Weight: 1.00
Name: A2G_CD_9	<u>SEQ ID NO: 1189</u>	Len: 108	Check: 2213	Weight: 1.00
Name: A_BY_97_97	<u>SEQ ID NO: 1190</u>	Len: 108	Check: 4264	Weight: 1.00
Name: A_KE_93_Q2	<u>SEQ ID NO: 1191</u>	Len: 108	Check: 3668	Weight: 1.00

Name: A_SE_93_SE	SEQ ID NO: 1192	Len: 108	Check: 4159	Weight: 1.00
Name: A_SE_94_SE	SEQ ID NO: 1193	Len: 108	Check: 4323	Weight: 1.00
Name: A_SE_94_SE	SEQ ID NO: 1194	Len: 108	Check: 3099	Weight: 1.00
Name: A_SE_95_SE	SEQ ID NO: 1195	Len: 108	Check: 3717	Weight: 1.00
Name: A_SE_95_SE	SEQ ID NO: 1196	Len: 108	Check: 4178	Weight: 1.00
Name: A_SE_95_UG	SEQ ID NO: 1197	Len: 108	Check: 3954	Weight: 1.00
Name: A_UG_85_U4	SEQ ID NO: 1198	Len: 108	Check: 3663	Weight: 1.00
Name: A_UG_92_92	SEQ ID NO: 1199	Len: 108	Check: 4315	Weight: 1.00
Name: AC_IN_95_2	SEQ ID NO: 1200	Len: 108	Check: 5100	Weight: 1.00
Name: AC_RW_92_9	SEQ ID NO: 1201	Len: 108	Check: 4062	Weight: 1.00
Name: AC_SE_96_S	SEQ ID NO: 1202	Len: 108	Check: 6001	Weight: 1.00
Name: ACD_SE_95_	SEQ ID NO: 1203	Len: 108	Check: 4767	Weight: 1.00
Name: ACG_BE_ V	SEQ ID NO: 1204	Len: 108	Check: 5568	Weight: 1.00
Name: AD_SE_93_S	SEQ ID NO: 1205	Len: 108	Check: 4456	Weight: 1.00
Name: AD_SE_95_S	SEQ ID NO: 1206	Len: 108	Check: 4850	Weight: 1.00
Name: ADHK_NO_97	SEQ ID NO: 1207	Len: 108	Check: 6557	Weight: 1.00
Name: ADK_CD_85_	SEQ ID NO: 1208	Len: 108	Check: 4622	Weight: 1.00
Name: AG_BE_ VI	SEQ ID NO: 1209	Len: 108	Check: 3720	Weight: 1.00
Name: AG_NG_92_9	SEQ ID NO: 1210	Len: 108	Check: 4790	Weight: 1.00
Name: AGHU_GA_	SEQ ID NO: 1211	Len: 108	Check: 4548	Weight: 1.00
Name: AGU_CD_76_	SEQ ID NO: 1212	Len: 108	Check: 7456	Weight: 1.00
Name: AJ_BW_98_B	SEQ ID NO: 1213	Len: 108	Check: 4086	Weight: 1.00
Name: B_AU_ VH	SEQ ID NO: 1214	Len: 108	Check: 5824	Weight: 1.00
Name: B_CN_ RL4	SEQ ID NO: 1215	Len: 108	Check: 3342	Weight: 1.00
Name: B_DE_86_D3	SEQ ID NO: 1216	Len: 108	Check: 4538	Weight: 1.00
Name: B_DE_86_HA	SEQ ID NO: 1217	Len: 108	Check: 5673	Weight: 1.00
Name: B_FR_83_HX	SEQ ID NO: 1218	Len: 108	Check: 2953	Weight: 1.00
Name: B_GA_ OYI	SEQ ID NO: 1219	Len: 108	Check: 5056	Weight: 1.00
Name: B_GB_ CAM	SEQ ID NO: 1220	Len: 108	Check: 4131	Weight: 1.00
Name: B_GB_ GB8	SEQ ID NO: 1221	Len: 108	Check: 7783	Weight: 1.00
Name: B_GB_59_MA	SEQ ID NO: 1222	Len: 108	Check: 5562	Weight: 1.00
Name: B_KR_ WK	SEQ ID NO: 1223	Len: 108	Check: 6702	Weight: 1.00
Name: B_NL_86_32	SEQ ID NO: 1224	Len: 108	Check: 5027	Weight: 1.00
Name: B_TW_ TWC	SEQ ID NO: 1225	Len: 108	Check: 6611	Weight: 1.00
Name: B_US_ DH1	SEQ ID NO: 1226	Len: 108	Check: 5131	Weight: 1.00
Name: B_US_ P89	SEQ ID NO: 1227	Len: 108	Check: 5087	Weight: 1.00
Name: B_US_83_RF	SEQ ID NO: 1228	Len: 108	Check: 7745	Weight: 1.00
Name: B_US_83_SF	SEQ ID NO: 1229	Len: 108	Check: 4303	Weight: 1.00
Name: B_US_84_MN	SEQ ID NO: 1230	Len: 108	Check: 4888	Weight: 1.00
Name: B_US_86_JR	SEQ ID NO: 1231	Len: 108	Check: 5959	Weight: 1.00
Name: B_US_86_YU	SEQ ID NO: 1232	Len: 108	Check: 6104	Weight: 1.00
Name: B_US_87_BC	SEQ ID NO: 1233	Len: 108	Check: 5602	Weight: 1.00
Name: B_US_88_WR	SEQ ID NO: 1234	Len: 108	Check: 5031	Weight: 1.00
Name: B_US_90_WE	SEQ ID NO: 1235	Len: 108	Check: 5035	Weight: 1.00
Name: BF1_BR_93_	SEQ ID NO: 1236	Len: 108	Check: 3381	Weight: 1.00
Name: C_BR_92_92	SEQ ID NO: 1237	Len: 108	Check: 6035	Weight: 1.00
Name: C_BW_96_96	SEQ ID NO: 1238	Len: 108	Check: 5570	Weight: 1.00
Name: C_BW_96_96	SEQ ID NO: 1239	Len: 108	Check: 7348	Weight: 1.00
Name: C_BW_96_96	SEQ ID NO: 1240	Len: 108	Check: 5043	Weight: 1.00
Name: C_BW_96_96	SEQ ID NO: 1241	Len: 108	Check: 5056	Weight: 1.00
Name: C_ET_86_ET	SEQ ID NO: 1242	Len: 108	Check: 4199	Weight: 1.00
Name: C_IN_93_93	SEQ ID NO: 1243	Len: 108	Check: 5957	Weight: 1.00
Name: C_IN_93_93	SEQ ID NO: 1244	Len: 108	Check: 4573	Weight: 1.00
Name: C_IN_93_93	SEQ ID NO: 1245	Len: 108	Check: 5361	Weight: 1.00
Name: C_IN_94_94	SEQ ID NO: 1246	Len: 108	Check: 5479	Weight: 1.00
Name: C_IN_95_95	SEQ ID NO: 1247	Len: 108	Check: 5697	Weight: 1.00
Name: CRF01_AE_C	SEQ ID NO: 1248	Len: 108	Check: 2633	Weight: 1.00
Name: CRF01_AE_C	SEQ ID NO: 1249	Len: 108	Check: 4093	Weight: 1.00
Name: CRF01_AE_C	SEQ ID NO: 1250	Len: 108	Check: 2957	Weight: 1.00
Name: CRF01_AE_T	SEQ ID NO: 1251	Len: 108	Check: 2478	Weight: 1.00

Name:	CRF01_AE_T	SEQ ID NO: 1252	Len: 108	Check: 1857	Weight: 1.00
Name:	CRF01_AE_T	SEQ ID NO: 1253	Len: 108	Check: 1204	Weight: 1.00
Name:	CRF01_AE_T	SEQ ID NO: 1254	Len: 108	Check: 2024	Weight: 1.00
Name:	CRF01_AE_T	SEQ ID NO: 1255	Len: 108	Check: 913	Weight: 1.00
Name:	CRF01_AE_T	SEQ ID NO: 1256	Len: 108	Check: 1446	Weight: 1.00
Name:	CRF02_AG_F	SEQ ID NO: 1257	Len: 108	Check: 4840	Weight: 1.00
Name:	CRF02_AG_F	SEQ ID NO: 1258	Len: 108	Check: 6283	Weight: 1.00
Name:	CRF02_AG_G	SEQ ID NO: 1259	Len: 108	Check: 4683	Weight: 1.00
Name:	CRF02_AG_N	SEQ ID NO: 1260	Len: 108	Check: 3989	Weight: 1.00
Name:	CRF02_AG_S	SEQ ID NO: 1261	Len: 108	Check: 3401	Weight: 1.00
Name:	CRF02_AG_S	SEQ ID NO: 1262	Len: 108	Check: 4884	Weight: 1.00
Name:	CRF03_AB_R	SEQ ID NO: 1263	Len: 108	Check: 2749	Weight: 1.00
Name:	CRF03_AB_R	SEQ ID NO: 1264	Len: 108	Check: 3199	Weight: 1.00
Name:	CRF04_cpx	SEQ ID NO: 1265	Len: 108	Check: 2779	Weight: 1.00
Name:	CRF04_cpx	SEQ ID NO: 1266	Len: 108	Check: 2140	Weight: 1.00
Name:	CRF04_cpx	SEQ ID NO: 1267	Len: 108	Check: 4857	Weight: 1.00
Name:	CRF05_DF_B	SEQ ID NO: 1268	Len: 108	Check: 6229	Weight: 1.00
Name:	CRF05_DF_B	SEQ ID NO: 1269	Len: 108	Check: 4828	Weight: 1.00
Name:	CRF06_cpx	SEQ ID NO: 1270	Len: 108	Check: 4652	Weight: 1.00
Name:	CRF06_cpx	SEQ ID NO: 1271	Len: 108	Check: 5232	Weight: 1.00
Name:	CRF06_cpx	SEQ ID NO: 1272	Len: 108	Check: 4871	Weight: 1.00
Name:	CRF06_cpx	SEQ ID NO: 1273	Len: 108	Check: 5747	Weight: 1.00
Name:	CRF11_cpx	SEQ ID NO: 1274	Len: 108	Check: 4101	Weight: 1.00
Name:	CRF11_cpx	SEQ ID NO: 1275	Len: 108	Check: 3288	Weight: 1.00
Name:	D_CD_83_EL	SEQ ID NO: 1276	Len: 108	Check: 3640	Weight: 1.00
Name:	D_CD_83_ND	SEQ ID NO: 1277	Len: 108	Check: 4658	Weight: 1.00
Name:	D_CD_84_84	SEQ ID NO: 1278	Len: 108	Check: 6447	Weight: 1.00
Name:	D_UG_94_94	SEQ ID NO: 1279	Len: 108	Check: 6559	Weight: 1.00
Name:	F1_BE_93_V	SEQ ID NO: 1280	Len: 108	Check: 4812	Weight: 1.00
Name:	F1_BR_93_9	SEQ ID NO: 1281	Len: 108	Check: 4376	Weight: 1.00
Name:	F1_FI_93_F	SEQ ID NO: 1282	Len: 108	Check: 4918	Weight: 1.00
Name:	F1_FR_96_M	SEQ ID NO: 1283	Len: 108	Check: 3934	Weight: 1.00
Name:	F2_CM_95_M	SEQ ID NO: 1284	Len: 108	Check: 5318	Weight: 1.00
Name:	F2KU_BE_94	SEQ ID NO: 1285	Len: 108	Check: 4644	Weight: 1.00
Name:	G_BE_96_DR	SEQ ID NO: 1286	Len: 108	Check: 4391	Weight: 1.00
Name:	G_NG_92_92	SEQ ID NO: 1287	Len: 108	Check: 5855	Weight: 1.00
Name:	G_SE_93_SE	SEQ ID NO: 1288	Len: 108	Check: 2420	Weight: 1.00
Name:	H_BE__VI9	SEQ ID NO: 1289	Len: 108	Check: 5780	Weight: 1.00
Name:	H_BE__VI9	SEQ ID NO: 1290	Len: 108	Check: 2472	Weight: 1.00
Name:	H_CF_90_90	SEQ ID NO: 1291	Len: 108	Check: 3026	Weight: 1.00
Name:	J_SE_93_SE	SEQ ID NO: 1292	Len: 108	Check: 4542	Weight: 1.00
Name:	J_SE_94_SE	SEQ ID NO: 1293	Len: 108	Check: 4057	Weight: 1.00
Name:	K_CD_97_EQ	SEQ ID NO: 1294	Len: 108	Check: 2222	Weight: 1.00
Name:	K_CM_96_MP	SEQ ID NO: 1295	Len: 108	Check: 4681	Weight: 1.00
Name:	N_CM_95_YB	SEQ ID NO: 1296	Len: 108	Check: 3679	Weight: 1.00
Name:	O_CM__ANT	SEQ ID NO: 1297	Len: 108	Check: 1276	Weight: 1.00
Name:	O_CM_91_MV	SEQ ID NO: 1298	Len: 108	Check: 814	Weight: 1.00
Name:	O_SN__99S	SEQ ID NO: 1299	Len: 108	Check: 9132	Weight: 1.00
Name:	O_SN__99S	SEQ ID NO: 1300	Len: 108	Check: 2342	Weight: 1.00
Name:	U_CD__83C	SEQ ID NO: 1301	Len: 108	Check: 4773	Weight: 1.00

SEQ ID NO	1	50
1136	00BW0762_1 ...MEQVDPN LEPWNHPGSQ PKTPCNKCFC KSCSYHCLVC FQTKGLGISY	
1137	00BW0768_2 ...MDPVDPN LEPWNHPGSQ PKTACNNCYC KYCSYHCLVC FQKKGLGISY	
1138	00BW0874_2 ...MEPVDPN LEPWNHPGSQ PKTACNSCYC KHCCYHCRVC FLTKGLGISY	
1139	00BW1471_2 ...MDPVDPK LEPWNHPGSQ PKTACNTCYC KKCCYHCQVC FLNKGLGISY	
1140	00BW1616_2 ...MEPIDPN LEPWNHPGSQ PSTACNKCYC KQCCYHCPAC FLTKGLGISY	
1141	00BW1686_8 ...MEPVDPK LEPWNHPGSQ PTTPTCTCFC KVCSYHCLVC FQTKGLGIYY	

1142	00BW1759_3	...MEPIDPN	LEPWNHPGSQ	PKTACNKCYC	KSCSYHCLVC	FQKKGLGISY
1143	00BW1773_2	...MEPVDPN	LEPWNHPGSQ	PKTPCTKCYC	KLCSYHCLVC	FQTKGLSISY
1144	00BW1783_5	...MEPVDPN	LEPWNHPGSQ	PKTPCTKCYC	KKCSYHCLVC	FQTKGLGISY
1145	00BW1795_6	...MEPVDPN	LEPWNHPGSQ	PKTPCNHCYC	KHCSYHCLVC	FQTKGLGISY
1146	00BW1811_3	...MEPVDPN	LEPWKHPGSQ	PKTACNTCYC	KRCSYHCPVC	FLTKGLGISY
1147	00BW1859_5	...MEPVDPN	LEPWNHPGSQ	PKTACNKCYC	KRCSYHCLVC	FQTKGLGISY
1148	00BW1880_2	...MEPVDPN	LEPWNHPGSQ	PQTPCNKCYC	KRCSYHCLVC	FQTKGLGISY
1149	00BW1921_1	...MEPIDPK	LEPWNHPGSQ	PNTPTPCYC	KKCSYHCLVC	FQTKGLGIYY
1150	00BW2036_1	...MEPVDPK	LEPWNHPGSQ	PKTPCNKCYC	KKCSYHCLVC	FQTKGLGISY
1151	00BW2063_6	...MEIVDPN	LDPWDHPGSQ	PSTPCNKCYC	KYCSYHCLVC	FQTKGLGISY
1152	00BW2087_2	...MEPIDPN	LEPWNHPGSQ	PKTACNKCFC	KRCCYHCPAC	FLTKGLGISY
1153	00BW2127_2	...MEPVDPN	LEPWNHPGSQ	PKTACSPCYC	KNCSYHCLVC	FQTKGLGISY
1154	00BW2276_7	...MEPVDPN	LEPWKHPGSQ	PKTACTSCYC	KRCSYHCLVC	FQTKGLGISY
1155	00BW3819_3	...MEPVDPN	LEPWNHPGSQ	PKTACNQCYC	KHCCYHCLVC	FQTKGLGISY
1156	00BW3842_8	...MEPVDPK	LEPWNHPGSQ	PRTPCNKCFC	KVCSYHCQSC	FLTKGLGISY
1157	00BW3871_3	...MDPVDPN	LEPWNHPGSQ	PKTPCNKCYC	KKCSYHCVVC	FQTKGLGIYY
1158	00BW3876_9	...MELIDPK	LEPWNHPGSQ	PAAPCNKCYC	KHCSYHCLVC	FQTKGLGISY
1159	00BW3886_8	...MEPIDPN	LEPWNHPGSQ	PKTPCNKCYC	KHCSYHCLVC	FQTKGLGISY
1160	00BW3891_6	...MEPVDPN	LEPWNHPGSQ	PNTACNKCYC	KQCSYHCLVC	FQKKGLGISY
1161	00BW3970_2	...MEPVDPN	LEPWNHPGSQ	PKTACNSCYC	KKCSYHCQVC	FLTKGLGISY
1162	00BW5031_1	...MEPVDPN	LEPWNHPGSQ	PKTPCNKCYC	KQCSYHCPVC	FLTKGLGIYY
1163	96BW01B21	...MEPVDPN	LEPWNHPGSQ	PKTACNNCYC	KHCSYHCLVC	FQTKGLGIYY
1164	96BW0407	...MEPIDPN	LEPWNHPGSQ	PKTACNKCYC	KHCSYHCLVC	FQTKGLGISY
1165	96BW0502	...MEPVDPN	LEPWKHPGSQ	PRTACTKCYC	KYCCYHCLVC	FQTKGLGISY
1166	96BW06_J4	...MEPVDPK	LEPWNHPGGQ	PKTPCNTCYC	KKCSYHCLVC	FQKKGLGIYY
1167	96BW11_06	...MEQVDPN	LEPWNHPGSQ	PKTPCNKCYC	KYCSYHCLVC	FQTKGLGISY
1168	96BW1210	...MEPVDPN	LEPWNHPGSQ	PKIACNKCYC	KACCYHCLVC	FQTKGLGISY
1169	96BW15B03	...MEPVDPK	LEPWNHPGSQ	PKTPCTKCF	KGCSYHCLVC	FQTKGLGISY
1170	96BW16_26	...MEPVDPK	LEPWNHPGSQ	PKTACNKCYC	KRCSYHCLVC	FQTKGLGISY
1171	96BW17A09	...MDPVDPN	LEPWNHPGSQ	PKTACNTCYC	KKCCYHCQVC	FLNKGLGISY
1172	96BWM01_5	...MEPVDPN	LEPWKHPGSQ	PETPCNKCYC	KSCSYHCLVC	FQKKGLGISY
1173	96BWM03_2	...MEPVDPN	LEPWNHPGSQ	PKTACNNCCC	KRCSYHCLVC	FQKKGLGISY
1174	98BWMC12_2	...MEPVDPN	LEPWNHPGSQ	PKTACNNCYC	KRCCYHCQRC	FLTKGLGISY
1175	98BWMC13_4	...MEPVDPN	LEPWNHPGSQ	PKTSCNNCYC	KKCSYHCLVC	FQKKGLGISY
1176	98BWMC14_a	...MDPVDPK	LEPWNHPGSQ	PSTPCNTCFC	KKCSYHCLVC	FQKKGLGIYY
1177	98BWM014_1	...MEPIDPN	LEPWNHPGSQ	PKTACNKCHC	KRCCYHCTVC	FLTKGLGISY
1178	98BWM018_d	...MEPIDPN	LEPWNHPGSQ	PKTDCNKCYC	KRCCYHCLVC	FQKKGLGISH
1179	98BWM036_a	...MEPVDPN	LEPWNHPGSQ	PRTACNTCYC	KKCSYHCLVC	FQKKGLGISY
1180	98BWM037_d	...MEPVDPN	LEPWNHPGSQ	PKTACNKCYC	KHCSYHCLVC	FQTKGLGISY
1181	99BW3932_1	...MEPVDPN	LEPWNHPGSQ	PKTACNKCYC	KSCSYHCPVC	FLSKGLGISY
1182	99BW4642_4	...MEPVDPN	LEPWNHPGSQ	PKTPCTTCFC	KRCSYHCLVC	FQTKGLGIYY
1183	99BW4745_8	...MEPVDPN	LEPWNHPGSQ	PSTACNKCYC	KHCSYHCLVC	FQTKGLAISY
1184	99BW4754_7	...MEPVDPN	LEPWNHPGSQ	PETPCNKCFC	KACSYHCLVC	FQKKGLGISY
1185	99BWMC16_8	...MDPVDPN	LEPWNHPGSQ	PKTACNRCYC	KKCSYHCLVC	FHTKGLGISY
1186	A2_CD___97	...MEPVDPN	LEPWNHPGSQ	PKTACNNCYC	KKCCYHCQRC	FLNKGLGISY
1187	A2_CY___94	...MEPVDPK	LEPWNHPGSQ	PKTACTKCYC	KRCCYHCQLC	FINKGLGISY
1188	A2D___97_9	...MDPVDPN	LEPWNHPGSQ	PRTACNKCYC	KRCCYHCPVC	FLNKGLGISY

1189	A2G_CD__9	...MDPVDPN	LEPWNHPGSQ	PKTACNKCYC	KACCWHCQVC	FLNKGLGISY
1190	A_BY_97_97	...XDPVDPN	LEPXNHXXSQ	PKTXCRNCYC	KKCCWHCQIC	FLKKGLGISY
1191	A_KE_93_Q2	...MDPVDPN	LEPWNHPGSQ	PTTACNKCYC	KKCCYHCQVC	FLNKGLGISY
1192	A_SE_93_SE	...MDPVDPN	LEPWNHPGSQ	PSTACNKCYC	KICCYHCPVC	FLNKGLGISY
1193	A_SE_94_SE	...MDPVDPN	LEPWNHPGSQ	PTTPCSKCYC	KKCCYHCIVC	FQNKGLGISY
1194	A_SE_94_SE	...MDPVDPN	LEPWNHPGSQ	PTTACNKCYC	KKCCYHCQAC	FLNKGLGISY
1195	A_SE_95_SE	...MEPVDPN	IEPWNHPGSQ	PTTPCTKCYC	KKCCYHCPAC	FLNKGLGISY
1196	A_SE_95_SE	...MDPVDPN	LEPWNHPGSQ	PATACSACYC	KKCCYHCPVC	FLNKGLGISY
1197	A_SE_95_UG	...MDPVDPN	LEPWNHPGSQ	PTTPCNKYFC	KRCCYHCLVC	FQHKGLGISY
1198	A_UG_85_U4	...MEPVDPN	LEPWKHPGSQ	PTTACSNCYC	KVCCWHCQLC	FLKKGLGISY
1199	A_UG_92_92	...MDPVDPN	LEPWNHPGSQ	PKTPCNKCYC	KVCCYHCQCC	FLNKGLGISY
1200	AC_IN_95_2	...MEPVDPN	LEPWNHPGSQ	PRTACNNCYC	KRCSYHCLVC	FQKKGLGISY
1201	AC_RW_92_9	...MEPVDPK	LEPWNHPGSQ	PKTACNNCYC	KHCSYHCLVC	FQAKGLGISY
1202	AC_SE_96_S	...MEPIDPN	LEPWNHPGSQ	PKTACNRCYC	KRCSYHCLVC	FQTKGLGISY
1203	ACD_SE_95_	...MDLVDPN	LEPWNHPGSQ	PTTPCSKCYC	KKCCYHCQHC	FITKGLGISY
1204	ACG_BE__V	...MEPVDPK	LEPWNHPGSQ	PKTACNKCFC	KKCSYHCLVC	FQTKGLGISY
1205	AD_SE_93_S	...MDPVDPN	LEPWNHPGSQ	PTTPCTKCYC	KKCCYHCQVC	FITKGLGISY
1206	AD_SE_95_S	...MDPVDPN	LEPWNHPGSQ	PTTPCSKCYC	KKCCYHCQSC	FLNKGLGISY
1207	ADHK_NO_97	...MDPVDPN	LEPWNHPGSQ	PNTPCNNCYC	KQCCYHCQLC	FLRKGLGISY
1208	ADK_CD_85_	...MDPVDPN	LEPWNHPGSQ	PRTPCNKCYC	KKCCYHCQMC	FITKGLGISY
1209	AG_BE__VI	...MDPVDPN	LEPWNHPGSQ	PKTACNKCYC	KKCCWHCQVC	FLNKGLGISY
1210	AG_NG_92_9	...MELVDPS	LEPWNHPGSQ	PTTACNKCYC	KICCWHCQLC	FLNKGLGISY
1211	AGHU_GA__	...MDPVDPN	IEPWNQPGSQ	PKTACNQCYC	KRCCYHCQHC	FLKKGLRISY
1212	AGU_CD_76_	...MEPVDPN	LEPWNQPGSQ	PQTACNNCYC	KKCCFHCQVC	FSSKGLGISY
1213	AJ_BW_98_B	...MEPVDPN	IEPWNQPGSQ	PKTACTPCYC	KKCCFHCQVC	FLKKGLGISY
1214	B_AU__VH_	...MDPVDPN	LEPWKHPGSQ	PKTACTNCYC	KQCCFHCQVC	FIRKGLGISY
1215	B_CN__RL4	...MEPVDPN	LEPWKHPGSQ	PKTACNNCYC	KKCCCLHCQVC	FMKKGLGIFY
1216	B_DE_86_D3	...MEPVDPN	LEPWEHPGSQ	PKTACTNCYC	KKCCFHCQVC	FTHKGLGISY
1217	B_DE_86_HA	...MEPVDPN	LEPWKHPGSQ	PRTPTCTNCYC	KKCCCLHCQVC	FTRKGLSISY
1218	B_FR_83_HX	...MEPVDPN	LEPWKHPGSQ	PKTACTNCYC	KKCCFHCQVC	FITKALGISY
1219	B_GA__OYI	...MEPVDPN	LEPWKHPGSQ	PKTASNNCYC	KRCCCLHCQVC	FTHKGLGISY
1220	B_GB__CAM	...MEPVDPN	LEPWKHPGSQ	PRTACTNCYC	KQCCFHCQVC	FITKGLGISY
1221	B_GB__GB8	...MEPVDPN	LEPWKHPGSQ	PRTACTNCYC	KKCCFHCQVC	FLRKGLGISY
1222	B_GB_59_MA	...MEPVDPN	LEPWNHPGSQ	PKTACTKCYC	KKCCCLHCQVC	FITKGLGISY
1223	B_KR__WK_	...MEPVDPN	LEPWKHPGSQ	PKTPCTKCYC	KKCCCLHCQVC	FMTKGLGISY
1224	B_NL_86_32	...MEPVDPK	LEPWKHPGSQ	PKTACNNCYC	KKCCFHCQVC	FTHKGLGISY
1225	B_TW__TWC	...MDPVDPN	LEPWKHPGSQ	PKTACTNCYC	KKCCCLHCQVC	FMTKALGISE
1226	B_US__DH1	...MEPVDPN	LEPWKHPGSQ	PKTACTNCYC	KKCCCLHCQVC	FITKGLGISY
1227	B_US__P89	...MEPVNPS	LEPWKHPGSQ	PKTACTNCYC	KKCCFHCQAC	FITKGLGISY
1228	B_US_83_RF	...MEPVDPN	LEPWKHPGSQ	PKTACNNCYC	KKCCYHCQVC	FLTKGLGISY
1229	B_US_83_SF	...MEPVDPN	LEPWKHPGSQ	PRTACNNCYC	KKCCFHCYAC	FTRKGLGISY
1230	B_US_84_MN	...MEPVDPN	LEPWKHPGSQ	PKTACTTCYC	KKCCFHCQVC	FTHKALGISY
1231	B_US_86_JR	...MEPVDPN	LEPWKHPGSQ	PKTACTNCYC	KKCCCLHCQVC	FTHKGLGISY
1232	B_US_86_YU	...MEPVDPN	LEPWKHPGSQ	PRTACNNCYC	KKCCFHCQVC	FTHKGLGISY
1233	B_US_87_BC	...MEPVDPN	LEPWKHPGSQ	PKTACTKCYC	KKCCCLHCQVC	FMTKGLGISY
1234	B_US_88_WR	...MDPVDPN	LEPWKHPGSQ	PKTACTNCYC	KKCCFHCQVC	FITKGLGISY
1235	B_US_90_WE	...MEPVDPN	LEPWKHPGSQ	PKTACTNCYC	KRCCFHCQVC	FMTKGLGISY

1236	BF1_BR_93_	...	MEPVDP	LEPWKHPGSR	PQTACNSCYC	KKCCFHCQVC	FTTKGLGISY
1237	C_BR_92_92	...	MEPVDPN	LEPWNHPGSQ	PKTACNNCYC	KRCSYHCLVC	FQTKGLGISY
1238	C_BW_96_96	...	MEPIDPN	LEPWNHPGSQ	PKTACNKCFC	KHCSYHCLVC	FQTKGLSISY
1239	C_BW_96_96	...	MEQVDPN	LEPWNRPGSQ	PKTPCNNCYC	KYCSYHCLVC	FQTKGLGISY
1240	C_BW_96_96	...	MEPVDPN	LEPWNHPGSQ	PKIACNKCVC	KACCYHCLVC	FQTKGLGISY
1241	C_BW_96_96	...	MEPVDPK	LEPWNHPGSQ	PKTPCTKCFC	KGCSYHCLVC	FQTKGLGISY
1242	C_ET_86_ET	...	MEPVDPN	LEPWNHPGSQ	PKTACNQCYC	KKCSYHCLVC	FLTGLGISY
1243	C_IN_93_93	...	MEPVDPN	LEPWNHPGSQ	PKTACNQCYC	KRCSYHCLVC	FQKKGLGISY
1244	C_IN_93_93	...	MEPVDPN	LEPWNHPGSQ	PKTACNNCYC	KHCSYHCLVC	FQKKGLGISY
1245	C_IN_93_93	...	MEPVDPN	LEPWNHPGSQ	PRTACNNCFC	KSCSYHCLVC	FQKKGLGISY
1246	C_IN_94_94	...	MEPIDPN	LEPWNHPGSQ	PKTACNNCYC	KHCSYHCLVC	FQKKGLGISY
1247	C_IN_95_95	...	MEPVDPN	LEPWNHPGSQ	PKTACNNCYC	KKCSYHCLVC	FQKKGLGISY
1248	CRF01_AE_C	...	MEPVDP	LEPWNHPGSQ	PTTACSKCYC	KKCCWHCQLC	FLKKGLGISY
1249	CRF01_AE_C	...	MEPVDPN	LEPWKHPGSQ	PTTACSKCYC	KMCCWHCQLC	FLKKGLGISY
1250	CRF01_AE_C	...	MELVDPK	LEPWNHPGSQ	PTTACNKCVC	KICCWHCQLC	FLKKGLGISY
1251	CRF01_AE_T	...	MELVDPN	LEPWNHPGSQ	PTTACSKCYC	KKCCWHCQLC	FLKKGLGISY
1252	CRF01_AE_T	...	MELVDPN	LEPWKHPGSQ	PSTACSKCYC	KICCWHCQLC	FLKKGLGISY
1253	CRF01_AE_T	...	MEPVDPN	LEPWNHPGSQ	PTTACSKCYC	KICCWHCQLC	FLKKGLGISH
1254	CRF01_AE_T	...	MELVDPN	LEPWNHPGSQ	PTTACSKCYC	KKCCWHCQLC	FLKKGLGISH
1255	CRF01_AE_T	...	MELVDPN	LEPWNHPGSQ	PTTACSKCYC	KKCCWHCQLC	FLKKGLGISH
1256	CRF01_AE_T	...	MELVDPN	LEPWNHPGSQ	PTTACSKCYC	KKCCWHCQLC	FLKKGLGISH
1257	CRF02_AG_F	...	MEPVDP	LEPWNHPGSQ	PTTACSKCYC	KICCWHCQLC	FLNKGLGISY
1258	CRF02_AG_F	...	MEPVDP	LEPWNHPGSQ	PTTACSNCYC	KICCWHCQLC	FLNKGLGISY
1259	CRF02_AG_G	...	MELIDPS	LEPWNHPGSQ	PTTACSKCYC	KICCWHCQLC	FLNKGLGISY
1260	CRF02_AG_N	...	MELVDPS	LEPWNHPGSQ	PTTACSKCYC	KMCC.HCQLC	FLNKGLGISY
1261	CRF02_AG_S	...	MELVDPS	LEPWNHPGSQ	PTTACSKCYC	KICCWHCQLC	FLNKGLGISY
1262	CRF02_AG_S	...	MELVDPK	LEPWNHPGSQ	PTTACSKCYC	KLCCWHCQLC	FLNKGLGISY
1263	CRF03_AB_R	...	MEPVDP	LEPWKHPGSQ	PKTACTNCYC	KKCCCLHCQVC	FMKKGLGISY
1264	CRF03_AB_R	...	MEPVDP	LEPWKHPGSQ	PKTACTNCYC	KKCCCLHCQVC	FMKKGLGISY
1265	CRF04_cpx_	...	MEPVDPD	LEPWNHPGSQ	PTTDCNKCFC	KKCCWHCQVC	FLKKGLGISY
1266	CRF04_cpx_	MEAVDLVYPN	LEPWNHPGSQ	PTTACNKCFC	KKCCWHCQAC	FLKKGLGISY	
1267	CRF04_cpx_	...	MEPVDPN	LEPWNHPGSQ	PTTACTKCFC	KVCCYHCQVC	FLRKGLGISY
1268	CRF05_DF_B	...	MDPVDPN	LEPWNHPGSQ	PRTACNQCYC	KMCCYHCQNC	FITKGLGISY
1269	CRF05_DF_B	...	MDPVDPN	LEPWNHPGSQ	PRTACNQCHC	KKCCYHCQVC	FITKGLGISY
1270	CRF06_cpx_	...	MEPVDPK	IEPWNQPGSR	PKTACTKCYC	KKCCYHCPVC	FLNKGLGISY
1271	CRF06_cpx_	...	MEPVDPN	IEPWNQPGSR	PKTACTPCYC	KKCSYHCQLC	FLNKGLGISY
1272	CRF06_cpx_	...	MEPVDPK	IEPWNQPGSR	PKTACTSCYC	KRCCYHCPLC	FLNKGLGISY
1273	CRF06_cpx_	...	MEPVDPN	IEPWNQPGSR	PKTACTSCYC	KQCCYHCPVC	FLNKGLGISY
1274	CRF11_cpx_	...	MEPVDPN	IEPWNQPGSR	PKTACNQCYC	KRCCYHCPHC	FLKKGLGIYY
1275	CRF11_cpx_	...	MEPGDIN	IDPWNQPGSQ	PKTACNQCYC	KRCCYHCQHC	FLKKGLGISY
1276	D_CD_83_EL	...	MDPVDPN	LEPWNHPGSQ	PRTPCNKCHC	KKCCYHCPVC	FLNKGLGISY
1277	D_CD_83_ND	...	MDPVDPN	LESWNHPGSQ	PRTACNKCHC	KKCCYHCQVC	FITKGLGISY
1278	D_CD_84_84	...	MDPVDPN	IDPWNHPGSQ	PRTACNNCYC	KKCCYHCQVC	FITKGLGISY
1279	D_UG_94_94	...	MEPVDPN	LEPWNHPGSQ	PRTPCNKCVC	KRCCYHCYVC	FVTKGLGISY
1280	F1_BE_93_V	...	MEPVDP	LDPWNHPGSQ	PTTPCTKCYC	KRCCFHCQWC	FTTKGLGISY
1281	F1_BR_93_9	...	MELVDPN	LDPWNHPGSQ	PTTPCTRCYC	KWCCFHCYWC	FTTKGLGISY
1282	F1_FI_93_F	...	MELVDPN	LDPWNHPGSQ	PPTPCNKCVC	KRCCFHCYWC	FATKGLGISY



1283	F1_FR_96_M	...	MELVDPN	LDPWNQPGSQ	PTTPCTKCYC	KKCCFHCYCC	FATKGLGISY
1284	F2_CM_95_M	...	MEVVDPN	LDPWKHPGSQ	PETPCNKCYC	KKCCFHCQLC	FTRKGLGISY
1285	F2KU_BE_94	...	MEQVDPN	LDPWNHPGSQ	PKTACNNCYC	KKCCFHCQVC	FTTKGLGISY
1286	G_BE_96_DR	...	MDPVDPK	LEPWKHPGSQ	PKTPCNNCYC	KS.VAALQVC	FLNKGLGISY
1287	G_NG_92_92	...	MDPVDPK	LEPWNHPGSQ	PTTPCNKCYC	KVCCWHCQVC	FLNKGLGISY
1288	G_SE_93_SE	...	MDPVDPN	LEPWNHPGSQ	PKTPCNKCFC	KVCCWHCQVC	FLNKGLGISY
1289	H_BE__VI9	...	MDPVDPN	QEPWNHPGSQ	PRTACNNCYC	KKCCYHCQLC	FLKKGLGIYY
1290	H_BE__VI9	...	MDPVDPN	QEPWNHPGNQ	PKTPCNNCYC	KQCSFHCQLC	FLKKGLGISY
1291	H_CF_90_90	...	MDPVDPK	LEPWNHPGSQ	PQTACNNCYC	KKCCYHCQMC	FLKKGLGISY
1292	J_SE_93_SE	...	MEPVDPN	REPWNHPGSQ	PKTACTNCYC	KKCCYHCQVC	FLQKGLGISY
1293	J_SE_94_SE	...	MEPVDPN	REPWNHPGSQ	PKTACTNCYC	KKCCYHCQVC	FLQKGLGISY
1294	K_CD_97_EQ	...	MEPVDPN	IEPWNQPGSQ	PKTACNQCYC	KKCCYHCQLC	FLQKGLGICY
1295	K_CM_96_MP	...	MDPVDPN	IEPWNQPGSQ	PKTACNQCYC	KRCCYHCQIC	FLKKGLGISN
1296	N_CM_95_YB	...	MEPVDPN	LEPWNHPGSQ	PKTACNNCYC	KRCCYHCLYC	FTTKGLGISY
1297	O_CM__ANT	...	MDPVDPN	VPPWHHPGSQ	PQIPCNNCYC	KRCCYHCYVC	FVRKGLGISY
1298	O_CM_91_MV	...	MDPVDPN	MPPWHHPGSQ	PQTPCNNCYC	KRCCYHCYVC	FTTKGLGISH
1299	O_SN__99S	...	MDPVDPN	MPPWHHPGSQ	PQTPCNKCYC	KACCYHCYVC	FASKGLGISY
1300	O_SN__99S	...	MDPVDPN	MPPWHHPGSQ	PQTPCNKCYC	KACCYHCYVC	FASKGLGLSY
1301	U_CD__83C	...	MDPVDPN	LEPWNHPGSQ	PKTACNSCYC	KRCCLHCQVC	FMTKGLGISY

	51					100
00BW0762_1	GRKKRRQRR.	.HAPPGSKDH	QNPISKQPLP	.QTRGDPTGS	EESKKKVESK	
00BW0768_2	GRKKRGQRR.	.NAPPSSEDH	QDLISKQPLS	.QTRGDPTGS	EESKKKAESK	
00BW0874_2	GRKKRRQRR.	.SAPPSGEDH	QSSLPKQPLP	.QARGNPTGS	EESKKKVESK	
00BW1471_2	GRKKRRQRR.	.SAPPSKDH	QDPLSKQPLS	.QTRGDPTGS	KESKKKVESK	
00BW1616_2	GRKKRRQRR.	.STPPSSKDH	QNPVSKQPLP	.RTQGNSTGS	EESKKKVESK	
00BW1686_8	GRKKRRQRR.	.SAPPSNKEH	QDPIPKQPLP	.RTPGDPTGP	EESKKKVESK	
00BW1759_3	GRKKRRQRR.	.SGPPSNKDH	QNLVSKQPLS	.QTQRDPTGS	EESKKKVESK	
00BW1773_2	GRKKRRQRR.	.STPPSSEDH	QDLISKQPLP	.RTQGDPTGS	EESKKKVESK	
00BW1783_5	GRKKRRQRR.	.SGPPSSEDH	QNPISKQPLS	.QTRGDPTGS	KESKKKVESK	
00BW1795_6	GRKKRRRRR.	.SAPPSSEDH	QNPISKQPLS	.QTRGDPTGS	EESKKKVESK	
00BW1811_3	GRKKRRQRR.	.RAPPSSEDH	QNPPIKQPLS	.RTQGDPTGS	EESKKKVESK	
00BW1859_5	GRKKRGQRR.	.SAPSSSEDH	QDNISKQPLP	.RTQGDPTGS	EESKKKVESK	
00BW1880_2	GRKKRRQRR.	.SAPPSSEDH	QNPISKQFPF	.QTRGDSTGS	EESKKKVESK	
00BW1921_1	GRKKRRQRR.	.SAPPSKDH	QNPISKQPLP	.RTPGNSTGS	EESKKKVESK	
00BW2036_1	GRKKRGQRR.	.STPPSNKAH	QNLISKQPLP	.RTQGDSTGS	EESKKKVESK	
00BW2063_6	GRKKWRQRRG	RSAPSSSKDH	QDLISKQPLP	.QTRGDPTSS	KESKKKVESK	
00BW2087_2	GRKKRRQRR.	.SAPPSGEDH	QNPISKQPLP	.QTRGNPTGS	EESKKKVESK	
00BW2127_2	GRKKRRQRR.	.SAPPSSEDH	QDPIKQPLP	.QTRGDPTGS	EEPKKKVESK	
00BW2276_7	GRKKRRQRR.	.SAPPSSEDH	QNHISKQPLP	.QTRGDQDTS	EESKKKVESK	
00BW3819_3	GRKKRRQRR.	.RSPQSSEAH	QDPIKQPLP	.QARGDPTGS	EESKKKVESK	
00BW3842_8	GRKKRGQRR.	.SAPSSSEDH	QNPPIKQPLP	.RTQGNSTGS	EESKKKVESK	
00BW3871_3	GRKKRRQRR.	.SAPPSNKH	QNPISKQPLP	.RTQGNSTGS	EESKKKVESK	
00BW3876_9	GRKKRRQRR.	.STPPRSEDH	QNLILKQPLP	.RTQGNPTGP	EESKKKVESK	
00BW3886_8	GRKKRRQRR.	.SAPPSSEDH	QNLISKQPLP	.RTPGNSTGS	EESKKKVGSK	
00BW3891_6	GRKKRRQRR.	.SAPPSSEDH	QNPISKQPLS	.QTRGDSTGS	EESKKKVESK	
00BW3970_2	GRKKRRQRR.	.SAPPSSEDH	QNLISKRPLP	.QTRGNQDTS	EESKKKVESK	
00BW5031_1	GRKKRRQRR.	.SAPSSSENH	QNPVSKQPLP	.QARGNSTGS	EESKKKVESK	
96BW01B21	GRKKRRQRR.	.SAPPSSEDH	QNLISKQPLP	.RTQGDPTGS	EESKKKVESK	
96BW0407	GRKKRRQRR.	.STPPSSEDH	QNPVSKQPLS	.QTRGDPTGS	EESKKKVESK	
96BW0502	GRKKRRQRR.	.STPPSSEH	QNLISEQPLP	.RTQGNPTGS	EESKKKVESK	
96BW06_J4	GRKKRRQRR.	.SAPSSSEDH	QDPIKQFPF	.RTQGESTGS	EESKKEVESK	
96BW11_06	GRKKRRQRR.	.SAPPSKDH	QNPVSKQPLP	.QTRGDPTGS	KESKRKVENK	
96BW1210	GRKKRRQRR.	.SAPPSSEDH	QDLVPKQPLS	.QARGNPTSS	KESKKKVESK	
96BW15B03	GRKKRGQRR.	.SAPPRSEDH	QNLISKQPLP	.RTQGDSTGS	EESKKKVESK	

96BW16_26	GRKKRRQRR.	.SAPPSSSEDH	QNPISKQPLP	.QTQGDPTGS	EESKKKVESK
96BW17A09	GRKKRRQRR.	.SAPPSNGDH	QNPISKQPLP	.QTRGDPTGS	KESKKEVESK
96BWM01_5	GRKKRRQRR.	.SAPPSSSEDH	QDLVSKQPLP	.QTRGDPTGS	KESKKKVESK
96BWM03_2	GRKKRGQRR.	.SAPSSSKDH	QNPVSKQPLP	.QTRGNSTGS	EESKKKVESK
98BWMC12_2	GRKKRRQRR.	.SAPPSCKDH	QNPLPEQPST	.QTRGDSTGS	EESKKKVESK
98BWMC13_4	GRKKRRQRR.	.SAPASSEDH	QDLISKQLLP	.QTRGDPTGS	KESKKKVESK
98BWMC14_a	GRKKRRQRR.	.STPPSSSKDH	QNPVSKQPTS	.RTQGDWTGS	IESEKKVESK
98BWM014_1	GRKKRRRRR.	.KAPPSSSEDH	QNLVSKQPLP	.QSRGNPTGS	EESKKKVESK
98BWM018_d	GRKKRRQRR.	.SAPSSSKDH	QNPPIPKQPLP	.QTRGDQDTS	EESKKKVESK
98BWM036_a	GRKKRSQRR.	.STPPSSSEDH	QDPIISKQPLP	QQPRGIPTGS	EESKKKVESK
98BWM037_d	GRKKRRQRR.	.SAPPSSSEDH	QNLISKQPLS	.QTRGDPTGP	EESKKKVESK
99BW3932_1	GRKKRRPRR.	.SAPPSNNDH	QDLVSKQPLP	.QTRGDPTGS	EESKKKVESK
99BW4642_4	GRKKRGQRRR	.STPSSSKDH	QDLVPKQPLP	.RTQGNSTGS	EESKKKVESK
99BW4745_8	GRKKRRQRR.	.SAPSSSEDH	QNLVSKQPLP	.QAQGDPTGS	EESKKKVESK
99BW4754_7	GRKKRRQRR.	.SAPPSSTDH	QTPISKQPLP	.QTRGDQDTS	EESKKKVESK
99BWMC16_8	GRKKRRQRR.	.SAPPSSSEDH	QNPISKQPLP	.RTQGDSTGS	EESKKKVESK
A2_CD_97	GRKKRRPRR.	.GPDQGNTH	QNPVPKQSLP	.QTQDSTGP	EESKKKVESK
A2_CY_94	GRKKRRPRR.	.KPSPSNNDH	QNPPIPKQSLP	.QAQRVPTGP	EEPKEVESK
A2D_97_9	GRKKRRPRR.	.RPPQGGTGH	QNPPIPEQSLP	.RPQRIPTGT	EESKTEVESK
A2G_CD_9	GRKKRKHRR.	.GAPPGSKDH	QNPPIPKQPLP	TTRG.NPTGP	KESKKEVASK
A_BY_97_97	GRKKRRHRR.	.GTSHSSSKDH	XIPISKQPLP	HTQK.DQTGX	EESKKKXESK
A_KE_93_Q2	GRKKRRQRR.	.GAPQSSSKDH	QNSIQKQPIP	QTQG.VSTGP	KESKKKMESK
A_SE_93_SE	GRKKRTRRR.	.GAPQSNNDH	QNPISKQPIP	QTQG.DSTGP	EESKKKVESK
A_SE_94_SE	GRKKRRQRR.	.RTPQSSSKDH	QNPPIPKQPIP	QTQG.VSTGP	EESKKKVESK
A_SE_94_SE	GRKKRKQRR.	.GAPQSNNDH	QNPQQQSIP	QTQG.IPTGP	EESKKKVESK
A_SE_95_SE	GRKKRKQRR.	.GTPQGNNDH	QNPPIPKQSTP	QTQG.ISTGP	EESKKKVESK
A_SE_95_SE	GRKKRRQRR.	.RTPQSSSKDH	QNPVPKQSLP	QAQG.DSTGP	EESKKKVESK
A_SE_95_UG	GRKKRRQRR.	.GTPQSSSKDH	QDPIPKQSLP	PAQG.IPTGP	EESKKKVESK
A_UG_85_U4	GKKRKPRR.	.GPPQGSNDH	QTLIPKQPLP	QSQR.VSAGQ	EESKKKVESK
A_UG_92_92	GRKKRKPRR.	.GTPQSNNDH	QNPPIPKQPIP	RTQG.DSTGP	EESKKKVESK
AC_IN_95_2	GRKKWRQRR.	.RAPPSSSEDH	QNLISKQPIP	.QTQGDSTGP	EESKKKMESK
AC_RW_92_9	GRKKRRQRR.	.NAPPSSSEDH	QNPISKQPLS	.QTRGDPTGS	EESKKKVESK
AC_SE_96_S	GRKKRRQRR.	.SAPSSSKDH	QNPISKQSLP	.QTQGDPTGP	EEPKEVESK
ACD_SE_95	GRKKRRQRR.	.GPPQSNNDH	QNPVQKQPIP	QTQR.ESTGP	EESKKKVESK
ACG_BE_V	GRKKRSQRR.	.RAPPSSSEDR	QNLISKQPLS	.QTRGDPTGP	EESKKEVESK
AD_SE_93_S	GRKKRRQRR.	.XTPEGGAH	QDPIPKQPS	QPRGD.PTGP	KEKKK.VASK
AD_SE_95_S	GRKKRKQRR.	.GAPSSSKDH	QNPPIPKQPIP	QTQG.ISTGP	KESKKEVESK
ADHK_NO_97	GRKKRRPRR.	.RPPQSSQDH	QDFIPKQPLS	.RTHGEPTGP	KEKKK.VASK
ADK_CD_85	GRKKRRQRR.	.RPPQGNQAH	QDPLPEQPSS	QHRGDHPTGP	KEKKK.VESK
AG_BE_VI	GRKNRKHRR.	.GTPQGSNDH	QNPVPKQSLP	LIRG.IPTGP	EESKKEVASK
AG_NG_92_9	GRKKRRRRR.	.GTPQSHQDH	QNPVPKQPLP	TTRG.NPTGP	KESKKEVESK
AGHU_GA	GRKKRSQRR.	.RAPKSSPDH	QNLVPKQPS	.RTNGNPTGP	KEKKK.VASK
AGU_CD_76	GRKKRRQRR.	.GTPQDRKDH	QNPVPRQPLP	TTRG.NPTGP	EESKKEVESK
AJ_BW_98_B	GRKKRRQRR.	.TAPPGNKNH	QDLVQEPLS	.QTQRKSTGP	EESKKEVESK
B_AU_VH	GRKKRRQRR.	.RAPEDSQTH	QVSLSKQSP	QPRGD.PTGP	KESKKKVESK
B_CN_RL4	GRKKRRQRR.	.RAPQDSQTH	QASLSKQPAS	QPRGD.PAGP	KESKKKVESE
B_DE_86_D3	GRKKRRQRR.	.RAPEDSQTH	QVSLSKQPAS	QPRGD.PTGP	KESKKKVESE
B_DE_86_HA	GRKKRRQRR.	.RAPQDSQTH	QVSLPKQPS	QQRGD.PDSP	KESKKKVERE
B_FR_83_HX	GRKKRRQRR.	.RAHQNSQTH	QASLSKQPTS	QPRGD.PTGP	KE.KKKVERE
B_GA_OYI	GRKKRRQRR.	.RAPQDSKTH	QVSLSKQPAS	QPRGD.PTGP	KESKKKVERE
B_GB_CAM	GRKKRRQRR.	.RTPQSSKTH	QASLSKQPAS	QFQGD.PTGP	KESKKKVEGE
B_GB_GB8	GRKKRRQRR.	.RLPEDSQIH	QVSLPKQPTS	QPQGD.PTGP	KESKKKVESK
B_GB_59_MA	GRKKRRQRR.	.RAPQDSQTH	QVSLSKQPTS	QPRGD.PTGP	EESKKKVERE
B_KR_WK	GRKKRRQRR.	.RAPQDNKNH	QVSLSKQPTS	RARGD.PTGP	EESKEKVEKE
B_NL_86_32	GRKKRRQRR.	.RSPQDSETH	QVSLSKQPAS	QPRGD.PTGP	KESKKKVERE
B_TW_TWC	GRKKRRQRR.	.RTPQNSQTH	QADLSKQPTS	QPRGD.QTGQ	KESTKKVERE
B_US_DH1	GRKKRRKRR.	.RSPQHSQTH	QASLSKQPAS	QPRGD.PTGP	KESKKKVESE
B_US_P89	GRKKRRQRR.	.RPPQDSQTH	QVSLSKQPS	QPRGD.PTGP	KEQKKKVERE
B_US_83_RF	GRKKRRQRR.	.GPPQGSQTH	QVSLSKQPTS	QPRGD.PTGP	KESKEKVERE
B_US_83_SF	GRKKRRQRR.	.RAPQDSQTH	QASLSKQPAS	QSRGD.PTGP	TESKKKVERE

B_US_84_MN	GRKKRRQRR.	.RAPEDSQTH	QVSLPKQPAP	QFRGD.PTGP	KESKKKVERE
B_US_86_JR	GRKKRRQRR.	.RPPQDSQTH	QVSLPKQPSS	QQRGD.PTGP	KESKKKVERE
B_US_86_YU	GRKKRRQRR.	.RPPQDSQTH	QSSLSKQPTS	QLRGD.PTGP	TESKKKVERE
B_US_87_BC	GRKKRRQRR.	.RAPQDSQTH	QASLSKQPTS	QPRGD.PTGP	KESKKKVERE
B_US_88_WR	GRKKRRQRR.	.RAPPEGLTH	QVPLSKQPSS	QFRGD.PTGP	KESKKKVVERE
B_US_90_WE	GRKKRRQRR.	.RSPQNSQTH	QDLSLKQPTS	QPRGD.PTGP	KESKKKVERE
BF1_BR_93	GRKKRRQRH.	.RTPQSSQLH	QDPVPKQPAS	QAQGN.PTGP	KESKKEVESQ
C_BR_92_92	GRKKRRQRR.	.SAPPSSSEDH	QNPVSKQPLP	.QTRGDQTS	EESKKKVESK
C_BW_96_96	GRKKRRQRR.	.SAPPSSSEDH	QNPVSKQPLP	.QTRGDPTGL	EESKKKVESK
C_BW_96_96	GRKKRRQRR.	.SAPPSSSKDH	QNPVSKQPLP	.QTRGDPTGS	KESKKKVESK
C_BW_96_96	GRKKRRQRR.	.SAPPSSSEDH	QDLVPKQPLS	.QARGNPTSS	KESKKKVESK
C_BW_96_96	GRKKRRQRR.	.SAPPSSSEDH	QNLISKQPLP	.RTQGDSTGS	EESKKKVESK
C_ET_86_ET	GRKKRRQRR.	.RAPQSSSKDH	QNLISKQPLS	.HTRGDPTGS	EESKKKVESK
C_IN_93_93	GRKKRRQRR.	.SAPPSSSEDH	QNLISKQPLP	.RTQGDPTGS	EESKKKVESK
C_IN_93_93	GRKKRRQRR.	.RAPQSSSEDH	QNLISKQPLP	.RTQGDPTGS	EESKKKVESK
C_IN_93_93	GRKKRRQRR.	.SAPPSSSEDH	QNLISKQPLP	.RTQGDPTGS	EESKKKVESK
C_IN_94_94	GRKKRRQRR.	.SAPPQSSSEDH	QDLISKQPLP	.RTQGDPTGS	EESKKKVEGK
C_IN_95_95	GRKKRRQRR.	.SAPPQSSSEDH	QNPISKQPLP	.RTPGDPTGS	EESKKKVESK
CRF01_AE_C	GRKKRKHRR.	.GPPPGSKDH	QNPVSKQPLP	TTRG.NPTGP	KESKKEVASK
CRF01_AE_C	GRKKRKHRR.	.GPSQDSKDH	QNSIPKQPLP	TSRG.NPTGP	KESKKKVESK
CRF01_AE_C	GRKKRKHRR.	.GTPQSSSKGH	QDPISKQPLP	IIRG.NPTGP	KESKKEVESK
CRF01_AE_T	GRKKRKHRR.	.GTPQSSSKDH	QNPVSKQPLP	IIRR.NPTDP	KESKKEVASK
CRF01_AE_T	GRKKRKHRR.	.GTPQSRKDH	QHPIEQPLS	IIRG.NPTDP	KESKKEVASK
CRF01_AE_T	GRKKRKHRR.	.GTPQSSSKDH	QSPIEQPLP	IIRG.NPTDP	KESKKEVASK
CRF01_AE_T	GRKKRKHRR.	.GTPQSRKDH	QYPIEQPLP	IIRG.NPTDP	KESKKEVASK
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CRF01_AE_T	GRKKRKHRR.	.RTPQSSSKDH	QYPIEQPSP	IIRG.IPTDP	KESKKEVASK
CRF02_AG_F	GRKKRRRRR.	.GTPQSRQDH	QNPVSKQPLP	TTRG.DPTDP	KESKKEVASK
CRF02_AG_F	GRKKRRRRR.	.GTPQSRQDR	QNPVSKQPLP	TTRG.NPTGP	KESKREVESK
CRF02_AG_G	GRKKRRRRR.	.GTPQSHQDH	QNPVSKQSLP	QTRG.DPTGP	KESKKEVESK
CRF02_AG_N	GRKKRRRRR.	.GTPQSRQDH	QNPVSKQPLP	TTRG.NPTDP	KESKKEVESK
CRF02_AG_S	GRKKRRRRR.	.GTPQSRQDH	QDPVSKQPLP	TTRG.NPAGP	KESKKEVASK
CRF02_AG_S	GRKKRRRRR.	.GTPQSRQDH	QNPVSKQPLP	TTRG.EQTGP	KESKKEVASK
CRF03_AB_R	GRKKRRQRR.	.RAPQDNQTD	QVSLPKQPAS	QPRGD.PTGP	KE.KKKMERE
CRF03_AB_R	GRKKRRQRR.	.RPPQDNQTD	QVSLPKQPAS	QPRGD.PTGP	KE.KKKVERE
CRF04_cpx	GRKKRKHRR.	.GSLQSGSKGH	QNLIPKQPLS	QQPNGDSTGP	EEQKKKVASK
CRF04_cpx	GRKKRKRNE.	.DLLGFSRDR	QNPVSKQPLS	Q.PNGNPEGP	KEQKKKVASK
CRF04_cpx	GRKKRKHRR.	.RPPQSGSRDR	QNPVSKQPLS	QQHSGDPTGP	KEQKEAVASK
CRF05_DF_B	GRKKRRPRR.	.RPPQGSQAH	QDPVPEQPPS	QPRGD.PTGP	KKQKKEVESK
CRF05_DF_B	GRKKRRSRR.	.RPPQGGQAH	QIPVPEQPPS	QARGD.PTGQ	KEQKKKVESK
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CRF06_cpx	GRKKRRQRR.	.TAPPQSGKNH	QDPVSKQPLS	.QTQRKSTGP	EESKKEVESK
CRF06_cpx	GRKKRRQRR.	.TAPLQSGSKH	QDPVSKQPLS	.QTQRESTGP	EKSKEVESK
CRF11_cpx	GRKKRRQRR.	.AASHSSSENH	QDPVSKQPLS	.QPNRKPTGP	EESKKEVESK
CRF11_cpx	GRKKRRQRR.	.TASRSSKNH	QDPVSKQPLP	.QASRNPTGP	EESKKEVESK
D_CD_83_EL	GRKKRRQRR.	.GPPQGGQAH	QVPIPKQPSS	QPRGD.PTGP	KEQKKKVESE
D_CD_83_ND	GRKKRRQRR.	.KPPQGDQAH	QVPIPKQPSS	QSRGD.PTGP	K.KKKKVESE
D_CD_84_84	GRKKRRQRR.	.RPPHSSQTH	QDPVSKQPLS	QPRGD.PTGQ	KEKKK.VESK
D_UG_94_94	GRKKRRPRR.	.RTPPQGGQAH	QDPVSKQPLS	QPRGN.PTGP	KEKKK.VESE
F1_BE_93_V	GRKKRRQRH.	.RTPQSSQVH	QNSLPKQPLS	QARGD.PTGP	KESKKEVESK
F1_BR_93_9	GRKKRRQRR.	.RTPQSSQVH	QDFVPKQPIS	QARGN.PTGP	KESKKEVESK
F1_FI_93_F	GRKKRRQRH.	.RTPQSSQVH	QDPVSKQPLS	QPRRN.PTGP	KESKKEVESK
F1_FR_96_M	GRKKRRQRR.	.RTPQSSQVH	KNPIEQPLS	QARGD.PTGP	KESKKEVESK
F2_CM_95_M	GRKKRRQRR.	.RTPQSGEVH	QDPVSKQPLS	QTRGD.PTGP	EESKKKVESK
F2KU_BE_94	GRKKRRQRR.	.RTPQSSQAH	QNPVSKQPLS	QARGD.PTGP	KEPKKEVESK
G_BE_96_DR	GRKKRKHRR.	.GTPHSSSKDH	QTPVSKQPLS	TTRG.NPTGP	QESKKEVESK
G_NG_92_92	GRKKRRPRR.	.GTPQSSSKDH	QNPVSKQPLP	ITSG.NPTGS	EKPKKEVASK
G_SE_93_SE	GRKKRKHRR.	.GTPQSSSKGH	QDPVSKQPLP	TTRG.NPTGP	KESKKEVASK
H_BE_VI9	GRKKRRQRR.	.GTPKSLQDH	QTLIPKQPLS	.RTSGDPTGP	EKKKK.VASK

H_BE__VI9	GRKKRSRRR.	.ATPASVQDH	QNHIPKQPLS	.RTRGDPTGP	KEKKK.VASK
H_CF_90_90	GRKKRSQRH.	.RTPASLQDH	QNSISKQPLS	.RTHGDPTGP	KEQKKEVASK
J_SE_93_SE	GRKKRRQRR.	.SAPPGSKTH	QDLIPKQPLS	.QTQRKPTGP	EESKKEVESK
J_SE_94_SE	GRKKRRQRR.	.SAPPGSKNH	QDLIPEQPLF	.QTQRKPTGP	EESKKEVESK
K_CD_97_EQ	GREKRRQRT.	.TTPYASKNH	KDPIPKQPLP	.QARGDPTGP	KESKKEVESK
K_CM_96_MP	GRKKRRPRR.	.TTPYNSENH	QDPLRKQPLS	.QPRGEQTDG	KESKKKVESK
N_CM_95_YB	GRKKRSQRR.	.RTPQSSKSH	QDLIPEQPLS	.QQQGDQGTGQ	KKQKEALESK
O_CM__ANT	GRKK...RGR	PAAAS.HPDH	KDPVPKQSPT	ITK.RKQERQ	EEQEEVEKK
O_CM_91_MV	GRKK...RRR	PAAAASYPDN	KDPVPEQSL	HTG.RKQKRQ	EEQEKKEVEKE
O_SN__99S	GRKK...RRR	PAAAARHPDN	QDIVPEQLTY	ITN.RKQKRQ	EEQEKEVEKE
O_SN__99S	GRKK...RRR	PAAAARNPDN	QDIVPEQPPP	ITNNRKHKRQ	EEQEKEVEKE
U_CD__83C	GRKKRGKRR.	.RTPQSGPNH	QNIVSKQPSS	QPRGD.PTGQ	EEPKKKVEKK

	101	108
00BW0762_1	TETDPFD.	
00BW0768_2	TKTDQFD.	
00BW0874_2	TKTDQFD.	
00BW1471_2	TEADPCD.	
00BW1616_2	TETDPFD.	
00BW1686_8	TKTDPFDD.	
00BW1759_3	TETDRFD.	
00BW1773_2	TETDPD..	
00BW1783_5	TETDPFD.	
00BW1795_6	TETDPFD.	
00BW1811_3	TETDPD..	
00BW1859_5	TETDPYD.	
00BW1880_2	TETNPFDD.	
00BW1921_1	TEADQFD.	
00BW2036_1	TEADRFDD.	
00BW2063_6	TETDPFD.	
00BW2087_2	TERDPFD.	
00BW2127_2	TTTDPFD.	
00BW2276_7	TETDPYD.	
00BW3819_3	TKTDPFDD.	
00BW3842_8	TETDRFD.	
00BW3871_3	TKTDQFD.	
00BW3876_9	TKADPFDD.	
00BW3886_8	AETDQFDY	
00BW3891_6	TETDPFA.	
00BW3970_2	TERDPFA.	
00BW5031_1	TETDPFDW	
96BW01B21	TKTDPFDD.	
96BW0407	TEADPFDD.	
96BW0502	TEADPFA.	
96BW06_J4	TETDQFD.	
96BW11_06	TETDQFD.	
96BW1210	TETDPFD.	
96BW15B03	TETDRFD.	
96BW16_26	TETDPCD.	
96BW17A09	TEADPFDD.	
96BWM01_5	TKTDQFD.	
96BWM03_2	TETDPFD.	
98BWMC12_2	TKAHPFD.	
98BWMC13_4	TETDQFD.	
98BWMC14_a	TETDQFA.	
98BWM014_1	TETDPCA.	
98BWM018_d	TETDQFD.	
98BWM036_a	TETDPFD.	
98BWM037_d	TETDPFD.	
99BW3932_1	TETDPFD.	

99BW4642_4	TETDQFA.
99BW4745_8	TEPDPCD.
99BW4754_7	TETDPFD.
99BWMC16_8	TEADRFD.
A2_CD__97	AETDRFD.
A2_CY__94	AETDRFD.
A2D__97_9	AETDPCD.
A2G_CD__9	TETDPD..
A_BY_97_97	AETDQFD.
A_KE_93_Q2	AEADRFD.
A_SE_93_SE	AETDRFD.
A_SE_94_SE	AEADRFD.
A_SE_94_SE	AETDRFD.
A_SE_95_SE	TEADRFD.
A_SE_95_SE	TETDRFA.
A_SE_95_UG	AETDRFA.
A_UG_85_U4	AKTDRFA.
A_UG_92_92	TEADRYA.
AC_IN_95_2	AKTDRFD.
AC_RW_92_9	TEADPFDD.
AC_SE_96_S	TETDRFD.
ACD_SE_95_	AETDRFD.
ACG_BE__V	TETHPLA.
AD_SE_93_S	AEADQFDW
AD_SE_95_S	TEPDRFD.
ADHK_NO_97	TXTDPPFDW
ADK_CD_85_	AEADQFDW
AG_BE__VI	TETHPGD.
AG_NG_92_9	TETDQCA.
AGHU_GA__	AEADPPFDW
AGU_CD_76_	TETDPPFAW
AJ_BW_98_B	AKPDRFD.
B_AU__VH_	TETNPSD.
B_CN__RL4	TETDPRD.
B_DE_86_D3	TETDPID.
B_DE_86_HA	TEADPFDD.
B_FR_83_HX	TETDPFD.
B_GA__OYI	TETDPED.
B_GB__CAM	TETHPGD.
B_GB__GB8	TETDPSDW
B_GB_59_MA	TETDPVA.
B_KR__WK_	TVVDPVT.
B_NL_86_32	TETDPVD.
B_TW__TWC	TETDPNDQ
B_US__DH1	TETDPVH.
B_US__P89	TETDPVH.
B_US_83_RF	TETDPAVQ
B_US_83_SF	TETDPFD.
B_US_84_MN	TETHPVD.
B_US_86_JR	TETDPDN.
B_US_86_YU	TETDPVH.
B_US_87_BC	TETDPVD.
B_US_88_WR	TETDPIA.
B_US_90_WE	TETDPED.
BF1_BR_93_	AKTDPD..
C_BR_92_92	TETDPFD.
C_BW_96_96	TETDPFD.
C_BW_96_96	TETDQFD.
C_BW_96_96	TETDPFD.
C_BW_96_96	TETDRFD.

C_ET_86_ET	AETDPYA.
C_IN_93_93	TKTDPFD.
C_IN_93_93	AKTDPFA.
C_IN_93_93	TKTDPFA.
C_IN_94_94	TTSDPFD.
C_IN_95_95	TKTDPFD.
CRF01_AE_C	AKTDPFA.
CRF01_AE_C	AETDPDW.
CRF01_AE_C	TKTDPCA.
CRF01_AE_T	AETDQCD.
CRF01_AE_T	AETDPCD.
CRF01_AE_T	AETDPCD.
CRF01_AE_T	AETDPCD.
CRF01_AE_T	AETDPD..
CRF01_AE_T	AETDQCD.
CRF02_AG_F	TETDQGD.
CRF02_AG_F	TKTDPCD.
CRF02_AG_G	TETDPFA.
CRF02_AG_N	TKTDPCD.
CRF02_AG_S	TETDPCD.
CRF02_AG_S	TETGPCD.
CRF03_AB_R	TETHPFD.
CRF03_AB_R	TETHPFD.
CRF04_cpx_	TEADPFA.
CRF04_cpx_	TEADPFD.
CRF04_cpx_	TESNPFD.
CRF05_DF_B	TEADQFDW
CRF05_DF_B	AETDPFDC
CRF06_cpx_	AEPDRFD.
CRF06_cpx_	AEPDRFD.
CRF06_cpx_	AETDRFD.
CRF06_cpx_	TEPDRFD.
CRF11_cpx_	AEPDRFD.
CRF11_cpx_	AEPAPFD.
D_CD_83_EL	AETDPDC.
D_CD_83_ND	AETDPFDW
D_CD_84_84	TEVHPFDW
D_UG_94_94	TEADPFDW
F1_BE_93_V	AKTDPCA.
F1_BR_93_9	AKTDPD..
F1_FI_93_F	AKTDPCD.
F1_FR_96_M	TETDPFD.
F2_CM_95_M	TKTDPSD.
F2KU_BE_94	TETDPLD.
G_BE_96_DR	TETDPFD.
G_NG_92_92	TETDPLD.
G_SE_93_SE	AEADQCD.
H_BE__VI9	TETDPFDW
H_BE__VI9	TEADPCD.
H_CF_90_90	TETDPD..
J_SE_93_SE	AEPDRFD.
J_SE_94_SE	AEPDRFD.
K_CD_97_EQ	TKTDPD..
K_CM_96_MP	TKTDQFD.
N_CM_95_YB	TEADPCD.
O_CM__ANT	AGPGGYPR
O_CM_91_MV	TGPGSQPC
O_SN__99S	ACP.RYPG
O_SN__99S	TGSDRYPR
U_CD__83C	TTTDPFD.



Table 17. HIV Vif Sequence Alignment  
GCG Multiple Sequence File.  
Written by Omega 1.1

Name: 00BW0762_1	<u>SEQ ID NO: 1302</u>	Len: 194	Check: 4675	Weight: 1.00
Name: 00BW0768_2	<u>SEQ ID NO: 1303</u>	Len: 194	Check: 4961	Weight: 1.00
Name: 00BW0874_2	<u>SEQ ID NO: 1304</u>	Len: 194	Check: 3755	Weight: 1.00
Name: 00BW1471_2	<u>SEQ ID NO: 1305</u>	Len: 194	Check: 3843	Weight: 1.00
Name: 00BW1616_2	<u>SEQ ID NO: 1306</u>	Len: 194	Check: 4613	Weight: 1.00
Name: 00BW1686_8	<u>SEQ ID NO: 1307</u>	Len: 194	Check: 4096	Weight: 1.00
Name: 00BW1759_3	<u>SEQ ID NO: 1308</u>	Len: 194	Check: 3523	Weight: 1.00
Name: 00BW1773_2	<u>SEQ ID NO: 1309</u>	Len: 194	Check: 4446	Weight: 1.00
Name: 00BW1783_5	<u>SEQ ID NO: 1310</u>	Len: 194	Check: 3151	Weight: 1.00
Name: 00BW1795_6	<u>SEQ ID NO: 1311</u>	Len: 194	Check: 4892	Weight: 1.00
Name: 00BW1811_3	<u>SEQ ID NO: 1312</u>	Len: 194	Check: 3877	Weight: 1.00
Name: 00BW1859_5	<u>SEQ ID NO: 1313</u>	Len: 194	Check: 3290	Weight: 1.00
Name: 00BW1880_2	<u>SEQ ID NO: 1314</u>	Len: 194	Check: 2555	Weight: 1.00
Name: 00BW1921_1	<u>SEQ ID NO: 1315</u>	Len: 194	Check: 4284	Weight: 1.00
Name: 00BW2036_1	<u>SEQ ID NO: 1316</u>	Len: 194	Check: 4019	Weight: 1.00
Name: 00BW2063_6	<u>SEQ ID NO: 1317</u>	Len: 194	Check: 4165	Weight: 1.00
Name: 00BW2087_2	<u>SEQ ID NO: 1318</u>	Len: 194	Check: 5068	Weight: 1.00
Name: 00BW2127_2	<u>SEQ ID NO: 1319</u>	Len: 194	Check: 5231	Weight: 1.00
Name: 00BW2128_3	<u>SEQ ID NO: 1320</u>	Len: 194	Check: 5469	Weight: 1.00
Name: 00BW2276_7	<u>SEQ ID NO: 1321</u>	Len: 194	Check: 5547	Weight: 1.00
Name: 00BW3819_3	<u>SEQ ID NO: 1322</u>	Len: 194	Check: 1251	Weight: 1.00
Name: 00BW3842_8	<u>SEQ ID NO: 1323</u>	Len: 194	Check: 4197	Weight: 1.00
Name: 00BW3871_3	<u>SEQ ID NO: 1324</u>	Len: 194	Check: 3487	Weight: 1.00
Name: 00BW3876_9	<u>SEQ ID NO: 1325</u>	Len: 194	Check: 4432	Weight: 1.00
Name: 00BW3886_8	<u>SEQ ID NO: 1326</u>	Len: 194	Check: 5175	Weight: 1.00
Name: 00BW3891_6	<u>SEQ ID NO: 1327</u>	Len: 194	Check: 3845	Weight: 1.00
Name: 00BW3970_2	<u>SEQ ID NO: 1328</u>	Len: 194	Check: 2268	Weight: 1.00
Name: 00BW5031_1	<u>SEQ ID NO: 1329</u>	Len: 194	Check: 3711	Weight: 1.00
Name: 96BW01B21	<u>SEQ ID NO: 1330</u>	Len: 194	Check: 4602	Weight: 1.00
Name: 96BW0407	<u>SEQ ID NO: 1331</u>	Len: 194	Check: 5108	Weight: 1.00
Name: 96BW0502	<u>SEQ ID NO: 1332</u>	Len: 194	Check: 4385	Weight: 1.00
Name: 96BW06_J4	<u>SEQ ID NO: 1333</u>	Len: 194	Check: 5371	Weight: 1.00
Name: 96BW11_06	<u>SEQ ID NO: 1334</u>	Len: 194	Check: 6037	Weight: 1.00
Name: 96BW1210	<u>SEQ ID NO: 1335</u>	Len: 194	Check: 4343	Weight: 1.00
Name: 96BW15B03	<u>SEQ ID NO: 1336</u>	Len: 194	Check: 5690	Weight: 1.00
Name: 96BW16_26	<u>SEQ ID NO: 1337</u>	Len: 194	Check: 4471	Weight: 1.00
Name: 96BW17A09	<u>SEQ ID NO: 1338</u>	Len: 194	Check: 3907	Weight: 1.00
Name: 96BWMO1_5	<u>SEQ ID NO: 1339</u>	Len: 194	Check: 5608	Weight: 1.00
Name: 96BWMO3_2	<u>SEQ ID NO: 1340</u>	Len: 194	Check: 3079	Weight: 1.00
Name: 98BWMC12_2	<u>SEQ ID NO: 1341</u>	Len: 194	Check: 5336	Weight: 1.00
Name: 98BWMC13_4	<u>SEQ ID NO: 1342</u>	Len: 194	Check: 5304	Weight: 1.00
Name: 98BWMC14_a	<u>SEQ ID NO: 1343</u>	Len: 194	Check: 3984	Weight: 1.00
Name: 98BWMO14_1	<u>SEQ ID NO: 1344</u>	Len: 194	Check: 2480	Weight: 1.00
Name: 98BWMO18_d	<u>SEQ ID NO: 1345</u>	Len: 194	Check: 2801	Weight: 1.00
Name: 98BWMO36_a	<u>SEQ ID NO: 1346</u>	Len: 194	Check: 3762	Weight: 1.00
Name: 98BWMO37_d	<u>SEQ ID NO: 1347</u>	Len: 194	Check: 4971	Weight: 1.00
Name: 99BW3932_1	<u>SEQ ID NO: 1348</u>	Len: 194	Check: 4165	Weight: 1.00
Name: 99BW4642_4	<u>SEQ ID NO: 1349</u>	Len: 194	Check: 2912	Weight: 1.00
Name: 99BW4745_8	<u>SEQ ID NO: 1350</u>	Len: 194	Check: 5323	Weight: 1.00
Name: 99BW4754_7	<u>SEQ ID NO: 1351</u>	Len: 194	Check: 3964	Weight: 1.00
Name: 99BWMC16_8	<u>SEQ ID NO: 1352</u>	Len: 194	Check: 6325	Weight: 1.00
Name: A2_CD_97CD	<u>SEQ ID NO: 1353</u>	Len: 194	Check: 5849	Weight: 1.00
Name: A2_CY_94CY	<u>SEQ ID NO: 1354</u>	Len: 194	Check: 5097	Weight: 1.00
Name: A2D_97KR	<u>SEQ ID NO: 1355</u>	Len: 194	Check: 3871	Weight: 1.00
Name: A2G_CD_97C	<u>SEQ ID NO: 1356</u>	Len: 194	Check: 5705	Weight: 1.00
Name: A_BY_97BL0	<u>SEQ ID NO: 1357</u>	Len: 194	Check: 8467	Weight: 1.00



Name: A_KE_Q23_A	<u>SEQ ID NO: 1358</u>	Len: 194	Check: 5053	Weight: 1.00
Name: A_SE_SE659	<u>SEQ ID NO: 1359</u>	Len: 194	Check: 3808	Weight: 1.00
Name: A_SE_SE725	<u>SEQ ID NO: 1360</u>	Len: 194	Check: 5856	Weight: 1.00
Name: A_SE_SE753	<u>SEQ ID NO: 1361</u>	Len: 194	Check: 5873	Weight: 1.00
Name: A_SE_SE853	<u>SEQ ID NO: 1362</u>	Len: 194	Check: 5523	Weight: 1.00
Name: A_SE_SE889	<u>SEQ ID NO: 1363</u>	Len: 194	Check: 3207	Weight: 1.00
Name: A_SE_UGSE8	<u>SEQ ID NO: 1364</u>	Len: 194	Check: 5837	Weight: 1.00
Name: A_UG_92UG0	<u>SEQ ID NO: 1365</u>	Len: 194	Check: 5055	Weight: 1.00
Name: A_UG_U455_	<u>SEQ ID NO: 1366</u>	Len: 194	Check: 5386	Weight: 1.00
Name: AC_IN_2130	<u>SEQ ID NO: 1367</u>	Len: 194	Check: 3540	Weight: 1.00
Name: AC_RW_92RW	<u>SEQ ID NO: 1368</u>	Len: 194	Check: 3664	Weight: 1.00
Name: AC_SE_SE94	<u>SEQ ID NO: 1369</u>	Len: 194	Check: 4187	Weight: 1.00
Name: ACD_SE_SE8	<u>SEQ ID NO: 1370</u>	Len: 194	Check: 4653	Weight: 1.00
Name: ACG_BE_VI1	<u>SEQ ID NO: 1371</u>	Len: 194	Check: 6680	Weight: 1.00
Name: AD_SE_SE69	<u>SEQ ID NO: 1372</u>	Len: 194	Check: 6416	Weight: 1.00
Name: AD_SE_SE71	<u>SEQ ID NO: 1373</u>	Len: 194	Check: 8542	Weight: 1.00
Name: ADHK_NO_97	<u>SEQ ID NO: 1374</u>	Len: 194	Check: 1255	Weight: 1.00
Name: ADK_CD_MAL	<u>SEQ ID NO: 1375</u>	Len: 194	Check: 5519	Weight: 1.00
Name: AG_BE_VI11	<u>SEQ ID NO: 1376</u>	Len: 194	Check: 7396	Weight: 1.00
Name: AG_NG_92NG	<u>SEQ ID NO: 1377</u>	Len: 194	Check: 7120	Weight: 1.00
Name: AGHU_GA_VI	<u>SEQ ID NO: 1378</u>	Len: 194	Check: 5827	Weight: 1.00
Name: AGU_CD_Z32	<u>SEQ ID NO: 1379</u>	Len: 194	Check: 4744	Weight: 1.00
Name: AJ_BW_BW21	<u>SEQ ID NO: 1380</u>	Len: 194	Check: 4938	Weight: 1.00
Name: B_AU_VH_AF	<u>SEQ ID NO: 1381</u>	Len: 194	Check: 6911	Weight: 1.00
Name: B_CN_RL42_	<u>SEQ ID NO: 1382</u>	Len: 194	Check: 6101	Weight: 1.00
Name: B_DE_D31_U	<u>SEQ ID NO: 1383</u>	Len: 194	Check: 3568	Weight: 1.00
Name: B_DE_HAN_U	<u>SEQ ID NO: 1384</u>	Len: 194	Check: 6199	Weight: 1.00
Name: B_FR_HXB2_	<u>SEQ ID NO: 1385</u>	Len: 194	Check: 4714	Weight: 1.00
Name: B_GA_OYI_	<u>SEQ ID NO: 1386</u>	Len: 194	Check: 4534	Weight: 1.00
Name: B_GB_CAM1_	<u>SEQ ID NO: 1387</u>	Len: 194	Check: 4796	Weight: 1.00
Name: B_GB_GB8_A	<u>SEQ ID NO: 1388</u>	Len: 194	Check: 6277	Weight: 1.00
Name: B_GB_MANC_	<u>SEQ ID NO: 1389</u>	Len: 194	Check: 4800	Weight: 1.00
Name: B_KR_WK_AF	<u>SEQ ID NO: 1390</u>	Len: 194	Check: 3856	Weight: 1.00
Name: B_NL_3202A	<u>SEQ ID NO: 1391</u>	Len: 194	Check: 4181	Weight: 1.00
Name: B_TW_TWCYS	<u>SEQ ID NO: 1392</u>	Len: 194	Check: 5670	Weight: 1.00
Name: B_US_BC_L0	<u>SEQ ID NO: 1393</u>	Len: 194	Check: 4644	Weight: 1.00
Name: B_US_DH123	<u>SEQ ID NO: 1394</u>	Len: 194	Check: 5023	Weight: 1.00
Name: B_US_JRCSE	<u>SEQ ID NO: 1395</u>	Len: 194	Check: 6235	Weight: 1.00
Name: B_US_MNCG_	<u>SEQ ID NO: 1396</u>	Len: 194	Check: 2067	Weight: 1.00
Name: B_US_P896_	<u>SEQ ID NO: 1397</u>	Len: 194	Check: 6322	Weight: 1.00
Name: B_US_RF_M1	<u>SEQ ID NO: 1398</u>	Len: 194	Check: 5045	Weight: 1.00
Name: B_US_SF2_K	<u>SEQ ID NO: 1399</u>	Len: 194	Check: 3723	Weight: 1.00
Name: B_US_WEAU1	<u>SEQ ID NO: 1400</u>	Len: 194	Check: 4222	Weight: 1.00
Name: B_US_WR27_	<u>SEQ ID NO: 1401</u>	Len: 194	Check: 7503	Weight: 1.00
Name: B_US_YU2_M	<u>SEQ ID NO: 1402</u>	Len: 194	Check: 5093	Weight: 1.00
Name: BF1_BR_93B	<u>SEQ ID NO: 1403</u>	Len: 194	Check: 4341	Weight: 1.00
Name: C_BR_92BR0	<u>SEQ ID NO: 1404</u>	Len: 194	Check: 5265	Weight: 1.00
Name: C_BW_96BW0	<u>SEQ ID NO: 1405</u>	Len: 194	Check: 5846	Weight: 1.00
Name: C_BW_96BW1	<u>SEQ ID NO: 1406</u>	Len: 194	Check: 3799	Weight: 1.00
Name: C_BW_96BW1	<u>SEQ ID NO: 1407</u>	Len: 194	Check: 4343	Weight: 1.00
Name: C_BW_96BW1	<u>SEQ ID NO: 1408</u>	Len: 194	Check: 5690	Weight: 1.00
Name: C_ET_ETH22	<u>SEQ ID NO: 1409</u>	Len: 194	Check: 4205	Weight: 1.00
Name: C_IN_93IN1	<u>SEQ ID NO: 1410</u>	Len: 194	Check: 3033	Weight: 1.00
Name: C_IN_93IN9	<u>SEQ ID NO: 1411</u>	Len: 194	Check: 3201	Weight: 1.00
Name: C_IN_93IN9	<u>SEQ ID NO: 1412</u>	Len: 194	Check: 4905	Weight: 1.00
Name: C_IN_94IN1	<u>SEQ ID NO: 1413</u>	Len: 194	Check: 3129	Weight: 1.00
Name: C_IN_95IN2	<u>SEQ ID NO: 1414</u>	Len: 194	Check: 3351	Weight: 1.00
Name: CRF01_AE_C	<u>SEQ ID NO: 1415</u>	Len: 194	Check: 6355	Weight: 1.00
Name: CRF01_AE_C	<u>SEQ ID NO: 1416</u>	Len: 194	Check: 2596	Weight: 1.00
Name: CRF01_AE_C	<u>SEQ ID NO: 1417</u>	Len: 194	Check: 4412	Weight: 1.00

Name:	CRF01_AE_T	SEQ ID NO: 1418	Len: 194	Check: 5882	Weight: 1.00
Name:	CRF01_AE_T	SEQ ID NO: 1419	Len: 194	Check: 5558	Weight: 1.00
Name:	CRF01_AE_T	SEQ ID NO: 1420	Len: 194	Check: 5926	Weight: 1.00
Name:	CRF01_AE_T	SEQ ID NO: 1421	Len: 194	Check: 5579	Weight: 1.00
Name:	CRF01_AE_T	SEQ ID NO: 1422	Len: 194	Check: 2960	Weight: 1.00
Name:	CRF01_AE_T	SEQ ID NO: 1423	Len: 194	Check: 5867	Weight: 1.00
Name:	CRF02_AG_F	SEQ ID NO: 1424	Len: 194	Check: 1879	Weight: 1.00
Name:	CRF02_AG_F	SEQ ID NO: 1425	Len: 194	Check: 3893	Weight: 1.00
Name:	CRF02_AG_G	SEQ ID NO: 1426	Len: 194	Check: 5632	Weight: 1.00
Name:	CRF02_AG_N	SEQ ID NO: 1427	Len: 194	Check: 3187	Weight: 1.00
Name:	CRF02_AG_S	SEQ ID NO: 1428	Len: 194	Check: 5274	Weight: 1.00
Name:	CRF02_AG_S	SEQ ID NO: 1429	Len: 194	Check: 5177	Weight: 1.00
Name:	CRF03_AB_R	SEQ ID NO: 1430	Len: 194	Check: 5215	Weight: 1.00
Name:	CRF03_AB_R	SEQ ID NO: 1431	Len: 194	Check: 5211	Weight: 1.00
Name:	CRF04_cpx	SEQ ID NO: 1432	Len: 194	Check: 2914	Weight: 1.00
Name:	CRF04_cpx	SEQ ID NO: 1433	Len: 194	Check: 5450	Weight: 1.00
Name:	CRF04_cpx	SEQ ID NO: 1434	Len: 194	Check: 4358	Weight: 1.00
Name:	CRF05_DF_B	SEQ ID NO: 1435	Len: 194	Check: 7168	Weight: 1.00
Name:	CRF05_DF_B	SEQ ID NO: 1436	Len: 194	Check: 5710	Weight: 1.00
Name:	CRF06_cpx	SEQ ID NO: 1437	Len: 194	Check: 4977	Weight: 1.00
Name:	CRF06_cpx	SEQ ID NO: 1438	Len: 194	Check: 5603	Weight: 1.00
Name:	CRF06_cpx	SEQ ID NO: 1439	Len: 194	Check: 4458	Weight: 1.00
Name:	CRF06_cpx	SEQ ID NO: 1440	Len: 194	Check: 3711	Weight: 1.00
Name:	CRF11_cpx	SEQ ID NO: 1441	Len: 194	Check: 4246	Weight: 1.00
Name:	CRF11_cpx	SEQ ID NO: 1442	Len: 194	Check: 7186	Weight: 1.00
Name:	D_CD_84ZR0	SEQ ID NO: 1443	Len: 194	Check: 4173	Weight: 1.00
Name:	D_CD_ELI_K	SEQ ID NO: 1444	Len: 194	Check: 5080	Weight: 1.00
Name:	D_CD_NDK_M	SEQ ID NO: 1445	Len: 194	Check: 4285	Weight: 1.00
Name:	D_UG_94UG1	SEQ ID NO: 1446	Len: 194	Check: 3203	Weight: 1.00
Name:	F1_BE_VI85	SEQ ID NO: 1447	Len: 194	Check: 5281	Weight: 1.00
Name:	F1_BR_93BR	SEQ ID NO: 1448	Len: 194	Check: 2780	Weight: 1.00
Name:	F1_FI_FIN9	SEQ ID NO: 1449	Len: 194	Check: 3522	Weight: 1.00
Name:	F1_FR_MP41	SEQ ID NO: 1450	Len: 194	Check: 3777	Weight: 1.00
Name:	F2_CM_MP25	SEQ ID NO: 1451	Len: 194	Check: 5402	Weight: 1.00
Name:	F2KU_BE_VI	SEQ ID NO: 1452	Len: 194	Check: 6170	Weight: 1.00
Name:	G_BE_DRCBL	SEQ ID NO: 1453	Len: 194	Check: 6155	Weight: 1.00
Name:	G_NG_92NG0	SEQ ID NO: 1454	Len: 194	Check: 5616	Weight: 1.00
Name:	G_SE_SE616	SEQ ID NO: 1455	Len: 194	Check: 6641	Weight: 1.00
Name:	H_BE_VI991	SEQ ID NO: 1456	Len: 194	Check: 5850	Weight: 1.00
Name:	H_BE_VI997	SEQ ID NO: 1457	Len: 194	Check: 6598	Weight: 1.00
Name:	H_CF_90CF0	SEQ ID NO: 1458	Len: 194	Check: 4443	Weight: 1.00
Name:	J_SE_SE702	SEQ ID NO: 1459	Len: 194	Check: 6028	Weight: 1.00
Name:	J_SE_SE788	SEQ ID NO: 1460	Len: 194	Check: 5724	Weight: 1.00
Name:	K_CD_EQTB1	SEQ ID NO: 1461	Len: 194	Check: 6926	Weight: 1.00
Name:	K_CM_MP535	SEQ ID NO: 1462	Len: 194	Check: 6479	Weight: 1.00
Name:	N_CM_YBF30	SEQ ID NO: 1463	Len: 194	Check: 4619	Weight: 1.00
Name:	O_CM_ANT70	SEQ ID NO: 1464	Len: 194	Check: 412	Weight: 1.00
Name:	O_CM_MVP51	SEQ ID NO: 1465	Len: 194	Check: 6622	Weight: 1.00
Name:	O_SN_99SE	SEQ ID NO: 1466	Len: 194	Check: 8844	Weight: 1.00
Name:	O_SN_99SE	SEQ ID NO: 1467	Len: 194	Check: 9492	Weight: 1.00
Name:	U_CD_83C	SEQ ID NO: 1468	Len: 194	Check: 5631	Weight: 1.00

SEQ ID NO	1	50
<u>1302</u>	00BW0762_1	MENRWQVLIV WQVDRMKIRT WNSLVKHHMY VSKRANGWFY RHYESRHPK
<u>1303</u>	00BW0768_2	MENRWQGLIV WQVDRMKIRT WNSLVKHHMY VSRRANGWFY RHYESRHPK
<u>1304</u>	00BW0874_2	MENRWQVLIV WQVDRMKIRA WNSLVKHHMY ISRKASGWFY RHYESRHPK
<u>1305</u>	00BW1471_2	MENRWQVLIV WQVDRMKIRT WNSLVKHHMY ISRRAGWVY RHYESRHPK
<u>1306</u>	00BW1616_2	MENRWQVLIV WQVDRMRIRT WNSLVKHHMY VSRRASGWFY RHYESRHPK

<u>1307</u>	00BW1686_8	MENRWQVLIV	WQVDRMKIRT	WNSLVKHHMY	ISRRASGWSY	RHHYESRHPK
<u>1308</u>	0BW1759_3	MENRWQVLIV	WQVDRMKIRT	WNSLVKHHMY	ISKRAKGWLY	RHHYENRHPK
<u>1309</u>	00BW1773_2	MENRWQVLIV	WQVDRMKIKT	WNSLVKHHMY	VSKRAKGWLY	RHHYESRHPK
<u>1310</u>	00BW1783_5	MENRWQVLIV	WQVDRMKIRT	WNSLVKHHMY	ISKKARGWLY	RHHYESRHPK
<u>1311</u>	00BW1795_6	MENRWQVLIV	WQVDRMKIRT	WNSLVKHHMY	VSRKANGWLY	RHHYESRHPK
<u>1312</u>	00BW1811_3	MENRWQVLIV	WQVDRMKIKT	WNSLVKHHMY	ISKKARGWLY	RHHYESRHPK
<u>1313</u>	00BW1859_5	MENRWQVLIV	WQVDRMKIRT	WNSLVKHHMY	ISRRASGWLY	RHHYESRHPK
<u>1314</u>	00BW1880_2	MENRWQVLIV	WQVDRMKIRT	WNSLVKHHMY	ISRRASGWLY	RHHYESRHPK
<u>1315</u>	00BW1921_1	MENRWQVLIV	WQVDRMKIRT	WNSLVKHHMY	ISRRASGWLY	RHHYESRHPK
<u>1316</u>	00BW2036_1	MENRWQALIV	WQVDRMKIRT	WNSLVKHHMY	VSKRAKGWLY	RHHYESRHPK
<u>1317</u>	00BW2063_6	MENRWQGLIV	WQVDRMKIRT	WNSLVKHHMY	ISRRASGWLY	RHHYESRHPK
<u>1318</u>	00BW2087_2	MENRWQVLIV	WQVDRMKIRT	WNSLVKHHMY	ISRRASGWLY	RHHYESRHPK
<u>1319</u>	00BW2127_2	MENRWQVLIV	WQVDRMKIRT	WNSLVKHHMY	TSKATGWLY	RHHYESRHPK
<u>1320</u>	00BW2128_3	MENRWQVLIV	WQVDRMKIRT	WNSLVKHHMY	VSRRTNGWLY	RHHYESRHPK
<u>1321</u>	00BW2276_7	MENRWQVLIV	WQVDRMKIRT	WNSLVKHHMY	ISRRASGWLY	RHHYESRHPK
<u>1322</u>	00BW3819_3	MENRWQVLIV	WQVDRMKIRT	WNSLVKHHMY	ISKRAKGWLY	RHHYESRHPK
<u>1323</u>	00BW3842_8	MENRWQALIV	WQVDRMKIRT	WNSLVKHHMY	ISRRASGWLY	RHHYESRHPK
<u>1324</u>	00BW3871_3	MENRWQVLIV	WQVDRMKIRT	WNSLVKHHMY	ISRRASGWLY	RHHYESRHPK
<u>1325</u>	00BW3876_9	MENRWQVLIV	WQVDRMKIRT	WNSLVKHHMY	VSRKANGWLY	RHHYESRHPK
<u>1326</u>	00BW3886_8	MENRWQVLIV	WQVDRMKIRT	WNSLVKHHMY	ISKRAKGWLY	RHHYESRHPK
<u>1327</u>	00BW3891_6	MENRWQVIV	WQVDRMKIRT	WNSLVKHHMY	VSKKANGWLY	RHHYESRHPK
<u>1328</u>	00BW3970_2	MENRWQVLIV	WQVDRMKIRT	WNSLVKHHMY	VSRASGWLY	RHHYESRHPK
<u>1329</u>	00BW5031_1	MDNRWQGLIV	WQVDRMKIRT	WNSLVKHHMY	VSRASGWLY	RHHYESRHPK
<u>1330</u>	96BW01B21	MENRWQVLIV	WQVDRMKIRT	WNSLVKHHMY	VSRASGWLY	RHHYESRHPK
<u>1331</u>	96BW0407	MENRWQVIV	WQVDRMKIRT	WNSLVKHHMY	VSKKANGWLY	RHHYESRHPK
<u>1332</u>	96BW0502	MENRWQVLIV	WQVDRMKIRT	WNSLVKHHMY	ISKRAKGWLY	RHHYESRHPK
<u>1333</u>	96BW06_J4	MENRWQVLIV	WQVDRMKIRT	WNSLVKHHMY	ISKRAKGWLY	RHHYESRHPK
<u>1334</u>	96BW11_06	MENRWQALIV	WQVDRMKIRT	WNSLVKHHMY	VSRASGWLY	RHHYESRHPK
<u>1335</u>	96BW1210	MENRWQGLIV	WQVDRMKIRT	WNSLVKHHMY	VSKRADGWLY	RHHYESRHPK
<u>1336</u>	96BW15B03	MENRWQALIV	WQVDRMKIRT	WNSLVKHHMY	VSKRTNGWLY	RHHYESRHPK
<u>1337</u>	96BW16_26	MENRWQVLIV	WQVDRMKIKT	WNSLVKHHMY	ISRRASGWLY	RHHYESRHPK
<u>1338</u>	96BW17A09	MENRWQVLIV	WQVDRMKIRT	WNSLVKHHMY	ISRRASGWLY	RHHYESRHPK
<u>1339</u>	96BWMO1_5	MENRWQGLIV	WQVDRMKIRT	WNSLVKHHMY	VSKRAAGWLY	RHHYESRHPK
<u>1340</u>	96BWMO3_2	MENRWQVLIV	WQVDRMKIRT	WNSLVKHHMY	VSKRAAGWLY	RHHYESRHPK
<u>1341</u>	98BWMC12_2	MENRWQVLIV	WQVDRMKIRT	WNSLVKHHMY	TSGRASGWLY	RHHYESRHPK
<u>1342</u>	98BWMC13_4	MENRWQVLIV	WQVDRMKIRT	WNSLVKHHMY	VSKRAAGWLY	RHHYESRHPK
<u>1343</u>	98BWMC14_a	MENRWQGLIV	WQVDRMKIRT	WNSLVKHHMY	ISRRASGWLY	RHHYESRHPK
<u>1344</u>	98BWMO14_1	MENRWQVLIV	WQVDRMKIRT	WNSLVKHHMY	ISRRASGWLY	RHHYESRHPK
<u>1345</u>	98BWMO18_d	MENRWQVLIV	WQVDRMKIRT	WNSLVKHHMY	VSKRAAGWLY	RHHYESRHPK
<u>1346</u>	98BWMO36_a	MENRWQVLIV	WQVDRMKIRA	WNSLVKHHMY	ISKRAAGWLY	RHHYESRHPK
<u>1347</u>	98BWMO37_d	MENRWQVLIV	WQVDRMKIRT	WNSLVKHHMY	VSKRASKWLY	RHHYESRHPK
<u>1348</u>	99BW3932_1	MENRWQVLIV	WQVDRMKIRT	WNSLVKHHMY	ISRRASGWLY	RHHYESRHPK
<u>1349</u>	99BW4642_4	MENRWQVLIV	WQVDRMKIRT	WNSLVKHHMY	VSKRAAGWLY	RHHYESRHPK
<u>1350</u>	99BW4745_8	MENRWQVLIV	WQVDRMKIRT	WNSLVKHHMY	ISRRASGWLY	RHHYESRHPK
<u>1351</u>	99BW4754_7	MENRWQVIV	WQVDRMKIRT	WNSLVKHHMY	VSRASGWLY	RHHYESRHPK
<u>1352</u>	99BWMC16_8	MENRWQGLIV	WQVDRMKIRT	WNSLVKHHMY	VSRASGWLY	RHHYESRHPK
<u>1353</u>	A2_CD_97CD	MENRWQVIV	WQVDRMKIRT	WNSLVKHHMY	VSKKAREWLY	RHHYESRHPK

1354	A2_CY_94CY	MENRWQVMIV	WQVDRMRIRT	WNSLVKHHMY	ISRKAKGWVY	KHHYESRNPR
1355	A2D___97KR	MENRWQVMIV	WQVDRMRIRT	WNSLVKHHMY	VSKKAKDWCY	RHHYESINPR
1356	A2G_CD_97C	MENRWQVMIV	WQVDRMRIKR	WNSLVKHHMY	VSRKAKDWFY	RHHYESRHPK
1357	A_BY_97BL0	XENRWQVXIV	WQVDRMRIRT	WNSLVKHHMY	VSKKAR.EVY	RHHYESRQPR
1358	A_KE_Q23_A	MENRWQAMIV	WQVDRMRIRT	WNSLVKHHMH	VSKKAKRWFY	RHHYESRHPK
1359	A_SE_SE659	MENRWQVMIV	WQVDRMRIRT	WNSLVKHHMY	VSKKAKNWVY	RHHFESRHPK
1360	A_SE_SE725	MENRWQVMIV	WQVDRMRIRT	WNSLVKHHMY	VSRKAKDWFY	RHHYESRNPR
1361	A_SE_SE753	MENRWQVMIV	WQVDRMRIRT	WNSLVKHHMC	VSKKARNWFY	RHHYESRHPK
1362	A_SE_SE853	MENRWQVMIV	WQVDRMRIRT	WNSLVKHHMY	ISKKAKNWFY	RHHFESRHPK
1363	A_SE_SE889	MENRWQVMIV	WQVDRMRIRT	WNSLVKHHMY	ISKKAKGWLY	RHHFESRHPK
1364	A_SE_UGSE8	MENRWQVMIV	WQVDRMRIRT	WNSLVKHHMY	ISKKAAGWFY	RHHYESRHPK
1365	A_UG_92UG0	MENRWQVMIV	WQVDRMRIRT	WNSLVKHHMY	ISRRAKGWFY	RHHYESRHPK
1366	A_UG_U455_	MENRWQVMIV	WQVDRMKIRT	WNSLVKHHMY	VSKKAQGWFY	RHHYESRHSR
1367	AC_IN_2130	MENRWQALIV	WQVDRMKIRT	WNSLVKHHMY	VSRKANGWFY	RHHYDSRHPK
1368	AC_RW_92RW	MENRWQVMIV	WQVDRMKIRT	WNSLVKHHMY	ASRRAKGWFY	RHHYESRHPK
1369	AC_SE_SE94	MENRWQVMIV	WQVDRMRIRT	WNSLVKHHMY	ISKKAKRWFY	RHHYESRHPK
1370	ACD_SE_SE8	MENRWQVMIV	WQVDRMRIGT	N.SLVKHHMY	VSKKARGWFY	RHHYXTRHPR
1371	ACG_BE_VI1	MENRWQVMIV	WQVDRMRIRT	WNSLVKHHMY	TSKKAKNWCY	RHHYESMHPK
1372	AD_SE_SE69	MENRWQVMIV	WQVDRMRIRT	WNSLVKHHMY	VSKQARGWLY	RHHYDCLNPK
1373	AD_SE_SE71	MENRWQVMIV	WQVDRMRIKT	WNSLVKHHMY	VSKKAQNWVY	RHHYESRHPR
1374	ADHK_NO_97	MENRWQVMIV	WQVDRMRIRT	WNSLVKHHMY	VSKKANKWLF	RHHYESRHPK
1375	ADK_CD_MAL	MENRWQVMIV	WQVDRMRIRT	WNSLVKHHMY	VSKKAKNWFY	RHHYESRHPK
1376	AG_BE_VI11	MENRWQVMIV	WQVDRMRIRT	WNSLVKHHMY	VSKKAKGWFY	RHHYESRHPK
1377	AG_NG_92NG	MENRWQVIV	WQVDRMRIRT	WNSLVKHHMY	KSKKAKDWFY	RHHYESRHPK
1378	AGHU_GA_VI	MENRWQVMIV	WQVDRMRIST	WNSLVKHHMY	VSKKAQGWFY	RHHYDCTHPR
1379	AGU_CD_Z32	MENRWQVMIV	WQVDRMRINT	WNSLVKHHMY	KSKKAKNWFY	RHHYDSNHPK
1380	AJ_BW_BW21	MENRWQVMIV	WQVDRMRINT	WNSLVKHHMY	VSKKTKKWLY	RHHYDSNHPK
1381	B_AU_VH_AF	MENRWQVMIV	WQVDRMRIRT	WNSLVKHHMY	KSGKARRWVY	RHHYESTHPR
1382	B_CN_RL42_	MENRWQVMIV	WQVDRMRIKT	WNSLVKHHMY	ISRKAKGWFY	KHHYDSTHPK
1383	B_DE_D31_U	MENRWQVMIV	WQVDRMRIRT	WNSLVKHHMY	VSGKAEKWFY	KHHYESTNPR
1384	B_DE_HAN_U	MENRWAVMIV	WQVDRMRIRT	WNSLVKHHMY	CSRKAKNWVY	RHHYESTNPR
1385	B_FR_HXB2_	MENRWQVMIV	WQVDRMRIRT	WNSLVKHHMY	VSGKARGWFY	RHHYESPHPR
1386	B_GA_OYI__	MENRWQVMIV	WQVDRMRIRT	WNSLVKHHMY	VSKKAKGWFY	RHHYESTHPR
1387	B_GB_CAM1_	MENRWQVMIV	WQVDRMRIRT	WNSLVKHHMY	ISGKAKKWSY	RHHYESTHPR
1388	B_GB_GB8_A	MENRWQVMIV	WQVDRMRIRT	WNSLVKHHMY	ISGKAKKWVY	KHHYENTHPR
1389	B_GB_MANC_	MENRWQVMIV	WQVDRMRIRT	WNSLVKHHMY	ISGKAKRWSY	KHHYESTNPR
1390	B_KR_WK_AF	MENRWQVMIV	WQVDRMRIKT	WNSLVKHHMY	ISKKAKEWVY	RHHYESTHPR
1391	B_NL_3202A	MENRWQVMIV	WQVDRMRIRA	WNSLVKHHMY	KSKKAERWFY	RHHYESTHPR
1392	B_TW_TWCYS	MENRWQVMIV	WQVDRMRIRA	WNSLVKHHMY	ISKKAKGWLY	KHHYESTHPR
1393	B_US_BC_L0	MENRWQVMIV	WQVDRMRIRT	WNSLVKHHMY	ISRKAKGWFY	RHHYESTHPK
1394	B_US_DH123	MENRWQVMIV	WQVDRMRIRT	WNSLVKHHMY	VSKKAKGWFY	RHHYESTHPR
1395	B_US_JRCSF	MENRWQVMIV	WQVDRMRIRT	WNSLVKHHMY	ISGKAKGWIY	KHHYESTNPR
1396	B_US_MNCG_	MENRWQVMIV	WQVDRMRIRT	WNSLVKHHMY	ISKKAKGRFY	RHHYESTHPR
1397	B_US_P896_	MENRWQVMIV	WQVDRMRIRT	WNSLVKHHMY	ISGKAKGWSY	RHHYESTNPR
1398	B_US_RF_M1	MENRWQVMIV	WQVDRMRIRT	WNSLVKHHMY	ISRKAKGWFY	RHHYESTHPR
1399	B_US_SF2_K	MENRWQVMIV	WQVDRMRIRT	WNSLVKHHMY	ISKKAKGWFY	RHHYESTHPR
1400	B_US_WEAU1	MENRWQVMIV	WQVDRMRIRT	WNSLVKHHMY	ISKKAKGWSY	RHHYESTHPR

<u>1401</u>	B_US_WR27_	MENRWQVMIV	WQVDRMRIRT	WKS LVKHHXH	ISGKARRWXY	XHHYENNHPR
<u>1402</u>	B_US_YU2_M	MENRWQVMIV	WQVDRMRIRA	WKS LVKHHMY	ISGKARGWYF	RHHYESPHPR
<u>1403</u>	BF1_BR_93B	MENRWQVVIV	WQVDRMRINT	WKS LVKYHMH	VSKKAKRWYF	RHHFESRHPK
<u>1404</u>	C_BR_92BR0	MENRWQVLIV	WQVDRMKIRT	WNS LVKHHMY	VSRRASGWYF	RHHYESRHPK
<u>1405</u>	C_BW_96BW0	MENRWQVLIV	WQVDRMKIRT	WNS LVKHHMY	VSRKANGWYF	RHHYESRHPK
<u>1406</u>	C_BW_96BW1	MENRWQVLIV	WQVDRMRIRT	WTS LVKHHMY	VSRRANGWSY	RHHFESRHPK
<u>1407</u>	C_BW_96BW1	MENRWQGLIV	WQVDRMRIRT	WHS LKHHMY	VSKRADGWYF	RHHYESRHPK
<u>1408</u>	C_BW_96BW1	MENRWQALIV	WQVDRMRIRT	WNS LVKHHMY	VSKRTNGWYF	RHHFESRHPK
<u>1409</u>	C_ET_ETH22	MENRWQVLIV	WQVDRMKIRT	WNS LVKHHMH	ISRRANGWVY	RHHYDSRHPK
<u>1410</u>	C_IN_93IN1	MENRWQVLIV	WQVDRMKIRT	WNS LVKHHMY	VSRRAKGWYF	RHHYDSRHPK
<u>1411</u>	C_IN_93IN9	MENRWQVLIV	WQVDRMKIRT	WNS LVKHHMY	VSRRANGWYF	RHHYESRHPK
<u>1412</u>	C_IN_93IN9	MENRWQVLIV	WQVDRMKIRT	WNS LVKHHMY	VSRRATGWYF	RHHYESRNPK
<u>1413</u>	C_IN_94IN1	MENRWQVLIV	WQVDRMKIRT	WNS LVKHHMY	VSRRANGWYF	RHHYDSRNPK
<u>1414</u>	C_IN_95IN2	MENRWQVLIV	WQVDRMKIRT	WNS LVKHHMY	VSRRANGWYF	RHHYESRHPK
<u>1415</u>	CRF01_AE_C	MENRWQVMIV	WQVDRMRIRT	WYS LVKHHMY	ISKKAKNWYF	RHHYESQHPK
<u>1416</u>	CRF01_AE_C	MENRWQVMIV	WQVDRMRIRA	WNS LVKHHMY	SSKKA AKWYF	RHHYESQHPK
<u>1417</u>	CRF01_AE_C	MENRWQVMIV	WQVDRMRIKT	WNS LVKHHMY	ISKKAKKWVY	RHHYESQHPK
<u>1418</u>	CRF01_AE_T	MENRWQVMIV	WQVDRMRIRT	WNS LVKHHMY	ISKKAKKWYF	RHHYESQHPK
<u>1419</u>	CRF01_AE_T	MENRWQVMIV	WQVDRMRIRT	WNS IVKHHMY	ISKKAKKWYF	RHHYESQHPK
<u>1420</u>	CRF01_AE_T	MENRWQVMIV	WQVDRMRIRT	WNS LVKHHMY	ISKKAKQWYF	RHHYESQHPK
<u>1421</u>	CRF01_AE_T	MENRWQVMIV	WQVDRMRIRT	WNS LVKHHMY	VSKKAKKWYF	RHHYESQNPK
<u>1422</u>	CRF01_AE_T	MENRWQVMIV	WQVDRMRIRT	WNS LVKHHMY	ISKKAKKWYF	RHHYESQHPK
<u>1423</u>	CRF01_AE_T	MENRWQVMIV	WRVDRMRIRT	WNS LVKHHMY	ISKKAKNWYF	RHHYESQHPK
<u>1424</u>	CRF02_AG_F	MENRWQVMIV	WQVDRMRIRT	WNS LVKHHMY	ISRKAKNWYF	RHHFESRHPK
<u>1425</u>	CRF02_AG_F	MENRWQVMIV	WQVDRMRIRT	WNS LVKHHMY	ISRKAKNWYF	RHHFESRHPK
<u>1426</u>	CRF02_AG_G	MENRWQVMIV	WQVDRMRIRT	WNS LVKHHMY	VSRKAKDWYF	RHHYESRHPK
<u>1427</u>	CRF02_AG_N	MENRWQVMIV	WQVDRMRIRT	WNS LVKHHMY	VSKKAKGWYF	RHHFESRHPK
<u>1428</u>	CRF02_AG_S	MENRWQVMIV	WQVDRMRIRT	WNS LVKYHMY	KSRKAKDWYF	RHHYESSHPR
<u>1429</u>	CRF02_AG_S	MENRWQVMIV	WQVDRMRIRT	WNS LVKHHMY	VSKKAHRWYF	RHHYESRHPK
<u>1430</u>	CRF03_AB_R	MENRWQVMIV	WQVDRMRIRT	WNS LVKHHIY	ISKKARGWVY	KHHYESRNPR
<u>1431</u>	CRF03_AB_R	MENRWQVMIV	WQVDRMRIRT	WNS LVKHHIY	ISKKARGWVY	KHHYESRNPR
<u>1432</u>	CRF04_cpx_	MANRWQVMIV	WQVDRMKIRT	WNS LVKHHMY	VSKKAKGF.Y	RHHYESRHPK
<u>1433</u>	CRF04_cpx_	MENRWQVMIV	WQVDRMKIRT	WNS LVKHHMY	ISKKAKGWSY	RHHYESRHPK
<u>1434</u>	CRF04_cpx_	MENRWQVMTV	WQVDRMKIRT	WNS LVKHHMH	ISKKAKGWVY	KHHYESRNPR
<u>1435</u>	CRF05_DF_B	MENRWQVMIV	WQVDRMRINT	WKS LVKYHMH	VSKKANRWCY	RHHFESRNPR
<u>1436</u>	CRF05_DF_B	MENRWQVMIV	WQVDRMRINT	WKS LVKYHMH	VSKKT KAWYF	RHHYESRHPK
<u>1437</u>	CRF06_cpx_	MENRWQVMIV	WQVDRMRINT	WKS LVKYHMH	ISKKAKRWNY	RHHYDSNHPK
<u>1438</u>	CRF06_cpx_	MENRWQVMIV	WQVDRMRINT	WKS LVKYHMH	ISKKAKRWTY	RHHYDSNHPK
<u>1439</u>	CRF06_cpx_	MENRWQVMIV	WQVDRMRINA	WKS LVKYHMN	VSKKAKGWLY	RHHYDSNHPK
<u>1440</u>	CRF06_cpx_	MENRWQVMIV	WQVDRMRINT	WKS LVKYHMH	ISKKARKWAY	RHHYDSHHPK
<u>1441</u>	CRF11_cpx_	MENRWQVMIV	WQVDRMRIRT	WHS LVKHHMY	VSKKARRWYF	RHHYESRHPK
<u>1442</u>	CRF11_cpx_	MENRWQVMIV	WQVARMRIRT	WNS LVKHHMY	VSKKAKGWLY	RHHYESRHPK
<u>1443</u>	D_CD_84ZR0	MENRWQVMIV	WQVDRMRINT	WKS LVKYHMH	ISKKAKGWYF	RHHYDSPHPK
<u>1444</u>	D_CD_ELI_K	MENRWQVMIV	WQVDRMRIKT	WKS LVKHHMY	VSKKANRWYF	RHHYESPHPK
<u>1445</u>	D_CD_NDK_M	MENRWQVMIV	WQVDRMRINT	WKS LVKYHMY	VSKKANRWYF	RHHYDSHHPK
<u>1446</u>	D_UG_94UG1	MENRWQVMIV	WQVDRMRIRT	WKS LVKHHMY	ISKKAKGWLY	RHHYDCPNPK
<u>1447</u>	F1_BE_VI85	MENRWQLMIV	WQVDRMRINT	WKS LVKYHMY	VSKKAKGWSY	RHHFQSRHPK

1448	F1_BR_93BR	MENRWQVMIV	WQVDRMRINT	WKS LVKYHMH	ISKKAKGWFY	RHHFESRHPK
1449	F1_FI_FIN9	MENRWQVTIV	WQVDRMRINT	WKS LVKYHMH	VSKKAKRWFY	RHHFESRHPK
1450	F1_FR_MP41	MENRWQVMIV	WQVDRMRIST	WKS LVKYHMH	VSKKAKNWFY	RHHFQSRHPK
1451	F2_CM_MP25	MENRWQVMIV	WQVDRMKIRT	WNSLVKHHMY	ISKRAAGWFY	RHHYESRHPR
1452	F2KU_BE_VI	MENRWQVMIV	WQVDRMRIKT	WNSLVKHHMY	VSRKTKGWSY	RHHYESINPR
1453	G_BE_DRCBL	MENRWQVMIV	WQVDRMRIRT	WNSLVKHHMY	ISKKAKGWFY	RHHYESRHPK
1454	G_NG_92NG0	MENRWQVVIV	WQVDRMRIRT	WNSLVKHHMY	VSKKAKGWFY	RHHYESRHPR
1455	G_SE_SE616	MENRWQVMIV	WQVDRMRIRT	WNSLVKHHMY	VSKKARGWFY	RPHYASRHPR
1456	H_BE_VI991	MENRWQVMIV	WQVDRMRIKT	WNSLVKHHMY	VSKKAKKVVY	RHHYESTNPK
1457	H_BE_VI997	MENRWQVMIV	WQVDRMRINK	WKS LVKYHMY	ISKKANRWVY	RHHYDSPHPR
1458	H_CF_90CF0	MENRWQVMIV	WQVDRMRINT	WKS LVKYHMH	ISRKARGWFY	RHHFESTHPR
1459	J_SE_SE702	MENRWQVMIV	WQVDRMRINT	WKS LVKYHMN	VSKKARQWLY	RHHYDSRHPK
1460	J_SE_SE788	MENRWQVMIV	WQVDRMRINT	WKS LVKYHMN	VSKKARKWLY	RHHYDSNHPK
1461	K_CD_EQTB1	MENRWQVMIV	WQVDRMRINT	WKS LVKYHMY	VSKKANRWRY	RHHYDSNHPK
1462	K_CM_MP535	MENRWQVMIV	WQVDRMRINT	WKS LVKYHMH	ISKKANRWYY	RHHYESRHPK
1463	N_CM_YBF30	MENRWQVMIV	WQVDRMKIRK	WNSLVKHHMY	VSKKAKGWYY	RHHYETHHPK
1464	O_CM_ANT70	MENRWQVLIV	WQVDRQKVKA	WNSLVKYHKY	RSRKTENWWY	RHHYESRNPR
1465	O_CM_MVP51	MENRWQVLIV	WQIDRQKVKA	WNSLVKYHKY	MSKKAANWRY	RHHYESRNPK
1466	O_SN_99SE_	MENRWQVLIV	WQVDRQRVKT	WNSLVKYHKY	RSKGTRDWYY	RHHFESRNPR
1467	O_SN_99SE_	MENRWQVLIV	WQVDRQRVKT	WNSLVKYHKY	RSKGTRDWYY	RHHFESKNPR
1468	U_CD___83C	MENRWQVMIV	WQVDRMRIKT	WNSLVKHHMY	ISKKAKGWVY	KHHYESTNPR

	51				100
00BW0762_1	LSSEVHIPLG	D.ARLVIKTY	WGLHTGERDW	HLGHGVSIEW	KLRRYSTQVD
00BW0768_2	VSSEVHIPLG	D.ARLVIITY	WGLHTGERDW	HLGHGVSIEW	RLRRYSTQVD
00BW0874_2	ISSEVHIPLG	D.ARLVIKTY	WGLQTGEREW	HLGHGVSIEW	RLRRYSTQVD
00BW1471_2	ISSEVHIPLG	D.AKLVIKTY	WGLHTGEREW	HLGHGVSIEW	RLKSFSTQVD
00BW1616_2	ISSEVHIPLG	D.ARLIIKTY	WGLQTGEKDW	HLGHGVSIEW	RLRKYSTQVD
00BW1686_8	ISSEVHIPLG	E.ARLVITTY	WGLQTGEREW	HLGHGVSIEW	RLRRYSTQVD
00BW1759_3	ISSEVHIPLG	D.ARLVITTY	WGLNTGERDW	HLGHGVSIEW	RLGRYSTQVD
00BW1773_2	VSSEIHIPLG	E.ARLVIKTY	WGLQTGEREW	HLGHGVSIEW	RWKRYSTQVE
00BW1783_5	ISSEVHIPLG	D.ARLVIKTY	WGLHTGEREW	HLGHGVSIEW	RLRKYSTQID
00BW1795_6	ISSEVHIPLG	E.ARLVIITY	WGLQTGEREW	HLGHGVSIEW	RLRRYSTQVD
00BW1811_3	ISSEVHIPLG	D.ARLVIKTY	WGLQTGERDW	HLGHGVSIEW	RLRKYSTQVE
00BW1859_5	ISSEVHIPLG	E.ARLVVKTY	WGLQTGEREW	HLGHGVSIEW	RLRGYSTQVD
00BW1880_2	ISSEVHIPLG	E.ARLVIKTY	WGLHTGERDW	HLGHGVSIEW	KLKRYSTQVD
00BW1921_1	VSSEVHIPLG	E.ARLVITTY	WGLQTGEREW	HLGHGVSIEW	RLRRYKTQVD
00BW2036_1	VSSEVHIPLG	E.ARLVVITY	WGLQTGEREW	HLGQGVSI EW	RLRRYSTQVD
00BW2063_6	ISSEVHIPLG	D.ARLVIKTY	WGLQTGERDW	HLGHGVSIEW	RLRKYSTQVD
00BW2087_2	VSSEVHIPLG	D.ARLVIKTY	WGLQTGERAW	HLGHGVSIEW	RMKRYSTQVD
00BW2127_2	VSSEVHIPLG	E.ARLVIKTY	WGLQTGERDW	HLGHGASIEW	RLRRYSTQVV
00BW2128_3	VSSGVHIPLG	D.ARLVIKTY	WGLQTGEREW	HLGHGVSIEW	RLRKYSTQVE
00BW2276_7	VSSEVHIPLG	D.ARLVITTY	WGLQTGEREW	HLGHGVSIEW	RLKRYSTQVD
00BW3819_3	VSSEVHIPLG	D.ARLVIKTY	WGLQTGERDW	HLGHGVSIEW	RLGKYNTQVE
00BW3842_8	VSSEVHIPLG	E.ARLVIITY	WGLQTGEREW	HLGHGVSIEW	RLRRYSTQVD
00BW3871_3	VSSEVHIPLG	E.ARLVIRTY	WGLQTGEREW	HLGHGVSIEW	RLRKYSTQVD
00BW3876_9	VSSEVHIPLG	E.DKLVITTY	WGLQTGEREW	HLGHGVSIEW	RLKKYSTQVD
00BW3886_8	VSSEVHIPLG	E.ARLVITTY	WGLQTGEREW	HLGHGVSIEW	RLKRYSTQVD
00BW3891_6	ISSEVHIPLG	E.ARLIIKTY	WGLQTGERDW	HLGHGASIEW	RLRRYSTQVD
00BW3970_2	ISSEVHIPLG	E.ARLIIKTY	G.LQTGEGDW	HLGHGCSIEW	RLRKYSTQVD
00BW5031_1	VSSEVHIPLG	D.ARLVIKTY	WGLHTGERDW	HLGHGVSIEW	RLRRYNTQVD
96BW01B21	VSSEVHIPLG	E.ARLVIKTY	WGLQTGEREW	HLGHGVSIEW	RLRRYSTQVD
96BW0407	VSSEVHIPLG	D.ARLVIKTY	WGLQTGERDW	HLGHGVSIEW	RLRGYSTQVD
96BW0502	VSSEVHIPLG	E.ARLVIKTY	WGLQTGERDW	HLGHGVSIEW	RLRKYSTQVE

96BW06_J4	VSSEVHIPLG	D.ARLVITTY	WGLQTGEREW	HLGHGVSIEW	RLRRYSTQVD
96BW11_06	VSSEVHISLG	E.ARLVIKTY	WGLHTGERDW	HLGHGVSIEW	KLRGYSTQVD
96BW1210	VSSEVHIPLG	D.ARLVIITY	WGLQTGEREW	HLGHGVSIEW	RLRSYSTQVD
96BW15B03	VSSEVHIPLG	E.ARLVIITY	WGLQT.EREW	HLGHGVSIEW	RLRRYSTQVD
96BW16_26	VSSEVHIPLG	D.AKLVIKTY	WGLQTGERDW	HLGHGVSIEW	RWGNYSTQVE
96BW17A09	ISSEVHIPLG	D.AKLVITTY	WGLHTGEGDW	HLGHGVSIEW	RLKRFSTQVD
96BWM01_5	ISSEVHIPLG	D.ARLVIKTY	WGLNTGERDW	HLGHGVSIEW	RLRKYSTQVD
96BWM03_2	VSSEIHIPLG	D.ARLIVRTY	WGLQTGEKEW	QLGHGVSIEW	RLRSFSTQVD
98BWMC12_2	VSSEVHIPLG	K.ARLVITTY	WGLQIGERDW	HLGHGVSIEW	RLRKYSTQVD
98BWMC13_4	ISSEVHIPLG	D.ARLVIKTY	WGLNTGERDW	HLGHGVSIEW	RLRKYSTQVD
98BWMC14_a	VSSEVHIPLG	E.AKLVIITY	WGLQPGEREW	HLGHGASIEW	RLRRYSTQVD
98BWM014_1	ISSEIHIPLG	E.ARLVIKTY	WGLNTGERDW	HLGHGVSIEW	RMRGYSTQVD
98BWM018_d	ISSEVHIPLG	D.AKLVIKTY	WGLQTGEREW	HLGHGTSIEW	ILGGYSTQVD
98BWM036_a	ISSEVHIPLG	D.ARLVVKTY	WGLQTGERDW	HLGHGVSIEW	RLRRYSTQVD
98BWM037_d	VSSEVHIPLG	D.ARLVIKTY	WGLQTGERDW	HLGHGCSIEW	RLRRYSTQVD
99BW3932_1	VSSEVHIPLG	E.ARLVIKTY	WGLQTGEKDW	HLGHGVSIEW	RLKRYSTQVD
99BW4642_4	VSSEVHIPLG	E.ARLIVRAY	WGLQTGEREW	HLGHGVSIEW	RLRRYSTQVD
99BW4745_8	VSSEVHIPLG	E.ARLVITTY	WGLLPGEREW	HLGHGVSIEW	RLRRYSTQVD
99BW4754_7	ISSEVHIPLR	D.ARLVIKTY	WGLHTGERDW	HLGHGVSIEW	RLGRYSTQVD
99BWMC16_8	VSSEVHIPLG	D.ARLVITTY	WGLHTGEREW	HLGHGVSIVW	RLRRYSTQVD
A2_CD_97CD	VSSEVHIPLK	E.ARLIVRTY	WGLHPGEKDW	HLGHGVSIEW	RQGRYSTQID
A2_CY_94CY	ISSEVHIPLG	E.ARIIVRTY	WGLHIGEKDW	HLGHGVSIEW	RQNRHYTQID
A2D_97KR	VSSEVHIPLG	G.AKIIVKTY	WGLHPGEKDW	HLGQGVSIW	RQERYSTQID
A2G_CD_97C	VSSEVHIPLG	E.ATLVIRTY	WGLQTGEKDW	QLGHGVSIEW	RQKRYSTQID
A_BY_97BL0	VSSEVHIPLG	D.ARLVVKTY	XGLHAXEKDW	QLGHXVSIEX	RQEXYSTQID
A_KE_Q23_A	VSSEVHIPLG	D.ATLVVRAY	WGLHTGEKDW	HLGHGVSIEW	RLKRYSTQIT
A_SE_SE659	VSSEVHIPLG	D.AKLVVRTY	WGLHTGEKEW	HLGHGVSIEW	RLNRYSTQID
A_SE_SE725	TSSEVHIPLG	D.ARLVVRTY	WGLHTGEKDW	QLGHGVSIEW	RLRRYSTQID
A_SE_SE753	VSSEVHIPLG	D.ARLVVRTY	WGLQTGEKDW	HLGHGVSIEW	RLKRYSTQID
A_SE_SE853	VSSEVHIPLG	E.AKLVVRTY	WGLQTGEKDW	QLGHGVSIEW	RLRRYSTQID
A_SE_SE889	VSSEVHIPLG	E.ARLVVRTY	WGLQTGEKDW	HLGHGVSIEW	RLRRYSTQID
A_SE_UGSE8	VSSEVHIPLG	D.ARLIVRTY	WGLHPGERDW	QLGHGVSIEW	RLRRYSTQID
A_UG_92UG0	VSSEVHIPIG	D.ARIVVRTY	WGLQTGEKDW	HLGHGVSIEW	RLKRYSTQID
A_UG_U455_	VSSEVHIPLG	E.ARLVVRTY	WGLHTGEKDW	HLGHGVSIEW	RLKRYSTQVD
AC_IN_2130	VSSEVHIPLG	E.AKLVIKTY	WGLQTGERDW	HLGHGVSIEW	RLRRYSTQVE
AC_RW_92RW	ISSEVHIPLG	E.ARLVIKTY	WGLQTGERDW	HLGHGVSIEW	RLRRYKTQVD
AC_SE_SE94	TSSEVHIPLG	E.ARLVIITY	WGLQTGERDW	HLGHGVSIEW	RLGRYRTQVD
ACD_SE_SE8	ISSEVHIPLG	D.AKIVVRTY	WGLHTGEKDW	HLGHGVSIEW	RLRKYSTQID
ACG_BE_VI1	VSSEVHIPLG	D.ARIVVRTY	WGLHTGEKAW	QLGHGVSIEW	RQRRYSTQID
AD_SE_SE69	VSSEVHIPLG	E.ARLVVKTY	WGLHTGERDW	HLGQGVSIW	RKRRYSTQVD
AD_SE_SE71	VSSEVHIPLG	D.AKLVVRTY	WGLHTGEKDW	HLGHGVSIEW	RLRRYSTQID
ADHK_NO_97	VSSEVHIPLG	D.ARLVVRTY	WGLQTGEKAW	HLGHGVSIEW	RQKRYSTQID
ADK_CD_MAL	VSSEVHIPLG	D.ARLVVRTY	WGLQTGEKDW	HLGHGVSIEW	RQKRYSTQLD
AG_BE_VI11	VSSEVHIPLG	D.ARLVVRTY	WGLHTGEKDW	HLGHGVSIEW	RQRRYSTQID
AG_NG_92NG	VSSEVHIPLG	E.ARLVVRTY	WGLHTGERDW	HLGQGVSIW	KQRRYSTQID
AGHU_GA_VI	VSSEVHIPLG	D.ARLVIKTY	WGLHTGERDW	HLGQGVSIW	RKGRYSTQVD
AGU_CD_Z32	ISSEVHIPLG	E.AKLVVTTY	WGLHTGEREW	HLGQGVSIW	RLRRYRTQVD
AJ_BW_BW21	ISSEVHIPLG	S.AELVVTTY	WGLNTGEREW	HLGQGLSIEW	RLKRYRTQVD
B_AU_VH_AF	ISSEVHIPLG	E.ARLVITTY	WGLHTGERDW	HLGQGVSIW	RKRRYSTQVD
B_CN_RL42_	ISSEVHIPLG	D.ARLVITTY	WGLHTGERDW	HLGQGVSIW	RKKRYSTQVD
B_DE_D31_U	ISSEVHIPLG	D.ARLVITTY	WGLHTGERDW	QLGHGVSIEW	RKKRYSTQVD
B_DE_HAN_U	VSSEVHIPLG	E.AKLVIITY	WGLHTGERDW	HLGQGASIEW	RKKRYSTQVD
B_FR_HXB2_	ISSEVHIPLG	D.ARLVITTY	WGLHTGERDW	HLGQGVSIW	RKKRYSTQVD
B_GA_OYI_	ISSEVHIPLG	D.ATLVVTTY	WGLHTGEREW	HLGQGASIEW	RKKRYSTQVD
B_GB_CAM1_	ISSEVHIPLG	E.ARLVVTTY	WGLHTGERDW	HLGQGVSIW	RTKGYNTQVD
B_GB_GB8_A	ISSEVHIPLG	E.ARLVITTY	WGLHTGERDW	HLGQGVSIW	RKRRYRTQVD
B_GB_MANC_	VSSEVHIPLG	D.AKLVIKTY	WGLHTGERDW	HLGQGASIEW	RKKGYSIQVD
B_KR_WK_AF	ISSEVHIPLG	D.AKLVIITY	WGLHTGEREW	HLGQGVSIW	RKKRYNTQVD
B_NL_3202A	ISSEVHIPVG	E.ARLVITTY	WGLHTGERDW	HLGQGVSIW	RKKRYSTQVD
B_TW_TWCYS	ISSEVHIPLG	D.ATLVITTY	WGLHTGERDW	HLGQGVSIW	RKRRYSTQVD

B_US_BC_L0	ISSEVHIPLG	D.ARLVITTY	WGLHTGERDW	HLGHGVSVIEW	RKKRYSTQVD
B_US_DH123	ISSEVHIPLG	D.ASLVVTTY	WGLHTGERDW	HLGQGVSIIEW	RKKRYSTQVD
B_US_JRCSF	VSSEVQIPLG	D.ARLVITTY	WGLHTGERDW	HLGQGVSMIEW	RTRRYSTQVD
B_US_MNCG	ISSEVHIPLG	D.ARLVITTY	WGLHTGERDW	HLGQGVSIIEW	RKKRYSTQVD
B_US_P896	ISSEVHIPLG	D.AKLVVTTY	WGLHTGERDW	HLGQGVSIIEW	RKKRYSTQVD
B_US_RF_M1	ISSEVHIPPG	D.ERLVITTY	WGLHTGERDW	HLGQGVSIIEW	RKKRYSTQVD
B_US_SF2_K	VSSEVHIPLG	D.AKLVITTY	WGLHTGEREW	HLGQGVAIIEW	RKKKYSTQVD
B_US_WEAU1	ISSEVHIPLG	E.GKLVITTY	WGLHTGERDW	HLGQGVSIIEW	RKQRYSTQVD
B_US_WR27	ISSEVHIPLG	D.AMLVITTY	WGLHTGERDW	HLGQGVSIIEW	RKQNYRTQVT
B_US_YU2_M	ISSEVHIPLG	D.AKLVITTY	WGLHTGERDW	HLGQGVSIIEW	RKKRYSTQVD
BF1_BR_93B	VSSEVHIPLG	E.AKLVITTY	WGLHTGERDW	HLGQGVSIIEW	RQGRYRTQID
C_BR_92BR0	ISSEVHIPLG	E.ARLVIITY	WGLQTGERDW	HLGHGVSIIEW	RLRRYSTQVD
C_BW_96BW0	VSSEVHIPLG	D.ARLVIKTY	WGLQTGERDW	HLGHGVSIIEW	RLRRYSTQVD
C_BW_96BW1	VSSEVHIPLG	E.ARLVIRTY	WGLHTGERDW	HLGHGVSIIEW	TVRGYST.VD
C_BW_96BW1	VSSEVHIPLG	D.ARLVIITY	WGLQTGEREW	HLGHGVSIIEW	RLRSYSTQVD
C_BW_96BW1	VSSEVHIPLG	E.ARLVIITY	WGLQT.EREW	HLGHGVSIIEW	RLRRYSTQVD
C_ET_ETH22	VSSEVHIPLG	E.ARLIIKTY	WGLQTGERDW	HLGHGVSIIEW	RLRSYNTQVD
C_IN_93IN1	VSSEVHIPLG	E.ARLVIKTY	WGLQTGERDW	HLGHGVSIIEW	RLRRYNTQIE
C_IN_93IN9	VSSEVHIPLG	E.ATLVIKTY	WGLQTGERDW	HLGHEVSIIEW	RLRRYNTQIE
C_IN_93IN9	ISSEVHIPLG	E.ARLVIKTY	WGLQTGERDW	HLGHGVSIIEW	RLRRYSTQVE
C_IN_94IN1	VSSEVHIPLG	E.AILVIKTY	WGLQTGERDW	HLGHGVSIIEW	RLRRYNTQIE
C_IN_95IN2	VSSEVHIPLG	E.ARLVITTY	WGLQTGERDW	HLGHGVSIIEW	RLRKYSTQVE
CRF01_AE_C	VSSEVHIPIG	D.ARLVIRTY	WGLHTGEKDW	HLGHGVSIIEW	RQRKYSTQVD
CRF01_AE_C	VSSEVHIPLG	D.ARLIIRTY	WGLHTGEKDW	HLGHGVSIIEW	RQR.KSTQID
CRF01_AE_C	VSSEVHIPLG	E.ARLVIRTY	WGLHTGEKDW	HLGHGVSIIEW	RQEKYSTQID
CRF01_AE_T	VSSEVHIPLG	E.ARLVIRTY	WGLQTGEKDW	QLGHGVSIIEW	RQRNYSTQID
CRF01_AE_T	VSSEVHIPLG	E.ARLVIRTY	WGLQTGEKDW	QLGHEVSIIEW	RQRTYSTQID
CRF01_AE_T	VSSEVHIPLG	E.ARLVIRTY	WGLQTGEKDW	QLGHGVSIIEW	RQRKYSTQID
CRF01_AE_T	VSSEVHIPLG	E.ARLVIRTY	WGLQTGEKDW	QLGHGVSIIEW	RQRKYSTQID
CRF01_AE_T	VSSEVHIPLG	E.ARLVIRTY	WGLQTGEKDW	QLGHGVSIIEW	RQRKYSTQID
CRF01_AE_T	VSSEVHIPLG	E.AKLIIIRTY	WGLQTGEKDW	QLGHGVSIIEW	RQRKYSTQID
CRF01_AE_T	VSSEVHIPLG	E.ARLVIRTY	WGLQTGEKDW	HLGHGVSIIEW	RQRKYSTQID
CRF01_AE_T	VSSEVHIPLG	E.AKLVIIRTY	WGLQTGEKDW	QLGHGVSIIEW	RQRKYSTQID
CRF02_AG_F	VSSEVHIPLG	D.ARLIVRTY	WGLHAGERDW	HLGHGVSIIEW	KQRKYSTQID
CRF02_AG_F	VSSEVHIPLG	D.ARLIVRTY	WRLHAGERDW	YLGHGVSIIEW	KQRKYSTQID
CRF02_AG_G	VSSEVHIPLG	D.ARIVVRTY	WGLHTGERDW	HLGHGVSIIEW	RQKRYSTQID
CRF02_AG_N	VCSEVHIPLG	D.ARLVVRTY	WGLHTGERDW	HLGHGVSIIEW	KQKRYSTQID
CRF02_AG_S	VSSEVHIPLG	D.ARLVVRTY	WGLHTGERDW	HLGHGVSIIEW	KQRRYSTQID
CRF02_AG_S	VSSEVHIPLG	D.ATLIVRTY	WGLQPGERDW	HLGHGVSIIVW	QQKRYSTQID
CRF03_AB_R	ISSEVHIPLG	D.AKLVIKTY	WGLHTGERDW	HLGQGASIEW	RKERYSTQVD
CRF03_AB_R	ISSEVHIPLG	D.AKLVIKTY	WGLHTGERDW	HLGQGASIEW	RKERYSTQVD
CRF04_cpx	VSSEVHIPLG	E.ARLVVRTY	WGLQPGEQDW	HLGHGVSIIEW	RLRRYSTQVD
CRF04_cpx	VSSEVQIPLG	D.ARLVIRTY	WGLQPGEKDW	HLGHGVSMIEW	RLRRYSTQVD
CRF04_cpx	ASSEVHIPLG	E.AKLVVRTY	WGLQPGKKDW	HLGHGVSIIXW	RLRSYSTQVD
CRF05_DF_B	ISSEVHIPLG	D.AKLVVTTY	WGLHTGERDW	HLGQGVSIIEW	RKKRYSTQVD
CRF05_DF_B	ISSEVHIPLG	E.AKLVIITY	WGLHTGEREW	HLGQGVSIIEW	RKGRYSTQID
CRF06_cpx	ISSEVHIPLG	S.AELVITTY	WGLNTGERKW	HLGQGVSIIEW	RLRRYRTQVD
CRF06_cpx	VSSEVHIPLG	C.AELVITTY	WGLNTGERKW	HLGQGVSIIEW	RLRRYRTQVD
CRF06_cpx	ISSEVHIPLG	C.AELVVTTY	WGLNTGEREW	HLGQGVSIIEW	RLKKYRTQVD
CRF06_cpx	ISSEVHIPLG	K.AELVVTTY	WGLNTGERKW	HLGQGVSIIEW	RLKRYRTQVD
CRF11_cpx	ISSEVHIPLG	D.ADLVVTTY	WGLHTGEREW	HLGQGVSIIEW	RMKRYRTQVD
CRF11_cpx	VSSEVHIPLG	E.DMLVVTTY	WGLHTGEREW	HLGQGVSIIEW	RRKRYRTQVD
D_CD_84ZR0	ISSEVHIPLG	D.ARLVVTTY	WGLHTGEREW	HLGQGVSIIEW	RKKRYSTQVD
D_CD_ELI_K	ISSEVHIPLG	E.ARLVIKTY	WGLHTGEREW	HLGQGVSIIEW	RKKRYSTQVD
D_CD_NDK_M	ISSEVHIPLG	E.ARLVVTTY	WGLHTGEKEW	HLGQGVSIIEW	RKKRYSTQVD
D_UG_94UG1	ISSEVHIPLG	E.ARLVVKTY	WGLHTGEREW	HLGQGVSIIEW	RKGRYNTQID
F1_BE_VI85	VSSEVHIPLG	E.VKLVITTY	WGLHPGEREW	HLGQGVSIIEW	RQGKYRTQID
F1_BR_93BR	ISSEVHIPLG	T.AELVITTY	WGLLPGEREW	HLGQGVSIIEW	RQGRYRTQID
F1_FI_FIN9	ISSEVHIPLG	E.AELVITTY	WGLNTGERDW	HLGQGVSIIEW	RQGRYRTQID
F1_FR_MP41	ISSEVHIPLG	E.AKLVVTTY	WGLHTGERDW	HLGQGVSIIEW	RQGRYRTQID
F2_CM_MP25	VSSEVHIPLG	EDSKLVIITY	WGLHTGERDW	HLGQGVSIIEW	RQKRYRTQVD
F2KU_BE_VI	VSSEVHIPLG	E.AKLVVTTY	WGLNTGERDW	HLGQGVSIIEW	RLKKYSTQID



G_BE_DRCBL	VSSEVHIPLG	D.AKLVVRTY	WGLHTGDKW	HLGHGVSIEW	RQGRYSTQVD
G_NG_92NG0	VSSEVHIPLR	D.ATLVVRTY	WGLHAGEKDW	QLGHGVSIEW	RQKRYSTQID
G_SE_SE616	VSSEVHIPLG	D.ATLVVTTY	WGLHTGEKDW	QLGHGVSIEW	RQRRYRTQVE
H_BE_VI991	TSSEVHIPVG	D.ARLVITTY	WGLHTGERDW	HLGHGVSIEW	RQERYSTQID
H_BE_VI997	ISSEVHIPLG	D.ARLVITTY	WGLHTGERDW	HLGQGVSI EW	RQKRYSTQVD
H_CF_90CF0	ISSEVHIPLG	E.ARLVITTY	WGLNTGEREW	HLGQGVSI EW	RLKRYSTQVE
J_SE_SE702	ISSEVHIPLG	E.ARLVVTTY	WGLQTGERDW	HLGQGVSI EW	RRKRYRTQVD
J_SE_SE788	ISSEVHIPLG	E.AILVITTY	WGLQTGERDW	HLGQGVSI EW	RQRRYRTQVD
K_CD_EQTB1	ISSEVHIPLG	D.AELVVTTY	WGLHTGEREW	HLGQGVSI EW	RLKRYRTQVD
K_CM_MP535	ISSEVHIPLG	D.AELVVTTY	WGLLTGERDW	HLGQGVSI EW	RLKRYRTQVE
N_CM_YBF30	ISSEVHIPVG	Q.ARLVTVTY	WGLTTGEQSW	HLGHGVSIEW	RLRKYKTQVD
O_CM_ANT70	VSSSVYIPVG	V.AHVVVTTY	WGLMPGERDE	HLGHGVSIEW	RYKKYKTQID
O_CM_MVP51	VSSAVYIPVA	E.ADIVVTTY	WGLMPGEREE	HLGHGVSIEW	QYKEYKTQID
O_SN_99SE_	VSSGVYIPVG	G.PWIVVTTY	WGLMPGERDE	HLGHGVSIEW	RYKKYKTQID
O_SN_99SE_	VSSGVYIPVG	G.PWIVVTTY	WGLMPGERDE	HLGHGVSIDW	RYRKYTTQID
U_CD___83C	ISSEVHIPLG	N.ARIVVTAY	WGLHTGERDW	HLGQGVSI EW	RQGRYSTQID

	101		150
00BW0762_1	PGLADQLIHM	HYFDCFADSA	IRKALLGQVV
00BW0768_2	PGLADQLIHM	HYFDCFADSA	IRQAILGHIV
00BW0874_2	PGLADQLIHI	HYFDCFADSA	IRKAILGHIV
00BW1471_2	PGLADQLIHM	HYFDCFAGSA	IRKAILGQIV
00BW1616_2	PGLADQLIHM	HYFDCFADSA	IRKALLGQVV
00BW1686_8	PGLADQLIHM	HYFDCFADSA	IRKAILGHIV
00BW1759_3	PGLADQLIHM	HYFDCFADSA	IRKALLGHIV
00BW1773_2	PGLADQLIHM	HYFDCFADSA	IRKAILGHIV
00BW1783_5	PGLADQLIHM	HYFDCFADSA	IRKALLGHIV
00BW1795_6	PGLADQLIHT	HYFDCFADSA	IRKAILGHRV
00BW1811_3	PDLADQLIHI	HYFDCFADSA	IRKAILGHIV
00BW1859_5	PGLADQLIHM	HYFDCFADSA	IRKAILGHRV
00BW1880_2	PGLADL.IHM	HYFDCFADSA	IRKALLGQVV
00BW1921_1	PGLADQLIHM	HYFDCFADSA	IRQAILGHIV
00BW2036_1	PGLADQLIHM	HYFDCFADSA	IRKAILGHIV
00BW2063_6	PGLADQLIHM	HYFDCFADSA	IRKAILGHIV
00BW2087_2	PGLADQLIHM	HYFDCFADSA	IRKAILGHIV
00BW2127_2	PGLADQLIHM	HYFDCFADSA	IRKAILGHIV
00BW2128_3	PGLADQLIHM	HYFDCFADSA	IRRAILGHIV
00BW2276_7	PGLADQLIHM	HYFDCFADSA	IRQAILGHIV
00BW3819_3	PGLADQLIHM	HYFDCFADSA	IRKAILGHIV
00BW3842_8	PGLADQLIHI	HYFDCFADSA	IRKAILGHIV
00BW3871_3	PGLADQLIHM	HYFDCFADSA	IRKAILGHIV
00BW3876_9	PGLADQLIHM	HYFDCFADSA	IRKAILGHIV
00BW3886_8	PGLADQLIHM	HYFDCFADSA	IRKAILGHIV
00BW3891_6	PGLADQLIHM	HYFDCFADSA	IRKAILGHIV
00BW3970_2	PGLADQLIHM	HYFDCFADSA	IRKAILGHIV
00BW5031_1	PGLADQLIHM	HYFDCFADSA	IRKAILGRIV
96BW01B21	PGLADQLIHM	HYFDCFADSA	IRKAILGHIV
96BW0407	PGLADQLIHM	HYFDCFADSA	IRKAILGQIV
96BW0502	PGLADQLIHM	HYFDCFADSA	IRKAILGEIV
96BW06_J4	PGLADQLIHM	YYFDCFADSA	IRKAILGHIV
96BW11_06	PGLADQLIHM	HYFDCFADSA	IRKALLGQVV
96BW1210	PGLADQLIHM	HYFDCFAGSA	IRQAILGHIV
96BW15B03	PGLADQLIHM	YYFDCFADSA	IRKAILGHIV
96BW16_26	PGLADQLIHM	HYFDCFADSA	IRKAILGNKI
96BW17A09	PGLADQLIHT	HYFDCFADSA	IRKAILGEIV
96BWM01_5	PGLADQLIHM	YYFDCFADSA	IRRAILGYIV
96BWM03_2	PGLADQLIHM	HYFDCFADSA	IRKAILGHIV
98BWMC12_2	PGLADQLIHM	HYFDCFADSA	IRKAILGHIV
98BWMC13_4	PGLADQLIHM	YYFDCFADSA	IRKAILGHIV
98BWMC14_a	PGLADRLIHM	HYFDCFADSA	IRNAILGHIV

98BWM014_1	PGLADQLIHM	HYFDCFADSA	IRQAILGNLV	IPRCDYQAGH	NKVGSLQYLA
98BWM018_d	PGLADQLIHM	HYFDCFADSA	IRKAILGDRV	SPRCDYQAGH	NKVGSLQYLA
98BWM036_a	PGLADQLIHM	HYFDCFADSA	IRKAILGHIV	IPRCDYQAGH	SKVGSLQYLA
98BWM037_d	PGLADQLIHM	HYFDCFADSA	IRQAILGHIV	IPRCDYQAGH	NKVGSLQYLA
99BW3932_1	PSMADQLIHM	HYFDCFADSA	IRKAILGHIV	IPRCDYQAGH	NKVGFLQYLA
99BW4642_4	PGLADQLIHM	HYFDCFADSA	IRKAILGHIV	IPRCDYQAGH	NKVGSLQYLA
99BW4745_8	PGMADQLIHM	HYFDCFADSA	IRKAILGHIV	IPRCDYQAGH	NKVGSLKYLA
99BW4754_7	PGLADQLIHM	HYFDCFADSA	IRKAILGHIV	IHRCEYPAGH	NKVGSLQYLA
99BWMC16_8	PSLADQLIHM	HYFDCCADSA	IRQAILGHIV	IPRCNYPAGH	NKVGSLQYLA
A2_CD_97CD	PDLADHLIHL	YYFDCFSESA	IRRAILGEIV	RPRCEYQAGH	NKVGSLQYLA
A2_CY_94CY	PDLADHLIHL	YYFDCFSESA	IRKAIIGEIV	SPRCEYQAGH	NKVGSLQYLA
A2D_97KR	PDLAGHLIHL	HYFDCFSDSA	IRKAILGKIV	RPRCEYQAGH	NKVGSLQYLA
A2G_CD_97C	PELADQLIHL	HYFDCFSESA	IRKAILGQVV	RPRCQYQAGH	TKVGSLQYLA
A_BY_97BL0	PDLADQLIHL	YYFDCFSESA	IRKAIVGHIV	SPRCNYPAGH	NKVGSLQYLA
A_KE_Q23_A	PDLADQLIHM	HYFDCFSDSA	IRKAIVGQVV	SPKCEYQAGH	NKVGSLQYLA
A_SE_SE659	PDQADQLIHL	HYFDCFSDSA	IRKALLGQVV	SPRCEYQAGH	KKVGSLQYLA
A_SE_SE725	PDLADQQLIHL	HYFDCFSDSA	IRKAILGHVV	SPICEYHTGH	NKVGSLQYLA
A_SE_SE753	PDLADQLIHL	YYLDCFSDSA	IRKALLGQVV	SPSCEYHTGH	NQVGSLQYLA
A_SE_SE853	PDLADQLIHM	HYXNCFSDSA	IRKAILGQVV	SPSCEYQAGH	NKVGSLQYLA
A_SE_SE889	PDLADQLIHL	HYFKCFSDSA	IRKAILGEIV	SPRCEYQAGH	NKVGSLQYLA
A_SE_UGSE8	PDLADQLIHL	HYFNCFSDSA	IRKAILGRVV	SPSCEYQTGH	NKVGSLQYLA
A_UG_92UG0	PDLADQLIHL	HYFNCFSDSA	IRKAILGQVV	SPRCDYQTGH	NKVGSLQYLA
A_UG_U455_	PDLADHLIHL	HYFDCFSESA	IRRAILGQIV	RPRCEYQAGH	NKVGSLQYLA
AC_IN_2130	PGLADQLIHM	HYFDCFADSA	IRQAILGHIV	IPRCDYQAGH	.KVGSLQYLA
AC_RW_92RW	PGLAGQLIHM	HYFDCFADSA	IRKAILGHIV	SPRCDYQAGH	NKVGSLQYLA
AC_SE_SE94	PGLADQLIHM	HYFDCFADSA	IRKAILGHIV	SPRCDYQAGH	NKVGSLQYLA
ACD_SE_SE8	PDPADQLIHL	HYFDCFSDSA	IRKAILGQVV	SPRCDYTAGH	NKVGSLQYLA
ACG_BE_VI1	PDLADQLIHL	YYFDCFSDSA	IRKAILGQVV	RPRCEYQAGH	NKVGSLQYLA
AD_SE_SE69	PGLADQLIHI	YYFDCFTESA	IRKAILGHIV	TTRCNYQTGH	NKVGSLQYLA
AD_SE_SE71	PDQADQLIHL	HYSNCFSESA	IRKAILGQVV	RPKCEYQTGH	NKVGSLQYLA
ADHK_NO_97	PDLADHLIHL	HYFDCFSDAV	IRKAILGQVV	RPRCEYQAGH	NQVGSLQYLA
ADK_CD_MAL	PDLADQLIHL	YYFDCFSESA	IRQAILGHIV	SPRCDYQAGH	NKVGSLQYLA
AG_BE_VI11	PDLADQLIHL	NYFDCFSDSA	IRKAILGQVV	RPRCEYQAGH	NKVGSLQYLA
AG_NG_92NG	PDLADQLIHL	HYFNCFSESA	VRKAILGEVV	RPRCEYQTGH	NQVGSLQYLA
AGHU_GA_VI	PGLADQLIHM	HYFDCFSDSA	IRKAILGQVV	RPRCEYSAGH	NQVGSLQYLA
AGU_CD_Z32	PGLADQLIHM	HYFDCFSESA	IRKAILGHRV	SPRCEYQAGH	NKVGSLQYLA
AJ_BW_BW21	PGLADQLIHM	HYFNCFSESA	IRKAILGHIV	SPICEYQAGH	NKVGSLQYLA
B_AU_VH_AF	PGLADQLIHM	YYFDCFSESA	IRNAILERIV	SPSCEHQAGH	NKVGSLQYLA
B_CN_RL42_	PGLADQLIHL	YYFDCFSESA	IRNAILGRVV	SPSCDYQAGH	NKVGSLQYLA
B_DE_D31_U	PGLADQLIHL	YYFDCFSESA	IRNAILGRIG	SPSCEYRAGH	NKVGSLQYLA
B_DE_HAN_U	PNLADQLIHL	YYFDCFSESA	IRNAILGRIV	SPRCEYQAGH	SKVGSLQYLA
B_FR_HXB2_	PELADQLIHL	YYFDCFSDSA	IRKALLGHIV	SPRCEYQAGH	NKVGSLQYLA
B_GA_OYI_	PGLADQLIHT	YYFDCFSESA	IRNAILGNIV	SPRCEYPAGH	NKVGSLQYLA
B_GB_CAM1_	PDLADQLIHL	YYFDCFSESA	IRKAIVGRLV	SPRCEYQAGH	NKVGSLQYLA
B_GB_GB8_A	PGLADQLIHQ	YYFDCFSESA	IRNALLGRTV	SPSCKYQAGH	NKVGSLQYLA
B_GB_MANC_	PGLADQLIHL	YYFDCFSESA	IRNAILGHIV	SPRCEYQAGH	NKVGSLQYLA
B_KR_WK_AF	PDLADKLIHL	HYFDCFSDSA	IRHAILGHRV	RPKCEYQAGH	NKVGSLQYLA
B_NL_3202A	PGLADQLIHL	YYFDCFSESA	IRNAILGHVV	SPRCEYQAGH	NKVGSLQYLA
B_TW_TWCYS	PDQADQLIHL	YYFDCFSESA	IRKAIVGCRV	SPRCEYQAGH	NKVGSLQYLA
B_US_BC_L0	PDLADQLIHL	YYFDCFSESA	IRNAILGHIV	SPRCEYQAGH	NKVGSLQYLA
B_US_DH123	PDLADQLIHL	YYFDCFSESA	IRNAILGHRV	SPRCEYQAGH	NKVGSLQYLA
B_US_JRCSF	PDLADQLIHL	YYFDCFSESA	IRNAILGHIV	SPRCEYQAGH	SKVGSLQYLA
B_US_MNCG_	PDLADHLIHL	HYFDCFSDSA	IRKAILGHRV	SPICEFQAGH	NKVGPLQYLA
B_US_P896_	PGLADRLIHL	YYFDCFSDSA	IRKSILGHIV	SPSCEYQAGH	NKVGSLQYLA
B_US_RF_M1	PDLADQLIHL	YYFDCFSESA	IRKPSLGHIV	SPRCEYQAGH	NKVGSLQYLA
B_US_SF2_K	PGLADQLIHL	HYFDCFSESA	IKNAILGYRV	SPRCEYQAGH	NKVGSLQYLA
B_US_WEAU1	PDLADQLIHL	YHFDCFSESA	IRNAILGHLV	IPRCEYQAGH	NKVGSLQYLA
B_US_WR27_	PDLADQLIHR	YYFDCFSEPA	IRNTIVGRIV	SPRCEYQTGH	NKVGSLQYLA
B_US_YU2_M	PDLADQLIHL	YYFDCFSESA	IRKAILGYRV	SPRCEYQAGH	NKVGSLQYLA
BF1_BR_93B	PGLADQLIHI	YYFDCFSESA	IRKAILGHRI	SPRCDYQAGH	NKVGSLQYLA

C_BR_92BR0	PGLADQLIHM	HYFDCFADSA	IRKAILGHRV	SSRCDYQAGH	NKVGSLQYLA
C_BW_96BW0	PGLADQLIHM	HYFDCFADSA	IRKAILGQIV	SPRCEYQAGH	NKVGSLQYLA
C_BW_96BW1	PGLADQLIHM	HYFDCFADSA	IRKALLGQVV	IPRCDYQAGH	NKVGSLQYLA
C_BW_96BW1	PGLADQLIHM	HYFDCFAGSA	IRQAILGHIV	IPRCDYQAGH	KKVGSLQYLA
C_BW_96BW1	PGLADQLIHM	YYFDCFSAESA	IRKAILGHIV	IPRCNYQAGH	NKVGSLQYLA
C_ET_ETH22	PGLADHLIHM	HYFDCFSAESA	IRKAILGYRV	SPRCDYQAGH	NKVGSLQYLA
C_IN_93IN1	PGLADQLIHM	HYFDCFADSA	IRKAILGHIV	IPRCDYQAGH	NKVGSLQYLA
C_IN_93IN9	PGLADQLIHM	HYFDCFADSA	IRKAILGHIV	IPRCDYQAGH	NKVGSLQYLA
C_IN_93IN9	PGLADQLIHM	HYFDCFADSA	IRKAILGHIV	IPRCDYQAGH	NKVGSLQYLA
C_IN_94IN1	PGLADQLIHM	HYFDCFADSA	IRKAILGRIV	IPRCDYQAGH	NKIGSLQYLA
C_IN_95IN2	PGLADQLIHM	HYFDCFADSA	IRKAILGHIV	IPRCDYQAGH	NKVGSLQYLA
CRF01_AE_C	PDLADRQIHL	QYFDCFSDSA	IRKAMLGQVV	RPRCEYPTGH	NKVGSLQYLA
CRF01_AE_C	PDLADQLIHL	QYFDCFSDSA	IRKALLGQIV	RPRCEYPAGH	NKVGSLQYLA
CRF01_AE_C	PDLADRLIHL	QYFDCFSESA	IRKAILGQVV	RPRCDYPEGH	NKVGSLQYLA
CRF01_AE_T	PDLADRLIHL	QYFDCFSDSA	IRRAILGQVV	RRRCEYPSGH	NKVGSLQYLA
CRF01_AE_T	PDLADQLIHL	QYFDCFSDSA	IRKAILGQVV	RRRCEYPSGH	NKVGSIQYLA
CRF01_AE_T	PDLADQLIHL	QYFDCFSDST	IRRAILGQVV	RRRCEYPSGH	NKVGSLQYLA
CRF01_AE_T	PDLADQLIHL	HYFDCFSDSA	IRRAILGQVV	RRRCEYPSGH	NKVGSLQYLA
CRF01_AE_T	PDLADQLIHL	QYFGCFSDSA	IRKAILGQVV	RRRCEYPSGH	NKVGSLQYLA
CRF01_AE_T	PDLADQLIHL	QYFDCFSDSA	IRKAILGQVV	RRRCEYPSGH	NKVGSLQYLA
CRF02_AG_F	PDLADQLIHL	HYFDCFSAESA	IRKAILGEVV	RPRCEYQAGH	KQVGSLSQYLA
CRF02_AG_F	PDLADQLIHL	HYFDCFADSA	IRKAILGQVV	SPRCEYQAGH	NQVGSLSQYLA
CRF02_AG_G	PDLADQLIHL	HYFTCFSESA	IRKAILGEVV	RPRCEYQAGH	NKVGSLQYLA
CRF02_AG_N	PDLADQLIHL	YYFNCFSDSA	IRKAILGEIV	RPRCEYQAGH	NKVGSLQYLA
CRF02_AG_S	PDLADQLIHL	HYFDCFSDSA	IRKAILGQIV	RPRCEYQAGH	TKVGSLSQYLA
CRF02_AG_S	PDLADQLIHL	HYFDCFSESA	IRKALLGQVV	RPKCEYQAGH	NKVGSLQYLA
CRF03_AB_R	PNLADQLIHL	YYFDCFSESA	IRNAILGHRV	SPSCEYRAGH	NKVGSLQYLA
CRF03_AB_R	PNLADQLIHL	YYFDCFSDSA	IRNAILGHRV	SPSCEYRAGH	NKVGSLQYLA
CRF04_cpx_	PDLADQLIHM	HYFDCFSESA	IRKAILGHRV	SPRCEYQAGH	NKVGSLQYLA
CRF04_cpx_	PDLADQLIHM	HYFDCFSESA	IRQAILGYRV	SPRCEYQAGH	NEVGSLSQYLA
CRF04_cpx_	PDLADQLIHV	HYFDCFSESA	IRKAILGHRV	SPRCEYQAGH	NKPGSLQYLA
CRF05_DF_B	PSLADQLIHV	YYFDCFSESA	IRNAILGRIV	SPRCEYQAGH	NKVGSLQYLA
CRF05_DF_B	PGLADQLIHM	YYFDCFSESA	IRKAILGYRV	SPRCEYQAGH	NKVGSLQYLA
CRF06_cpx_	PSMADQLIHI	HYFDCFSESA	IRKALLGHRV	SPRCDYQAGH	NKVGSLQYLA
CRF06_cpx_	PGLADQLIHM	HYFDCFSESA	IRKAILGQIV	SPQCDYQAGH	NKVGSLQYLA
CRF06_cpx_	PSLADQLIHM	HYFDCFSESA	IRKAILGHVV	SPKCDYQAGH	NKVGSLQYLA
CRF06_cpx_	PSLADQLIHM	HYFDCFSESA	IREAILGHIV	SPRCDFEAGH	NKVGSLQYLA
CRF11_cpx_	PGLADQLIHI	HYFDCFSESA	IREAILGHRV	SPRCEYQAGH	NQVGSLSQYLA
CRF11_cpx_	PELADQLIHM	HYFDCFSAESA	IRKAILGHRV	SPRCEYPAGR	NKVGSLQYLA
D_CD_84ZR0	PGLADQLIHM	YYFDCFADSA	IRKAILGHIV	SPRCEYQAGH	NKVGSLQYLA
D_CD_ELI_K	PGLADQLIHM	YYFDCFSESA	IRKAILGDIV	SPRCEYQAGH	NKVGSLQYLA
D_CD_NDK_M	PGLADQLIHM	YYFDCFSAESA	IRKAILGHIV	SPSCEYQAGH	NKVGSLQYLA
D_UG_94UG1	PGLADQLIHI	HYFDCFADSA	IRKAILGQVV	YPRCNYQAGH	NKVGSLQYLA
F1_BE_VI85	PGLADQLIHI	YYFDCFSESA	IRKAILGHRI	SPRCNYQAGH	NKVGSLQYLA
F1_BR_93BR	PGLADQLIHI	YYFDCFSESA	IRKAILGHKI	SPRCNYQAGH	NKVGSLQYLA
F1_FI_FIN9	PGLADQLIHI	YYFDCFSESA	IRKAILGHRI	SPRCDYQAGH	NKVGSLQYLA
F1_FR_MP41	PDLADQLIHI	YYFDCFSESA	IRKAILGHRI	SPRCNYQAGH	NKVGSLQYLA
F2_CM_MP25	PGLADQLIHL	HYFDCFSDSA	IRKAILGQRV	SPRCNYQAGH	NKVGSLQYLA
F2KU_BE_VI	PGLADQLIHM	HYFDCFADSA	IRKALIGLRV	SPRCEYQAGH	NKVGSLQYLA
G_BE_DRCBL	PDLADHLIHL	HYFNCFSESA	IRKAILGQTV	RPSCEYPAGH	NKVGSLQYLA
G_NG_92NG0	PNTADHLIHL	YYFDCFSESA	IRKAILGEIV	SPRCEYPAGH	NKVGSLQYLA
G_SE_SE616	PDLADHLIHL	HYFDCFSDSA	IRKAILGQIV	SPRCEYQAGH	NQVGSLSQYLA
H_BE_VI991	PDLADQLIHL	HYFDCFSDSA	IRKAILGHRV	SPICDYQAGH	RKVGSLQYLA
H_BE_VI997	PGLADQLIHT	HYFDCFSESA	IRGAILGRVV	SPRCEYQAGH	NQVGSLSQYLA
H_CF_90CF0	PGLADQLIHM	HYFDCFSESA	IRKAILGRVV	RPRCNYPAGH	KQVGTLSQYLA
J_SE_SE702	PGLADQLIHM	HYFDCFSDSA	IRKAILGQIV	SPRCDYQAGH	NKVGSLQYLA
J_SE_SE788	PGLADQLIHM	CYFDCFSDSA	IRKAILGQIV	SPRCDYQAGH	NKVGSLQYLA
K_CD_EQTB1	PGLADQLIHI	YYFDCFSESA	IRKALLGHRV	SPRCEYQAGH	TQVGSLSQYLA
K_CM_MP535	PDLADQLIHI	YYFDCFSESA	VRKAILGHRV	SPRCEYQAGH	NKVGSLQYLA
N_CM_YBF30	PEMADKLIHL	HYFDCFADSA	IRQAVLGRPV	LPRCEYPAGH	KQVGTLSQYLA

O_CM_ANT70	PETADRMHL	HYFTCFRTASA	VRKAILGQRV	LTKCEYPTGH	SQVGTLLQLLA
O_CM_MVP51	PETADRMHL	HYFTCFRTESA	IRKAILGQRV	LTKCEYLAGH	SQVGTLLQFLA
O_SN_99SE_	PETADRMHL	YFACFTESA	IRKAILGQRV	LTRCEYPAGH	SQVGTLLQLLA
O_SN_99SE_	PETADRMHT	YFACFTESA	IRKAILGQRV	LTRCEYSAGH	SQVGTLLQLLA
U_CD___83C	PDLADQLIHL	HYFDCFSDSA	IRKAILGHIV	SPRCEYQTGH	NKVGSLQYLA

	151		194
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00BW1471_2	LTALIKPKRI	KPPLPSLQKL	VEDKWNPNPQK
00BW1616_2	LTALIKPKKI	KPPLPSVRKL	VEDRWNNPQK
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00BW1773_2	LTALIKPKKI	KPPLPSVRKL	VEDRWNNPQK
00BW1783_5	LTALIKPKKR	KPPLPSVRKL	VEDRWNPQK
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00BW2036_1	LTALIKPKKR	KPPLPSVRKL	VEDRWNPQK
00BW2063_6	LTALIKPKKR	KPPLPSVRKL	VEDRWNNPQK
00BW2087_2	LTALVKKKI	KPPLPSVKKL	VEDRWNPQK
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00BW2276_7	LTALIKPKRR	KPPLPSVRKL	VEDRWNPQK
00BW3819_3	LTAIK.PKKR	KPPLPSVRKL	VEDRWNPQK
00BW3842_8	LTALIKPKKR	KPPLPSVRKL	VEDRWNSQK
00BW3871_3	LTALIKPKKI	KPPLPSIRKL	VEDRWNSQK
00BW3876_9	LTALIKPKKI	KPPLPSVRKL	AEDRWNNPQK
00BW3886_8	LTALIKPKKR	KPPLPSVRKL	VEDRWNSQK
00BW3891_6	LTALIKPKKR	KPPLPSVRKL	VEDRWNNPQK
00BW3970_2	LTALIKPKRR	KPPLPSVRKL	AEDRWNNPQK
00BW5031_1	LTALIKPKRP	KPPLPSVRKL	AEDRWNPQK
96BW01B21	LTALIKPKKR	KPPLPSVKKL	VEDRWNPQK
96BW0407	LTALIKPKKR	KPPLPSVRKL	VEDRWNPQK
96BW0502	LTALIKPKQR	KPPLPSVRKL	VEDRWNPQK
96BW06_J4	LTALIKPKKR	KPPLPSISKL	VEDRWNPQR
96BW11_06	LTALVKKKI	KPPLPSVRKL	VEDRWNPQK
96BW1210	LTALIKPKKR	KPPLPSVRKL	VEDRWNPQK
96BW15B03	LTALIKPKQI	KPPLPSVRKL	VEDRWNPQK
96BW16_26	LTALIKPKKI	KPPLPSVNLK	VEDRWNNPQK
96BW17A09	LTALIKPKKI	KPPLPSVQKL	VEDRWNPQK
96BWM01_5	LTALIKPKKR	KPPLPSVRKL	VEDRWNPQK
96BWM03_2	LTALIKPKRI	KPPLPSVRKL	TEDRWNPQK
98BWMC12_2	LTALIKPKQR	KPPLPSVRKL	VEDRWNNPQK
98BWMC13_4	LTALIKPKKR	KPPLPSVKKL	VEDRWNPQK
98BWMC14_a	LTALIKTKKR	KPPLPSVSKL	VEDRWNPQK
98BWM014_1	LTALIKPKKR	KPPLPSVRKL	VEDRWNPQK
98BWM018_d	LTALIKPKKI	KPPLPSVKKL	VEDRWNPQK
98BWM036_a	LTALIKPKRR	KPPLPSVRKL	VEDRWNPQK
98BWM037_d	LTALIKPKRR	KPPLPSVRKL	TEDRWNPQK
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99BW4745_8	LTALLKTKRR	KPPLPSVRKL	VEDRWNNPQK
99BW4754_7	LTALIKPKRI	KPPLPSVRKL	VEDRWNPQK
99BWMC16_8	LTALIKPKVI	KPPLPSVRKL	VEDRWNPQK
A2_CD_97CD	LRALVASTRT	KPPLPSVRKL	VEDRWNPQK
A2_CY_94CY	LKAVVASTRT	KPPLPSVRKL	VEDRWNPQK

A2D__97KR	LKALVGETRT	KPPLPSVRKL	TEDRWNPQK	TKGHRGSHTM	NGH.
A2G_CD_97C	LRALVKPTKI	KPPLPSVKKL	TEDRWNPQK	TRGHRENPTM	SGY.
A_BY_97BL0	LKALVTPTRE	RPPLPSVRXL	TEDRXNKPQK	TRGRRXNHTM	NXC.
A_KE_Q23_A	LKALVTPKKT	KPPLPSVRIL	TEDRWNPQK	TRGLRESHTM	NGC.
A_SE_SE659	LRALVAPRKT	KPPLPSVRIL	AEDRWNPQK	TRDPRESHTM	NGC.
A_SE_SE725	LKALVTPTRT	KPPLPSVRKL	AEDRWSKPQK	TRGHRGSHTM	NGC.
A_SE_SE753	LKALVTPKKT	RPPLPSVRIL	AEDRWNSRK	TRGPRGSHTM	NGC.
A_SE_SE853	LKALVTPKKI	KPPLPSVKKL	TEDRWNPQK	TRGHRGNHTM	HGY.
A_SE_SE889	LKALVTPKKI	RPPLPSVRKL	AEDRWNPQK	TKGHRGSHTM	NGH.
A_SE_UGSE8	LKALVTPKRT	KPPLPSVRKL	TEDRWNPQK	TKGHRGSHTM	NGC.
A_UG_92UG0	LKALVTPSRM	KPPLPSVKKL	AEDRWNPQK	TRGRRESHTM	NGC.
A_UG_U455_	LKALVTPTRA	KPPLPSVKKL	TEDRWNPQK	TRGHRGSRTL	NRH.
AC_IN_2130	LTALIKPKKR	KPPLPSIRKL	VEDRWNNPQK	TRGRRGNHTM	NGH.
AC_RW_92RW	LTALIKPKKI	KPPLPSVSKL	VEDKWNKPQK	TRGRRGNHTM	NGH.
AC_SE_SE94	LTALIKPKKI	KPPLPSVRKL	VEDKWNKPQK	TRGRRGNHTM	NGH.
ACD_SE_SE8	LKALVTPTRV	KPPLPSVRKL	AEDRWSKSQK	TRGLRGSMTM	NGC.
ACG_BE_VI1	LKALVTPQI	RPPLPSVRKL	TEDRWNPQK	TRGHRGNHTM	NGH.
AD_SE_SE69	LTALITPKKE	KPPLPSVKKL	TEDRWNPQR	TKGHRGSHTM	NGH.
AD_SE_SE71	LKALVTPTKT	KPPLPSVRIL	TEDRWNPQK	TRGLRESHTM	NGC.
ADHK_NO_97	LTALVAPKKI	KPPLPSIKKL	AEDRWNPQK	TRGHRGSHTM	NGC.
ADK_CD_MAL	LTALIAPKKT	RPPLPSVRKL	TEDRWNPQK	TKGHRGSHTM	NGH.
AG_BE_VI11	LKALVTPTRI	RPPLPSVRKL	TEDRWNPQK	TRGHRGSHTM	NGQW
AG_NG_92NG	LKALVTPQT	KPPLPSVKKL	TEDRWNEPQK	TRGHRGSHTM	NGH.
AGHU_GA_VI	LKALVTPTRE	RPPLPSVQKL	TEDRWNPQK	TKDHRGSHTM	NGC.
AGU_CD_Z32	LTALITPKKT	KPPLPSVKKL	VEDRWNPQK	TRGHRENQTM	NEH.
AJ_BW_BW21	LKAILKTEKR	KPPLPSVQKL	VEDRWNPQR	TRGHRESHTM	NGH.
B_AU_VH_AF	LAALITPRQT	KPPLPSVTKL	TEDRWNPQR	TKGHRGSHTM	SGH.
B_CN_RL42_	LTALTTPKNR	KPPLPSVTKL	TEDRWNPQR	TKGHRGSHTM	SGH.
B_DE_D31_U	LAALITPKKI	KPPLPSVAKL	TEDRWNPQR	TKGHRGSHTM	NGH.
B_DE_HAN_U	LAALITPKKI	KPPLPIVTKL	TEDRWNPQK	TKGHRGSHTM	HGH.
B_FR_HXB2_	LAALITPKKI	KPPLPSVTKL	TEDRWNPQK	TKGHRGSHTM	NGH.
B_GA_OYI_	LAALIKPKKI	KPPLPSVTKL	TEDRWNPQK	TKGHRGSHTM	NGH.
B_GB_CAM1_	LTALIAPKKI	KPPLPSVRKL	TEDRWNPQK	TKGHRGSHTM	NGH.
B_GB_GB8_A	LTALITPKKI	KPPLPSVTKL	TEDRWNPQK	TKGHRGSHTM	NGH.
B_GB_MANC_	LAALITPKKT	KPPLPSVTKL	TEDRWNPQK	TKGHRESHTM	NGH.
B_KR_WK_AF	LTALITPKKI	KPPLPSVRKL	TEDRWNPQK	TKGHRGSHTM	NGH.
B_NL_3202A	LAALIKPKKI	KPPLPSVTKL	TEDRWNPQK	TKGHRGSHTM	NGH.
B_TW_TWCYS	LTALVQPKKI	KPPLPSVVKL	TEDRWNPQK	TKGHRGSHTM	HGH.
B_US_BC_L0	LAALITPKRI	KPPLPSVTKL	TEDRWNPQK	TKGHRGSHTM	NGH.
B_US_DH123	LAALVTPRKI	KPPLPSVAKL	TEDRWNSHK	TKGHRGSHTM	NGH.
B_US_JRCSF	LTALIKPKKI	KPPLPSVKKL	TEDRWNPQK	TKGHRGSHTM	NGH.
B_US_MNCG_	LTALITPKKI	KPPLPSVKKL	TEDRWNPQK	TKGHRGSHTI	NGH.
B_US_P896_	LAALTTPRRI	KPPFPSVTKL	TEDRWNPQK	TKGHRGSHTM	TGH.
B_US_RF_M1	LAALTTPKKI	KPPLPSVKKL	TEDRWNPQK	TKGHRGSHTM	NGH.
B_US_SF2_K	LAALITPKKT	KPPLPSVKKL	TEDRWNPQK	TKGHRGSHTM	NGH.
B_US_WEAU1	LTALITPKKI	KPPLPSVKKL	TEDRWNPQK	TKGHRGSHTM	NGH.
B_US_WR27_	LTALIKPKKI	KPPLPSVKKL	TEDRWNPQK	TKGHRGSHTM	NGH.
B_US_YU2_M	LTALITPKKT	KPPLPSVKKL	TEDRWNPQK	TKGHRGSRTM	NGH.
BF1_BR_93B	LTALIKPKKR	KPPLPSVKKL	TEDRWNPQK	TKDHRGSHTM	NGH.
C_BR_92BR0	LTALIKPKKI	KPPLPSVKKL	VEDRWNPQK	TRDRRGNHTM	NGH.
C_BW_96BW0	LTALIKPKKR	KPPLPSVRKL	VEDRWNEPQK	TRGRRGNHTM	NGH.
C_BW_96BW1	LTALIKPKKI	KPPLPSVRKL	VEDRWNPQK	TRGRRGNHTM	NGH.
C_BW_96BW1	LTALIKPKKR	KPPLPSVRKL	VEDRWNPQK	TRGRKGNHTM	NGH.
C_BW_96BW1	LTALIKPKQI	KPPLPSVRKL	VEDRWNPQK	TRGRRGNRTM	NGH.
C_ET_ETH22	LTALIKPKKA	KPPLPSVSKL	VEDKWNKPQK	TRGRRGNHTM	NGH.
C_IN_93IN1	LTALIKPKKI	KPPLPSIKKL	VEDRWNNPQK	IRGRRGNHTM	NGH.
C_IN_93IN9	LTALIKPKKI	KPPLPSIKKL	VEDRWNNPQK	IRGRRGNHTM	NGH.
C_IN_93IN9	LTALIKPKKI	KPPLPSVRKL	VEDRWNNPLK	TRGRRGNHTM	NGH.
C_IN_94IN1	LTALIKPKKI	KPPLPSIKKL	VEDRWNNPQK	IRGRRGNHTM	NGH.
C_IN_95IN2	LTALIKPKKI	KPPLPSIKKL	VEDRWNNPQK	IRGRKGNHIM	HGH.

CRF01_AE_C	LKALATPKKT	RPPLPSVRKL	TEDRWNPQK	TRGHRENPTM	NGH.
CRF01_AE_C	LKALTCTKKT	KPPLPSVRKL	TEDRWNPQK	TKGHRESPTM	NGH.
CRF01_AE_C	LKALATPKKI	RPPLPSVRKL	TEDRWNPQK	TRGHRENPTM	SGH.
CRF01_AE_T	LKALTTPKRI	RPPLPSVKKL	TEDRWNPQK	IWGHRENPTM	NGH.
CRF01_AE_T	LKALTTPKRI	KPPLPSVKKL	TEDRWNPQK	IRDHREYRTM	NGH.
CRF01_AE_T	LKALTTPKRI	RPPLPSVKKL	TEDRWNPQK	IKGHRENPTM	NGH.
CRF01_AE_T	LKALTTPKRI	RPPLPSVKKL	TEDRWNPQK	KGDHRENPTM	NGH.
CRF01_AE_T	LKALTTPKRI	RPPLPSV.EI	TEDRWNPQK	KRGHRENPTM	NGH.
CRF01_AE_T	LKALTTPKRI	KPPLPSVRKL	TEDRWNPQK	IRGHREYPTM	NGH.
CRF02_AG_F	LKALVTPAKT	KPPLPSVKKL	AEDRWNPQK	TRGHRGNRSM	NGH.
CRF02_AG_F	LKALVTPVKT	KPPLPSVKKL	AEDRWNPQK	TRGHRGNRSM	NGQ.
CRF02_AG_G	LKALVTPTRK	KPPLPSVRKL	AEDRWNPQK	TRGHRGSRPM	NGR.
CRF02_AG_N	LNALVAPTCT	KPPLPSVRKL	AEDRWNPQK	TRGHRGSRPM	NGH.
CRF02_AG_S	LKALVTPTRT	KPPLPSVKKL	AEDRWNPQK	TRGHRGSRSM	NGH.
CRF02_AG_S	LKALVTPTRR	KPPLPSVKKL	AEDRWNPQK	TRGHRGNRSM	NGH.
CRF03_AB_R	LAALRTPKKI	KPPLPSVTKL	TEDRWNPQR	TKDHRSHTM	SGH.
CRF03_AB_R	LAALRTPKKI	KPPLPSVTKL	TEDRWNPQR	TKDHRSHTM	SGH.
CRF04_cpx	LAALISPCKT	KPPLPSVKKL	VEDRWNPQK	TRGRRENQIM	NGH.
CRF04_cpx	LAALISPCKT	KPPLPSVKKL	VEDRWNPQK	TRGRRENQIM	NGH.
CRF04_cpx	LAALISPCKT	KPPLPSVKKL	VEDRWNSQK	TKGRRESHIM	NGH.
CRF05_DF_B	LTALITPKKT	KPPLPSVRKL	TEDRWNPQK	TKGRRGNHTM	NGY.
CRF05_DF_B	LTALITPQKI	KPPLPSVRKL	TEDRWNPQR	TKGHRGCHTM	NGY.
CRF06_cpx	LTALIKPEKR	KPPLPSVQKL	VEDRWNPQK	TRGHRESHTM	NGH.
CRF06_cpx	LTALIKPKKR	KPPLPSVQKL	VEDRWNPQK	TRDHRESHTM	NGH.
CRF06_cpx	LTALIKPKKR	KPPLPSVQKL	VEDRWNPQK	TRDHRECHTM	NGH.
CRF06_cpx	LKALVTKRR	KPPLPSVQKL	VEDRWNPQK	TKDHRESHIM	DGH.
CRF11_cpx	LKALVTPTRA	KPPLPSVRKL	AEDRWNPQK	TRGHRGNHTA	NGC.
CRF11_cpx	LKALVTPKRT	KPPLPSVRKL	TEDRWNPQK	TRGRRGNHTV	NGC.
D_CD_84ZR0	LTALIAPKKR	KPPLPSVKKL	TEDRWNPQR	TKGRRGSHTM	NGH.
D_CD_ELI_K	LTALIAPQKI	KPPLPSVRKL	TEDRWNPQK	TRGHRGSHTM	NGH.
D_CD_NDK_M	LAALIAPKKI	KPPLPSVRKL	TEDRWNPQK	TKGRRGSHTM	NGH.
D_UG_94UG1	LTALVTPRKI	KPPLPSVGKL	TEDRWNPQR	TKGHRGSHTM	NGH.
F1_BE_VI85	LTALIAPEKT	KPPLPSVQKL	VEDRWNPQE	TRGHRGSHTM	NGH.
F1_BR_93BR	LTALIAPKKT	KPPLPSVQKL	VEDRWNPQK	TRGHRESHTM	NGH.
F1_FI_FIN9	LTALVSPKKA	KPPLPSVKKL	VEDRWNPQE	IRGHRGSHTM	NGH.
F1_FR_MP41	LTALIAPKKT	KPPLPSVKKL	VEDRWNPQE	TRGHRGSHTM	NGH.
F2_CM_MP25	LTALITPKKI	KPPLPSVRKL	VEDRWNPQK	TRGHRGSHTM	NGH.
F2KU_BE_VI	LTALVAPKKT	KPPLPSVRKL	VEDRWNPQK	TRDHRSHTM	NGH.
G_BE_DRCBL	LKVLVAPTRR	RPPLPSVRKL	TEDRWNPQK	TRGHRENPTM	NGH.
G_NG_92NG0	SKALVTPTRK	RPPLPSVGKL	AEDRWNPQK	TRDHRENPTM	NGH.
G_SE_SE616	LKVLVTSKRS	RPPLPSVTEL	AEDRWNPQK	TRGHRENPTM	NGH.
H_BE_VI991	LTALISPCKT	KPPLPSVRKL	VEDRWNPQK	TRGHRGSHTM	NGH.
H_BE_VI997	LTALVAPKKT	KPPLPSVKKL	VEDGWNKPQK	TRGHRGSHTM	NRH.
H_CF_90CF0	LTALVAPKKI	KPPLPSVRKL	VEDRWNPQK	TRGHRGSHTM	NGH.
J_SE_SE702	LTALIKPKRR	KPPLPSVQKL	VEDRWNPQK	TRDHRESHTM	NGH.
J_SE_SE788	LTALIRPKRR	KPPLPSVQKL	VEDRWNPQK	TTGHRESHTM	NGH.
K_CD_EQTB1	LTALIAPKKT	KPPVPSVQKL	VEDRWNPQK	TRGHRGSHTM	SGQ.
K_CM_MP535	LTALVAPRRP	KPPVPSVKKL	VEDRWNPQK	TRGHRGSQTM	NGH.
N_CM_YBF30	LTAVVGAKKR	KPPLPSVTKL	TEDRWNEHQK	MQGHRGNPIM	NGH.
O_CM_ANT70	LRAVVKARS	KPPLPSVQKL	TEDRWNKLHR	IRDQLKSPSM	NGH.
O_CM_MVP51	LKAVVKVRN	KPPLPSVQKL	TEDRWNPWK	IRDQLGSHSM	NGH.
O_SN_99SE	LRVVVKEKRN	KPPLPSVQKL	TEDRWSRHLR	IRDQLGSHSM	NGH.
O_SN_99SE	LRVVVKEKRH	KPPLPSVQKL	TEDRWSRHLR	IRDQLGSHSM	NGH.
U_CD_83C	LTTLVAPTKR	KPPLPSVRKL	VEDRWNPQK	TKGHKGSHTM	HGH.

Table 18. HIV Vpr Sequence Alignment  
GCG Multiple Sequence File.  
Written by Omega 1.1

Name: 00BW0762_1	<u>SEQ ID NO: 1469</u>	Len: 100	Check: 8179	Weight: 1.00
Name: 00BW0768_2	<u>SEQ ID NO: 1470</u>	Len: 100	Check: 8119	Weight: 1.00
Name: 00BW0874_2	<u>SEQ ID NO: 1471</u>	Len: 100	Check: 7661	Weight: 1.00
Name: 00BW1471_2	<u>SEQ ID NO: 1472</u>	Len: 100	Check: 6614	Weight: 1.00
Name: 00BW1616_2	<u>SEQ ID NO: 1473</u>	Len: 100	Check: 6361	Weight: 1.00
Name: 00BW1686_8	<u>SEQ ID NO: 1474</u>	Len: 100	Check: 6014	Weight: 1.00
Name: 00BW1759_3	<u>SEQ ID NO: 1475</u>	Len: 100	Check: 6894	Weight: 1.00
Name: 00BW1773_2	<u>SEQ ID NO: 1476</u>	Len: 100	Check: 7772	Weight: 1.00
Name: 00BW1783_5	<u>SEQ ID NO: 1477</u>	Len: 100	Check: 7149	Weight: 1.00
Name: 00BW1795_6	<u>SEQ ID NO: 1478</u>	Len: 100	Check: 7614	Weight: 1.00
Name: 00BW1811_3	<u>SEQ ID NO: 1479</u>	Len: 100	Check: 7968	Weight: 1.00
Name: 00BW1859_5	<u>SEQ ID NO: 1480</u>	Len: 100	Check: 6222	Weight: 1.00
Name: 00BW1880_2	<u>SEQ ID NO: 1481</u>	Len: 100	Check: 6941	Weight: 1.00
Name: 00BW1921_1	<u>SEQ ID NO: 1482</u>	Len: 100	Check: 8183	Weight: 1.00
Name: 00BW2036_1	<u>SEQ ID NO: 1483</u>	Len: 100	Check: 8175	Weight: 1.00
Name: 00BW2063_6	<u>SEQ ID NO: 1484</u>	Len: 100	Check: 8705	Weight: 1.00
Name: 00BW2087_2	<u>SEQ ID NO: 1485</u>	Len: 100	Check: 7388	Weight: 1.00
Name: 00BW2127_2	<u>SEQ ID NO: 1486</u>	Len: 100	Check: 8282	Weight: 1.00
Name: 00BW2128_3	<u>SEQ ID NO: 1487</u>	Len: 100	Check: 1723	Weight: 1.00
Name: 00BW2276_7	<u>SEQ ID NO: 1488</u>	Len: 100	Check: 6468	Weight: 1.00
Name: 00BW3819_3	<u>SEQ ID NO: 1489</u>	Len: 100	Check: 5670	Weight: 1.00
Name: 00BW3842_8	<u>SEQ ID NO: 1490</u>	Len: 100	Check: 7788	Weight: 1.00
Name: 00BW3871_3	<u>SEQ ID NO: 1491</u>	Len: 100	Check: 8574	Weight: 1.00
Name: 00BW3876_9	<u>SEQ ID NO: 1492</u>	Len: 100	Check: 7285	Weight: 1.00
Name: 00BW3886_8	<u>SEQ ID NO: 1493</u>	Len: 100	Check: 6446	Weight: 1.00
Name: 00BW3891_6	<u>SEQ ID NO: 1494</u>	Len: 100	Check: 8629	Weight: 1.00
Name: 00BW3970_2	<u>SEQ ID NO: 1495</u>	Len: 100	Check: 7113	Weight: 1.00
Name: 00BW5031_1	<u>SEQ ID NO: 1496</u>	Len: 100	Check: 5511	Weight: 1.00
Name: 96BW01B21	<u>SEQ ID NO: 1497</u>	Len: 100	Check: 7551	Weight: 1.00
Name: 96BW0407	<u>SEQ ID NO: 1498</u>	Len: 100	Check: 8226	Weight: 1.00
Name: 96BW0502	<u>SEQ ID NO: 1499</u>	Len: 100	Check: 8242	Weight: 1.00
Name: 96BW06_J4	<u>SEQ ID NO: 1500</u>	Len: 100	Check: 7544	Weight: 1.00
Name: 96BW11_06	<u>SEQ ID NO: 1501</u>	Len: 100	Check: 7942	Weight: 1.00
Name: 96BW1210	<u>SEQ ID NO: 1502</u>	Len: 100	Check: 8580	Weight: 1.00
Name: 96BW15B03	<u>SEQ ID NO: 1503</u>	Len: 100	Check: 7308	Weight: 1.00
Name: 96BW16_26	<u>SEQ ID NO: 1504</u>	Len: 100	Check: 7009	Weight: 1.00
Name: 96BW17A09	<u>SEQ ID NO: 1505</u>	Len: 100	Check: 6492	Weight: 1.00
Name: 96BWMO1_5	<u>SEQ ID NO: 1506</u>	Len: 100	Check: 5837	Weight: 1.00
Name: 96BWMO3_2	<u>SEQ ID NO: 1507</u>	Len: 100	Check: 5277	Weight: 1.00
Name: 98BWMC12_2	<u>SEQ ID NO: 1508</u>	Len: 100	Check: 7807	Weight: 1.00
Name: 98BWMC13_4	<u>SEQ ID NO: 1509</u>	Len: 100	Check: 9051	Weight: 1.00
Name: 98BWMC14_a	<u>SEQ ID NO: 1510</u>	Len: 100	Check: 7867	Weight: 1.00
Name: 98BWMO14_1	<u>SEQ ID NO: 1511</u>	Len: 100	Check: 7266	Weight: 1.00
Name: 98BWMO18_d	<u>SEQ ID NO: 1512</u>	Len: 100	Check: 7638	Weight: 1.00
Name: 98BWMO36_a	<u>SEQ ID NO: 1513</u>	Len: 100	Check: 7495	Weight: 1.00
Name: 98BWMO37_d	<u>SEQ ID NO: 1514</u>	Len: 100	Check: 6640	Weight: 1.00
Name: 99BW3932_1	<u>SEQ ID NO: 1515</u>	Len: 100	Check: 6974	Weight: 1.00
Name: 99BW4642_4	<u>SEQ ID NO: 1516</u>	Len: 100	Check: 6081	Weight: 1.00
Name: 99BW4745_8	<u>SEQ ID NO: 1517</u>	Len: 100	Check: 8860	Weight: 1.00
Name: 99BW4754_7	<u>SEQ ID NO: 1518</u>	Len: 100	Check: 6856	Weight: 1.00
Name: 99BWMC16_8	<u>SEQ ID NO: 1519</u>	Len: 100	Check: 8223	Weight: 1.00

<u>SEQ ID NO</u>		1				50
<u>1469</u>	00BW0762_1	MEQAPEDQGP	QREPYNEWTL	ELLEELKQEA	VRHFPRPWLH	SLGQHIYNTY
<u>1470</u>	00BW0768_2	MEQAPEDQGP	QREPYNEWTL	EILEELKQEA	VRHFPRPWLH	NLGEYIYETY
<u>1471</u>	00BW0874_2	MEQPPEDQGP	QREPYNEWTL	EILEELKQEA	VRHFPRPWLH	SLGQYIYETY
<u>1472</u>	00BW1471_2	MEQPPEDQGP	QREPYNEWTL	ELLEELKQEA	VRHFPRPWLH	SLGQHIYETY
<u>1473</u>	00BW1616_2	MEQPPEDQGP	QREPYNEWTL	ELLEELKQEA	VRHFPRPWLH	SLGQYIYENY
<u>1474</u>	00BW1686_8	MEQAPEDQGP	QREPYNEWAL	EILEELKQEA	VRHFPRPWLH	SIGQYIYETY
<u>1475</u>	00BW1759_3	MEQAPEDQGP	QREPYNEWTL	ELLEELKQEA	VRHFPRPWLH	GLGQHIYETY
<u>1476</u>	00BW1773_2	MEQPPEDQGP	QREPYNEWTL	ELLEELIQEA	VRHFPRPWLH	SLGQYIYETY
<u>1477</u>	00BW1783_5	MEQAPEDQGP	QREPYNEWTL	ELLEELKQEA	VRHFPRPWLH	SMGQHIYNTY
<u>1478</u>	00BW1795_6	MEQAPEDQGP	QREPIN . ETL	ELLEELKQEA	VRHFPRPWLH	NLGQYIYNTY
<u>1479</u>	00BW1811_3	MEQPPEDQGP	QREPYNEWAL	ELLEELKQEA	VRHFPRPWLH	GLGQYVYETY
<u>1480</u>	00BW1859_5	MEQPPEDQGP	QREPYNEWAL	EILEELKQEA	VRHFPRPWLH	SLGQYIYETY
<u>1481</u>	00BW1880_2	MEQAPEDQGP	QRELYNEWTL	ELLEELKQEA	ARHFPSWLH	GLGQHIYNTY
<u>1482</u>	00BW1921_1	MEQAPEDQGP	QREPYNEWTL	ELLEELKQEA	VRHFPRPWLH	NLGQYIYQTY
<u>1483</u>	00BW2036_1	MEQAPEDQGP	QREPYNEWTL	EILEELKQEA	VRHFPRPWLQ	SLGQYIYETY
<u>1484</u>	00BW2063_6	MEQPPEDQGP	QREPYNEWTL	GLLEELKQEA	VRHFPRPWLH	NLGQYIYNTY
<u>1485</u>	00BW2087_2	MEQAPEDQGP	QREPYNEWAL	ELLEELKQEA	VRHFPRPWLH	NLGQYIYETY
<u>1486</u>	00BW2127_2	MEQAPEDQGP	QREPYNEWTL	EILEELKQEA	VRHFPRPWLH	NLGQYIYETY
<u>1487</u>	00BW2128_3	MEQPPEDQGP	QREPYNEWTL	ELLEELKQEA	VRHFPRPWLH	GLGQYIYETY
<u>1488</u>	00BW2276_7	MEQTPEDQGP	QREPYNEWAL	EILEELKQEA	VRHFPRPWLH	SLGQYIYDTY
<u>1489</u>	00BW3819_3	MEQAPEDQGP	QREPYNEWTL	EILEELKQGA	VRHFPRPWLH	NLGQHIYETY
<u>1490</u>	00BW3842_8	MEQVPEDQGP	QREPYNEWTL	EILEELKQEA	VRHFPRPWLQ	GLGHYIYETY
<u>1491</u>	00BW3871_3	MEQVPEDQGP	QREPYNEWTL	EILEELKQEA	VRHFPRPWLH	NLGQYIYETY
<u>1492</u>	00BW3876_9	MEQSPEDQGP	QREPYNEWTL	ELLEELKQEA	VRHFPRPWLH	GIGQYIYETY
<u>1493</u>	00BW3886_8	MEQFPEDQGP	QREPYNEWTL	ELLEELKQEA	VKHFPRPWLH	NLGQHIYETY
<u>1494</u>	00BW3891_6	MEQPPEDQGP	QREPYNEWTL	EVLEELKQEA	VRHFPRPWLH	SLGQYVYETY
<u>1495</u>	00BW3970_2	MEQPPEDQGP	QREPYNEWAL	EILEELKQEA	VRHFPRPWLH	SLGQHIYETY
<u>1496</u>	00BW5031_1	MEQAPEDQGP	QREPYNEWTL	ELLEELKQEA	VRHFPRPWLH	SLGQHIYETY
<u>1497</u>	96BW01B21	MERPPEDQGP	QREPYNEWTL	ELLEELKQEA	VRHFPRPWLH	GLGQYIYETY
<u>1498</u>	96BW0407	MERAPEDQGP	QREPYNEWAL	ELLEELKQEA	VRHFPRPWLH	GLGQYIYETY
<u>1499</u>	96BW0502	MEQAPEDQGP	QREPYNEWTL	ELLEELKQEA	VRHFPRPWLH	GLGQYVYETY
<u>1500</u>	96BW06_J4	MEQAPEDQGP	QREPYNEWTL	EILEELKQEA	VRHFPRPWLH	SLGQYIYETY
<u>1501</u>	96BW11_06	MEQAPEDQGP	QREPYNEWTL	ELLEELKQEA	VRHFPRPWLH	SLGQHIYNTY
<u>1502</u>	96BW1210	MEQAPEDQGP	QREPYNEWTL	ELLEELKQEA	VRHFPRPWLH	SLGQYIYETY
<u>1503</u>	96BW15B03	TEQAPEDQGP	QREPYNEWAL	EILEELKQEA	VRHFPRPWLH	SLGQYIYETY
<u>1504</u>	96BW16_26	MEQPPEDQGP	QREPYTEWAL	ELLEELKQEA	VRHFPRPWLH	GLGQYIYDTY
<u>1505</u>	96BW17A09	MEQTPEDQGP	QREPHNEWTL	ELLEELKQEA	VRHFPRPWLH	SLGQHIYETY
<u>1506</u>	96BWM01_5	MEQAPEDQGP	QREPYNEWTL	ELLEELKQEA	VRHFPR . TLH	DLGQHIYNTY
<u>1507</u>	96BWM03_2	MEQAPEDQGP	QREPYNEWTL	EILEELKQEA	IRHFPIPYLQ	HLGQYIYETY
<u>1508</u>	98BWMC12_2	MEQPPEDQGP	QREPYNEWTL	EILEELKQEA	VRHFPRPWLH	SLGQYIYETY
<u>1509</u>	98BWMC13_4	MEQAPEDQGP	QREPYNEWTL	ELLEELKQEA	VRHFPRPWLH	NLGQYVYNTY
<u>1510</u>	98BWMC14_a	MEQAPEDQGP	QREPYNEWTL	EILEELKQEA	VRHLPWPWLH	SLGQHIYETY
<u>1511</u>	98BWM014_1	MEQAPEDQGP	QREPYNEWTL	ALLEDLKQEA	VRHVPRPWLH	SLGQHIYETY
<u>1512</u>	98BWM018_d	MEQAPEDQGP	QREPYNEWTL	ELLEELKQEA	VRHFPRPWLH	SLGQYIYETY
<u>1513</u>	98BWM036_a	MEQAPEDQGP	QREPYNEWTL	ELLEELKQEA	VRHFPRPWLH	NLGQYIYETY
<u>1514</u>	98BWM037_d	MEQAPEDQGP	QREPYNEWTL	EILEELKQEA	VRHFPRPWLH	DLGQYIYETY



<u>1515</u>	99BW3932_1	MEQAPEDQGP	QREPYNEWTL	EILEELKQEA	VRHFPRPWLH	NLGQYIYATY
<u>1516</u>	99BW4642_4	MEQPPEDQGP	QREPYNEWAL	EILEELKQEA	VRHFPRPWLH	NLGQYIYETY
<u>1517</u>	99BW4745_8	MEQPPEDQGP	QREPYNEWTL	EVLEDLKQEA	VRHFPRPWLH	SIGQYVYSTY
<u>1518</u>	99BW4754_7	MEQAPENQGP	QREPYNEWAL	ELLEELKQEA	VRHFPRPWLH	DLGQHIYNTY
<u>1519</u>	99BWMC16_8	MEQAPEDQGP	QREPYNEWTL	ELLEELKQEA	VRHFPRPWLH	SLGLYIYETY

	51					100
00BW0762_1	GDTWTGVEAI	IRILQQLLFI	HFRIGCQHSR	IGIMRQ....	RRTRNGASRS	
00BW0768_2	GDTWTGVEAL	IRVLQQLLFI	HFRIGCSHSR	IGIVRQ....	RRARNGSSRS	
00BW0874_2	GDTWTGVETI	IRTLQQLLFI	HFRIGCQHSR	IGILRQ....	KRARNGASRS	
00BW1471_2	GDTWAGVEAL	LRILQQLLFI	HFRIGCQHSR	IGIIPQ....	RRARNGSRRS	
00BW1616_2	GDTWAGVEAI	TRILQQLLFI	HFRIGCQHSR	IGILRQ....	RRARNGANRS	
00BW1686_8	GDTWTGVEAL	MRILQQLLFI	HFRIGCQHSR	IGILQR....	R.ARNGASRS	
00BW1759_3	GDTWTGVEAI	IRILQQLLFI	HYRIGCQHSR	IGIVRQ....	RRARNGANRS	
00BW1773_2	GDTWTGVEAI	IKILQQLLFI	HFRIGCQHSR	IGILRQ....	RRARNGASRS	
00BW1783_5	GDTWAGVEAI	IRILQQLLFI	HFRIGCQHSR	IGILRQ....	RRTRNGASRS	
00BW1795_6	GDTWTGVEAI	IRTLQQLLFV	HFRIGCQHSR	IGIMRQ....	RRARNGTSGS	
00BW1811_3	GDTWTGVEAI	IRILQQLLFV	HFRIGCQHSR	IGILQQ....	RRARNGASRS	
00BW1859_5	GDTWAGVEAL	IRILQQLLFI	HFRIGCQHSR	IGILQQ....	RRARNGASRS	
00BW1880_2	GDTWTGVEVL	IRILQQLLFI	HFRIGCQHSR	IGIIRQ....	RRTRNGASRP	
00BW1921_1	GDTWTGVEAL	IRILQQPLFI	HFRIGCQHSR	IGITLP....	RRARNGANRS	
00BW2036_1	GDTWTGVEAI	IRILQQLLFI	HFRSGCAHSR	IGTLPQ....	RRARNGASRS	
00BW2063_6	GDTWTGVEAI	IRILQQLLFI	HFRIGCQHSR	IGIIRQ....	RRTRNGDSRS	
00BW2087_2	GDTWTGVEAL	IRILQQLLFT	HYRFGCQHSR	IGILQQ....	RRARNGANRS	
00BW2127_2	GDTWTGVEVI	IRILQQLLFI	HFRIGCQHSR	IGILRQ....	RRTRNGASRS	
00BW2128_3	GDTWAGVESL	IRMLQHLLFI	HFRIGCQHSR	IDX.....	.....	
00BW2276_7	GDTWAGVEAI	IRILQQLLFT	HFRIGCHHSR	IGILRQ....	RRARNGASRS	
00BW3819_3	GDTWAGVEAL	LRILQQLLFI	HFRIGCQHSR	IGILRQ....	RRARNGASRP	
00BW3842_8	GDTWTGVETI	IRILQQLLFI	HFRIGCSRSR	IGPMRQ....	RRARNGASRS	
00BW3871_3	GDTWTGVEAL	LRVLQQLLFV	HFRIGCQHSR	IGILQQ....	RRARNGSSRS	
00BW3876_9	GDTWTGVEAI	IRILQQLLFI	HYRIGCAHSR	IGIVRQ....	RRARNGANRS	
00BW3886_8	GDTWTGVEAI	IRMLQQLLFI	HFRIGCQHSR	IGILRQ....	RRARNGANRS	
00BW3891_6	GDTWTGVEAL	IRMLQQLLFI	HFKIGCQHSR	IGILRR....	RRARNGASRS	
00BW3970_2	GDTWTGVEAL	IRILQQLLFI	HFRIGCQHSR	IGIILQ....	RRTRNGASRS	
00BW5031_1	GDTWMGVEAL	IRILQ....	HFRIGCQHSR	IGIILQ....	RRTRNGASRS	
96BW01B21	GDTWTGVENM	IRILQQLLFV	HFRIGCQHSR	IGILQQ....	RRARNGASRS	
96BW0407	GDTWTGVEAL	IRTLQQLLFI	HFRIGCQHSR	IGILRQ....	RRVRNGTNRS	
96BW0502	GDTWTGVETL	IRILQQLLFI	HFRIGCQHSR	IGILRQ....	RRTRNGASRS	
96BW06_J4	GDTWTGVETI	IRILQQLLFI	HFRIGCQHSR	IGILQQ....	RRARNGASRP	
96BW11_06	GDTWTGVEAI	IRILQQLLFI	HFRIGCQHSR	IGIIRQ....	RRTRNGASRP	
96BW1210	GDTWTGVEVL	TRILQQLLFI	HFRIGCQHSR	IGILRQ....	RRTRNGASRS	
96BW15B03	GDTWTGVEAI	IRILQQLLFI	HFRIGCLHSR	IGIMRQ....	RRARNGASRS	
96BW16_26	GDTWTGVEIK	IRILQQLLFI	HFRIGCQHSR	IGILQQ....	RRARNGARRS	
96BW17A09	GDTWAGVEAL	LRILQQLLFI	HFRIGCHHSR	IGITPQ....	RRARNGSRRS	
96BWM01_5	GDTWTGVEAI	TRILQQLLFI	HYRIGCQHSR	IGIMRQ....	RRARNGASRS	
96BWM03_2	GDTWAGVLAI	IRILQQLLFI	HFRIGCSHSR	IGIWR....	RRARNGASRS	
98BWMC12_2	GDTWTGVEAI	LRILQQLLFI	HFRIGCQHSR	IGILRQ....	RRARNGASRS	
98BWMC13_4	GDTWTGVEAI	IRILQQLLFI	HFRIGCQHSR	IGILRQ....	RRTRNGASRS	
98BWMC14_a	GDTWTGVEAI	IRILQQLLFI	HFRIGCQHSR	IGILPR....	RRARNGSSRS	
98BWM014_1	GDTWTGVEAI	IRILQQLLFI	HFRIGCQHSR	IGILRQ....	RRARNGANRS	
98BWM018_d	GDTWTGVEVI	IRILQQLLFI	HFRIGCQHSR	IGILRQ....	RRARNGANRS	
98BWM036_a	GDTWTGVEAL	IRTLQQLLFI	HFRIGCQHSR	IGILRQ....	RRARNGASRS	
98BWM037_d	GDTWTGVETI	IRVLQQLLFI	HFRIGCH.SR	IGIVRQ....	RRARNGASRS	
99BW3932_1	GDTWMGVEAL	LRILQQLLFI	HFRIGCQHSR	IGILRQ....	RRARNGASRS	
99BW4642_4	GDTWAGVEAI	IRVLQQLLFI	HFRIGCHHSR	IGIMQQ....	RRARNGASRS	
99BW4745_8	GDTWTGVEAL	MRILQQLLFI	HFRIGCRHSR	IGILRQ....	RGARNGASRS	
99BW4754_7	GDTWTGVEAI	IRILQQLLFI	HFRIGCHHSR	IGIIRQ....	RRTRNGASRP	
99BWMC16_8	GDTWTGVEVI	IRILQQLLFI	HFRIGCQHSR	IGILRQ....	RRARNGPSRS	

Table 19. HIV Vpu Sequence Alignment  
GCG Multiple Sequence File.  
Written by Omega 1.1

Name: 00BW0762_1	<u>SEQ ID NO: 1520</u>	Len: 106	Check: 4772	Weight: 1.00
Name: 00BW0768_2	<u>SEQ ID NO: 1521</u>	Len: 106	Check: 7115	Weight: 1.00
Name: 00BW0874_2	<u>SEQ ID NO: 1522</u>	Len: 106	Check: 7209	Weight: 1.00
Name: 00BW1471_2	<u>SEQ ID NO: 1523</u>	Len: 106	Check: 7341	Weight: 1.00
Name: 00BW1616_2	<u>SEQ ID NO: 1524</u>	Len: 106	Check: 3870	Weight: 1.00
Name: 00BW1686_8	<u>SEQ ID NO: 1525</u>	Len: 106	Check: 8787	Weight: 1.00
Name: 00BW1759_3	<u>SEQ ID NO: 1526</u>	Len: 106	Check: 7584	Weight: 1.00
Name: 00BW1773_2	<u>SEQ ID NO: 1567</u>	Len: 106	Check: 7507	Weight: 1.00
Name: 00BW1783_5	<u>SEQ ID NO: 1568</u>	Len: 106	Check: 7874	Weight: 1.00
Name: 00BW1795_6	<u>SEQ ID NO: 1569</u>	Len: 106	Check: 8721	Weight: 1.00
Name: 00BW1811_3	<u>SEQ ID NO: 1570</u>	Len: 106	Check: 3657	Weight: 1.00
Name: 00BW1859_5	<u>SEQ ID NO: 1571</u>	Len: 106	Check: 6137	Weight: 1.00
Name: 00BW1880_2	<u>SEQ ID NO: 1572</u>	Len: 106	Check: 5827	Weight: 1.00
Name: 00BW1921_1	<u>SEQ ID NO: 1573</u>	Len: 106	Check: 4605	Weight: 1.00
Name: 00BW2036_1	<u>SEQ ID NO: 1574</u>	Len: 106	Check: 6145	Weight: 1.00
Name: 00BW2063_6	<u>SEQ ID NO: 1575</u>	Len: 106	Check: 7187	Weight: 1.00
Name: 00BW2087_2	<u>SEQ ID NO: 1576</u>	Len: 106	Check: 9545	Weight: 1.00
Name: 00BW2127_2	<u>SEQ ID NO: 1577</u>	Len: 106	Check: 4898	Weight: 1.00
Name: 00BW2276_7	<u>SEQ ID NO: 1578</u>	Len: 106	Check: 7311	Weight: 1.00
Name: 00BW3819_3	<u>SEQ ID NO: 1579</u>	Len: 106	Check: 4879	Weight: 1.00
Name: 00BW3842_8	<u>SEQ ID NO: 1580</u>	Len: 106	Check: 1804	Weight: 1.00
Name: 00BW3871_3	<u>SEQ ID NO: 1581</u>	Len: 106	Check: 6650	Weight: 1.00
Name: 00BW3876_9	<u>SEQ ID NO: 1582</u>	Len: 106	Check: 6684	Weight: 1.00
Name: 00BW3886_8	<u>SEQ ID NO: 1583</u>	Len: 106	Check: 8701	Weight: 1.00
Name: 00BW3891_6	<u>SEQ ID NO: 1584</u>	Len: 106	Check: 8544	Weight: 1.00
Name: 00BW3970_2	<u>SEQ ID NO: 1585</u>	Len: 106	Check: 9375	Weight: 1.00
Name: 00BW5031_1	<u>SEQ ID NO: 1586</u>	Len: 106	Check: 7778	Weight: 1.00
Name: 96BW01B21	<u>SEQ ID NO: 1587</u>	Len: 106	Check: 6481	Weight: 1.00
Name: 96BW0407	<u>SEQ ID NO: 1588</u>	Len: 106	Check: 4225	Weight: 1.00
Name: 96BW0502	<u>SEQ ID NO: 1589</u>	Len: 106	Check: 5292	Weight: 1.00
Name: 96BW06_J4	<u>SEQ ID NO: 1590</u>	Len: 106	Check: 5367	Weight: 1.00
Name: 96BW11_06	<u>SEQ ID NO: 1591</u>	Len: 106	Check: 6477	Weight: 1.00
Name: 96BW1210	<u>SEQ ID NO: 1592</u>	Len: 106	Check: 6400	Weight: 1.00
Name: 96BW15B03	<u>SEQ ID NO: 1593</u>	Len: 106	Check: 2981	Weight: 1.00
Name: 96BW16_26	<u>SEQ ID NO: 1594</u>	Len: 106	Check: 5352	Weight: 1.00
Name: 96BW17A09	<u>SEQ ID NO: 1595</u>	Len: 106	Check: 6778	Weight: 1.00
Name: 96BWM01_5	<u>SEQ ID NO: 1596</u>	Len: 106	Check: 5954	Weight: 1.00
Name: 96BWM03_2	<u>SEQ ID NO: 1597</u>	Len: 106	Check: 6334	Weight: 1.00
Name: 98BWMC12_2	<u>SEQ ID NO: 1598</u>	Len: 106	Check: 6905	Weight: 1.00
Name: 98BWMC13_4	<u>SEQ ID NO: 1599</u>	Len: 106	Check: 7458	Weight: 1.00
Name: 98BWMC14_a	<u>SEQ ID NO: 1560</u>	Len: 106	Check: 4023	Weight: 1.00
Name: 98BWM014_1	<u>SEQ ID NO: 1561</u>	Len: 106	Check: 5708	Weight: 1.00
Name: 98BWM018_d	<u>SEQ ID NO: 1562</u>	Len: 106	Check: 7741	Weight: 1.00
Name: 98BWM036_a	<u>SEQ ID NO: 1563</u>	Len: 106	Check: 5445	Weight: 1.00
Name: 98BWM037_d	<u>SEQ ID NO: 1564</u>	Len: 106	Check: 8225	Weight: 1.00
Name: 99BW3932_1	<u>SEQ ID NO: 1565</u>	Len: 106	Check: 1112	Weight: 1.00
Name: 99BW4642_4	<u>SEQ ID NO: 1566</u>	Len: 106	Check: 8891	Weight: 1.00
Name: 99BW4745_8	<u>SEQ ID NO: 1567</u>	Len: 106	Check: 3424	Weight: 1.00
Name: 99BW4754_7	<u>SEQ ID NO: 1568</u>	Len: 106	Check: 5468	Weight: 1.00
Name: 99BWMC16_8	<u>SEQ ID NO: 1569</u>	Len: 106	Check: 6656	Weight: 1.00
Name: A2_CD_97CD	<u>SEQ ID NO: 1570</u>	Len: 106	Check: 6086	Weight: 1.00
Name: A2_CY_94CY	<u>SEQ ID NO: 1571</u>	Len: 106	Check: 4609	Weight: 1.00
Name: A2D_97KR	<u>SEQ ID NO: 1572</u>	Len: 106	Check: 2120	Weight: 1.00
Name: A2G_CD_97C	<u>SEQ ID NO: 1573</u>	Len: 106	Check: 4405	Weight: 1.00
Name: A_BY_97BL0	<u>SEQ ID NO: 1574</u>	Len: 106	Check: 913	Weight: 1.00
Name: A_KE_Q23_A	<u>SEQ ID NO: 1575</u>	Len: 106	Check: 3380	Weight: 1.00

Name: A_SE_SE659	SEQ ID NO: 1576	Len: 106	Check: 4192	Weight: 1.00
Name: A_SE_SE725	SEQ ID NO: 1577	Len: 106	Check: 3244	Weight: 1.00
Name: A_SE_SE753	SEQ ID NO: 1578	Len: 106	Check: 1918	Weight: 1.00
Name: A_SE_SE853	SEQ ID NO: 1579	Len: 106	Check: 5495	Weight: 1.00
Name: A_SE_SE889	SEQ ID NO: 1580	Len: 106	Check: 5422	Weight: 1.00
Name: A_SE_UGSE8	SEQ ID NO: 1581	Len: 106	Check: 4254	Weight: 1.00
Name: A_UG_92UG0	SEQ ID NO: 1582	Len: 106	Check: 4081	Weight: 1.00
Name: A_UG_U455_	SEQ ID NO: 1583	Len: 106	Check: 2987	Weight: 1.00
Name: AC_IN_2130	SEQ ID NO: 1584	Len: 106	Check: 7929	Weight: 1.00
Name: AC_RW_92RW	SEQ ID NO: 1585	Len: 106	Check: 5133	Weight: 1.00
Name: AC_SE_SE94	SEQ ID NO: 1586	Len: 106	Check: 7394	Weight: 1.00
Name: ACD_SE_SE8	SEQ ID NO: 1587	Len: 106	Check: 1852	Weight: 1.00
Name: ACG_BE_VI1	SEQ ID NO: 1588	Len: 106	Check: 6357	Weight: 1.00
Name: AD_SE_SE69	SEQ ID NO: 1589	Len: 106	Check: 5734	Weight: 1.00
Name: AD_SE_SE71	SEQ ID NO: 1590	Len: 106	Check: 4697	Weight: 1.00
Name: ADHK_NO_97	SEQ ID NO: 1591	Len: 106	Check: 6301	Weight: 1.00
Name: ADK_CD_MAL	SEQ ID NO: 1592	Len: 106	Check: 4338	Weight: 1.00
Name: AG_BE_VI11	SEQ ID NO: 1593	Len: 106	Check: 3500	Weight: 1.00
Name: AG_NG_92NG	SEQ ID NO: 1594	Len: 106	Check: 4859	Weight: 1.00
Name: AGHU_GA_VI	SEQ ID NO: 1595	Len: 106	Check: 6173	Weight: 1.00
Name: AGU_CD_Z32	SEQ ID NO: 1596	Len: 106	Check: 9411	Weight: 1.00
Name: AJ_BW_BW21	SEQ ID NO: 1597	Len: 106	Check: 6158	Weight: 1.00
Name: B_AU_VH_AF	SEQ ID NO: 1598	Len: 106	Check: 5007	Weight: 1.00
Name: B_CN_RL42	SEQ ID NO: 1599	Len: 106	Check: 4249	Weight: 1.00
Name: B_DE_D31_U	SEQ ID NO: 1600	Len: 106	Check: 4572	Weight: 1.00
Name: B_DE_HAN_U	SEQ ID NO: 1601	Len: 106	Check: 6819	Weight: 1.00
Name: B_FR_HXB2	SEQ ID NO: 1602	Len: 106	Check: 5240	Weight: 1.00
Name: B_GA_OYI_M	SEQ ID NO: 1603	Len: 106	Check: 5651	Weight: 1.00
Name: B_GB_CAM1	SEQ ID NO: 1604	Len: 106	Check: 5359	Weight: 1.00
Name: B_GB_GB8_A	SEQ ID NO: 1605	Len: 106	Check: 1955	Weight: 1.00
Name: B_GB_MANC	SEQ ID NO: 1606	Len: 106	Check: 6521	Weight: 1.00
Name: B_KR_WK_AF	SEQ ID NO: 1607	Len: 106	Check: 2320	Weight: 1.00
Name: B_NL_3202A	SEQ ID NO: 1608	Len: 106	Check: 4510	Weight: 1.00
Name: B_TW_TWCYS	SEQ ID NO: 1609	Len: 106	Check: 5491	Weight: 1.00
Name: B_US_BC_L0	SEQ ID NO: 1610	Len: 106	Check: 3142	Weight: 1.00
Name: B_US_DH123	SEQ ID NO: 1611	Len: 106	Check: 4669	Weight: 1.00
Name: B_US_JRCFS	SEQ ID NO: 1612	Len: 106	Check: 4070	Weight: 1.00
Name: B_US_MNCG	SEQ ID NO: 1613	Len: 106	Check: 3291	Weight: 1.00
Name: B_US_P896	SEQ ID NO: 1614	Len: 106	Check: 2280	Weight: 1.00
Name: B_US_RF_M1	SEQ ID NO: 1615	Len: 106	Check: 3104	Weight: 1.00
Name: B_US_SF2_K	SEQ ID NO: 1616	Len: 106	Check: 3857	Weight: 1.00
Name: B_US_WEAU1	SEQ ID NO: 1617	Len: 106	Check: 3817	Weight: 1.00
Name: B_US_WR27	SEQ ID NO: 1618	Len: 106	Check: 3329	Weight: 1.00
Name: B_US_YU2_M	SEQ ID NO: 1619	Len: 106	Check: 5184	Weight: 1.00
Name: BF1_BR_93B	SEQ ID NO: 1620	Len: 106	Check: 3243	Weight: 1.00
Name: C_BR_92B	SEQ ID NO: 1621	Len: 106	Check: 7645	Weight: 1.00
Name: C_BW_96BW0	SEQ ID NO: 1622	Len: 106	Check: 5235	Weight: 1.00
Name: C_BW_96BW1	SEQ ID NO: 1623	Len: 106	Check: 6477	Weight: 1.00
Name: C_BW_96BW1	SEQ ID NO: 1624	Len: 106	Check: 6400	Weight: 1.00
Name: C_BW_96BW1	SEQ ID NO: 1625	Len: 106	Check: 2981	Weight: 1.00
Name: C_ET_ETH22	SEQ ID NO: 1626	Len: 106	Check: 8303	Weight: 1.00
Name: C_IN_93IN1	SEQ ID NO: 1627	Len: 106	Check: 8376	Weight: 1.00
Name: C_IN_93IN9	SEQ ID NO: 1628	Len: 106	Check: 6231	Weight: 1.00
Name: C_IN_93IN9	SEQ ID NO: 1629	Len: 106	Check: 7626	Weight: 1.00
Name: C_IN_94IN1	SEQ ID NO: 1630	Len: 106	Check: 6889	Weight: 1.00
Name: C_IN_95IN2	SEQ ID NO: 1631	Len: 106	Check: 8199	Weight: 1.00
Name: CRF01_AE_C	SEQ ID NO: 1632	Len: 106	Check: 4437	Weight: 1.00
Name: CRF01_AE_C	SEQ ID NO: 1633	Len: 106	Check: 4082	Weight: 1.00
Name: CRF01_AE_C	SEQ ID NO: 1634	Len: 106	Check: 3725	Weight: 1.00
Name: CRF01_AE_T	SEQ ID NO: 1635	Len: 106	Check: 3201	Weight: 1.00

Name:	CRF01_AE_T	SEQ ID NO: 1636	Len: 106	Check: 3137	Weight: 1.00
Name:	CRF01_AE_T	SEQ ID NO: 1637	Len: 106	Check: 3484	Weight: 1.00
Name:	CRF01_AE_T	SEQ ID NO: 1638	Len: 106	Check: 3491	Weight: 1.00
Name:	CRF01_AE_T	SEQ ID NO: 1639	Len: 106	Check: 2300	Weight: 1.00
Name:	CRF01_AE_T	SEQ ID NO: 1640	Len: 106	Check: 2481	Weight: 1.00
Name:	CRF02_AG_F	SEQ ID NO: 1641	Len: 106	Check: 2748	Weight: 1.00
Name:	CRF02_AG_F	SEQ ID NO: 1642	Len: 106	Check: 4618	Weight: 1.00
Name:	CRF02_AG_G	SEQ ID NO: 1643	Len: 106	Check: 400	Weight: 1.00
Name:	CRF02_AG_N	SEQ ID NO: 1644	Len: 106	Check: 5979	Weight: 1.00
Name:	CRF02_AG_S	SEQ ID NO: 1645	Len: 106	Check: 5296	Weight: 1.00
Name:	CRF02_AG_S	SEQ ID NO: 1646	Len: 106	Check: 4213	Weight: 1.00
Name:	CRF03_AB_R	SEQ ID NO: 1647	Len: 106	Check: 952	Weight: 1.00
Name:	CRF03_AB_R	SEQ ID NO: 1648	Len: 106	Check: 431	Weight: 1.00
Name:	CRF04_cpx	SEQ ID NO: 1649	Len: 106	Check: 6986	Weight: 1.00
Name:	CRF04_cpx	SEQ ID NO: 1650	Len: 106	Check: 8606	Weight: 1.00
Name:	CRF04_cpx	SEQ ID NO: 1651	Len: 106	Check: 5826	Weight: 1.00
Name:	CRF05_DF_B	SEQ ID NO: 1652	Len: 106	Check: 5193	Weight: 1.00
Name:	CRF05_DF_B	SEQ ID NO: 1653	Len: 106	Check: 5092	Weight: 1.00
Name:	CRF06_cpx	SEQ ID NO: 1654	Len: 106	Check: 3214	Weight: 1.00
Name:	CRF06_cpx	SEQ ID NO: 1655	Len: 106	Check: 3831	Weight: 1.00
Name:	CRF06_cpx	SEQ ID NO: 1656	Len: 106	Check: 4862	Weight: 1.00
Name:	CRF06_cpx	SEQ ID NO: 1657	Len: 106	Check: 3114	Weight: 1.00
Name:	CRF11_cpx	SEQ ID NO: 1658	Len: 106	Check: 4492	Weight: 1.00
Name:	CRF11_cpx	SEQ ID NO: 1659	Len: 106	Check: 9106	Weight: 1.00
Name:	D_CD_84ZR0	SEQ ID NO: 1660	Len: 106	Check: 5829	Weight: 1.00
Name:	D_CD_ELI_K	SEQ ID NO: 1661	Len: 106	Check: 2669	Weight: 1.00
Name:	D_CD_NDK_M	SEQ ID NO: 1662	Len: 106	Check: 4007	Weight: 1.00
Name:	D_UG_94UG1	SEQ ID NO: 1663	Len: 106	Check: 2098	Weight: 1.00
Name:	F1_BE_VI85	SEQ ID NO: 1664	Len: 106	Check: 4208	Weight: 1.00
Name:	F1_BR_93BR	SEQ ID NO: 1665	Len: 106	Check: 4525	Weight: 1.00
Name:	F1_FI_FIN9	SEQ ID NO: 1666	Len: 106	Check: 5556	Weight: 1.00
Name:	F1_FR_MP41	SEQ ID NO: 1667	Len: 106	Check: 4332	Weight: 1.00
Name:	F2_CM_MP25	SEQ ID NO: 1668	Len: 106	Check: 5691	Weight: 1.00
Name:	F2KU_BE_VI	SEQ ID NO: 1669	Len: 106	Check: 4047	Weight: 1.00
Name:	G_BE_DRCBL	SEQ ID NO: 1670	Len: 106	Check: 3839	Weight: 1.00
Name:	G_NG_92NG0	SEQ ID NO: 1671	Len: 106	Check: 825	Weight: 1.00
Name:	G_SE_SE616	SEQ ID NO: 1672	Len: 106	Check: 4456	Weight: 1.00
Name:	H_BE_VI991	SEQ ID NO: 1673	Len: 106	Check: 2728	Weight: 1.00
Name:	H_BE_VI997	SEQ ID NO: 1674	Len: 106	Check: 3468	Weight: 1.00
Name:	H_CF_90CF0	SEQ ID NO: 1675	Len: 106	Check: 5568	Weight: 1.00
Name:	J_SE_SE702	SEQ ID NO: 1676	Len: 106	Check: 4413	Weight: 1.00
Name:	J_SE_SE788	SEQ ID NO: 1677	Len: 106	Check: 3659	Weight: 1.00
Name:	K_CD_EQTB1	SEQ ID NO: 1678	Len: 106	Check: 4999	Weight: 1.00
Name:	K_CM_MP535	SEQ ID NO: 1679	Len: 106	Check: 4729	Weight: 1.00
Name:	N_CM_YBF30	SEQ ID NO: 1680	Len: 106	Check: 8961	Weight: 1.00
Name:	O_CM_ANT70	SEQ ID NO: 1681	Len: 106	Check: 7210	Weight: 1.00
Name:	O_CM_MVP51	SEQ ID NO: 1682	Len: 106	Check: 8490	Weight: 1.00
Name:	O_SN_99SE	SEQ ID NO: 1683	Len: 106	Check: 726	Weight: 1.00
Name:	O_SN_99SE	SEQ ID NO: 1684	Len: 106	Check: 9615	Weight: 1.00
Name:	U_CD__83C	SEQ ID NO: 1685	Len: 106	Check: 6063	Weight: 1.00

SEQ ID NO	1	50
<u>1520</u>	00BW0762_1	.....MI ELIAAVDYRI GVA.ALIIAL IIAIVVWTIA YIEYRKLKQ
<u>1521</u>	00BW0768_2	.....ML ELTARVDYRL GVG.ALIVAI ILAIVVWIWA YIEYKELLRQ
<u>1522</u>	00BW0874_2	.....ML GLSEKAGYAL GVG.ALIVAL IIVIVVWTIV YIEYRKLVRQ
<u>1523</u>	00BW1471_2	.....MI NLLERVDX.. GVG.ALGIAL IIVIVVWTIV YIEYRKLVRQ
<u>1524</u>	00BW1616_2	..... ..MLDLDYKV AVG.AFTVAL ILAIVVWILV YREYRKLRLQ
<u>1525</u>	00BW1686_8	...MEDVILS FIA.KIDYRI GIA.AIIVAL ILAIVVWTIV YLEYRKLVRQ

1526	00BW1759_3	.....MID	LSA.RVDYRI	GVA.AFIIAL	IIAIVVWTIV	YIEYRKLRLQ
1527	00BW1773_2	MLKLATIVDY	ILAAKVDYRV	GIG.ALIAAL	IITIVVWIIV	YREYRKLRLQ
1528	00BW1783_5	...IVDVIFS	LTD.RVDYRI	AVA.ALTIAL	IIAIVVWTIV	YIEYRKLVRQ
1529	00BW1795_6	.....MVD	WTKXKVDYRI	AVV.AFIVAL	IIAIVVWTIV	YIEYRKLRLQ
1530	00BW1811_3	.....	..MLAIDYSL	GVG.ALLVAL	FIAIID....	....RKLVRQ
1531	00BW1859_5	.....ML	ELTARVDYRL	GVG.ALIVAL	IIAIVVWTIA	SLEYRKLRLQ
1532	00BW1880_2	.....MLS	LMT.RVDYRI	AVA.AFVIAL	ILAIIVWTIA	YLEYRKLVRQ
1533	00BW1921_1	.....MLD	LAA.IVDYRI	TIV.AFAIAL	FIAIVVWTIA	YLEYRKLVRQ
1534	00BW2036_1	.....ML	DLIAKVDYRV	GIG.ALIVAL	IIAVVWIIIA	YIEYRKLRLQ
1535	00BW2063_6	.....MID	WTE.QVDYRI	AIVXSFIVAL	IIAIVVWTIA	YIEYRKLRLQ
1536	00BW2087_2	.....ML	SLIERIDYRL	GVG.ALIVAL	IIVVWTIV	YIEYRKLVRQ
1537	00BW2127_2	.....ML	DLAARVDYRL	GVG.ALVVAL	IIAIVVWTIV	YIEYRKLVRQ
1538	00BW2276_7	.....M	VDLGRVDYRL	GVG.ALIVAL	IIAIVVWIIV	YIEYRKLVRQ
1539	00BW3819_3	.....ML	DLLTRVDYRL	GVG.ALIVAL	IIAIVVWTIA	YIEYRKLRLQ
1540	00BW3842_8	.....MF	DLLAGVDYRL	GVG.ALIIAL	IIAIVVWVIA	YIEYKWLRLQ
1541	00BW3871_3	.....MVD	LLE.KVDYRI	GIA.AFTVAL	LIAIVVWIIA	YIEYRKLVRQ
1542	00BW3876_9	.....M	LDLTQIGYEL	GIG.ALIVAL	IIAIVVWTIV	YIEYRKLVRQ
1543	00BW3886_8	.....	.MLAAVDYRL	GVG.ALTVAL	ILVIVVWTIV	YIEYRKLVRQ
1544	00BW3891_6	.....ML	DLLAGVDYRI	GVG.AFLVAL	SIAIVVWTIV	YIEYRKLRLQ
1545	00BW3970_2	.....MF	SLLERIDYRL	GVG.ALLVAL	IIAIVVWVIA	YIEYRKLVRQ
1546	00BW5031_1	.....M	FALFEVDYRL	TIG.AFIVAL	FLAIVVWTIA	YLEYRKLVRQ
1547	96BW01B21	.....ML	ELIAKIDYRL	GGG.ALIVAL	SIAIVVWIIA	YIEYKWLRLQ
1548	96BW0407	.....ML	SLAA.IDYRI	GVG.AFVVAL	IIAIVVWIIV	YIEYRKLVRQ
1549	96BW0502	.....MI	NFLAKVDYRL	GVG.ALIVAF	IIAIVVWIIA	YIEYRKLRLQ
1550	96BW06_J4	.....MID	LLA.RVDYRI	GLA.AFVVAL	LIAIVVWTIV	YLEYRKLVRQ
1551	96BW11_06	.....MVD	LLA.KVDYKI	AVA.AFIIAL	IIAIVVWIIV	YVEYRKLVRQ
1552	96BW1210	.....ML	YLLEKVDYRL	GVG.ALIIAL	IIAIVVWTIA	YLEYRKLVRQ
1553	96BW15B03	.....MVN	FLAAKVDYRL	GVG.ALIVAL	IIAIVVWSIV	YIEYKWLRLQ
1554	96BW16_26	.....MF	SLLAKVDYRV	GVG.ALIVAL	IIAIVVWIIV	YIEYRKLRLQ
1555	96BW17A09	.....ML	NLLAKVDYRL	GVG.ALVIAL	IIAIVVWIIA	YIEYRKLVRQ
1556	96BWM01_5	.....MID	WTA.RVDYRV	AVV.AFIVAL	ILAIIVWIIA	YLEYRKLRLQ
1557	96BWM03_2	.....ML	SLAALVDYRL	GVG.ALIVAL	IIAIVVWTIV	YLEYRKLVRQ
1558	98BWMC12_2	.....MV	VLGEKEIYIL	GIG.ALIVAL	IIAIVVWSIA	YIEYRKLVRQ
1559	98BWMC13_4	.....MSN	WTA.RVDYRI	AIA.AFIVAL	IIAIVVWTIV	YIEYRKLRLQ
1560	98BWMC14_a	.....MLD	LTE.GVDYRI	GIA.AFAVAL	FIAIVVWIIV	YLEYRKLVRQ
1561	98BWM014_1	.....ML	ELLEKVDYKI	TVA.AFIVAL	IIAIVVWTIA	YIEYRKLRLQ
1562	98BWM018_d	.....ML	DLIARVDYRL	GVG.ALIVAL	IIAIVVWTIV	YIEYRKLVRQ
1563	98BWM036_a	.....ML	AFLARVDYRL	GVG.AFIIAL	IIAIVVWTIA	YLEYRKLVRQ
1564	98BWM037_d	.....ML	NLVARVDYRL	GVG.ALIVAL	IIAIVVWTLV	YIEYRKLVRQ
1565	99BW3932_1	.....	.MLENIDYRL	GVG.ALIVAL	IIVVWTIV	YIEYRKLVRQ
1566	99BW4642_4	.....ML	DLTARVDYRL	GVG.ALIVAL	IIAIVVWTIV	YLEYRKLVRQ
1567	99BW4745_8	.....MI	NLIARVDYRL	GVG.ALIIAL	IIAIVVWTIA	YIEYRKLRLQ
1568	99BW4754_7	.....	.ML.ELDYRI	GIA.AFIIAL	IIAIVVWTIV	YIEYRKLRLQ
1569	99BWMC16_8	.....MF	NLAARVDYRL	GVG.ALVIAG	IIAIVVWTIV	YIEYRKLRLQ
1570	A2_CD_97CD	.....	.MSPLAILS	IVG..LVVAS	ILAIVVWTVV	FIEYRKLRLQ
1571	A2_CY_94CY	.....	.MLPLVILA	IVG..LIVAL	ILAIVVWTIV	FIEYRKLRLQ
1572	A2D___97KR	.....	.MNSLQILS	IVG..LIVAF	ILAVVWTVV	FIEYRKLRLQ

1573	A2G_CD_97C	.....	..MQALEISA	IVG..LIVAF	IAATVVWTIV	YIEYRKIRKQ
1574	A_BY_97BL0	.....	..MTPLXIYA	IVA..LVVVF	VIXXVVWTIV	GIXYXXLLKQ
1575	A_KE_Q23_A	.....	..MSPLEISA	IVG..LIVAL	ILAIIVWTIV	GIEYKKIRKQ
1576	A_SE_SE659	.....	..MQSLVILA	IVA..LVVVL	IIAIVVWTIV	FIEWGRLRRQ
1577	A_SE_SE725	.....	..MLPLSTIWA	IIG..LIVAL	ILAIIVWTIV	GIEYKKLLKQ
1578	A_SE_SE753	.....	..MIPLQIWA	IAG..LIVAL	ILAIIAWTIV	GIEYEKLLKQ
1579	A_SE_SE853	.....MSA	LEISALEIWS	IVG..LVVAL	IIAIVVWTIV	GIECKRLQKQ
1580	A_SE_SE889	.....	..MTPLEIWA	IVG..LVVVS	IIAIVVWTIV	GIEYKKLLKQ
1581	A_SE_UGSE8	.....	..MSPLEIWA	IVG..LIVAL	IIAIVVWTIV	GLEYKKLLKQ
1582	A_UG_92UG0	.....	..MQLLEICA	VVG..LVVAL	IIAIVVWTIV	GIEYKKLLKQ
1583	A_UG_U455_	.....	..MTPLEIWA	ITG..LIVAL	IIAIVVWTIV	GIE.KKLLKQ
1584	AC_IN_2130	.....	..MLNLNYEL	AVG.ALIVAL	IIAIVVWTIV	YVEYRKLLRQ
1585	AC_RW_92RW	.....	..MTSLEIYA	IVA..LIVAL	IIIVVVWTLA	GIEYKKLLKQ
1586	AC_SE_SE94	.....ML	DLLAEIDYRI	GVG.AFIIAL	IIAVVVWIIA	YIEYRKLVKQ
1587	ACD_SE_SE8	.....	..MQPLEICS	IVG..LIVAI	IIAIVVWTIV	GIEIKKLLRQ
1588	ACG_BE_VI1	.....ML	ELLAQVDYRI	GVG.ALILAL	FIAIVVWIIA	YLEYRKLVVRQ
1589	AD_SE_SE69	.....	..MQSLVILS	IVA..LVVAL	VIAIVVWTIV	FIEYRRLERQ
1590	AD_SE_SE71	.....	..MLSLLHICA	IVG..LLVAL	IIAIVVWTIV	GIEYKRLLRQ
1591	ADHK_NO_97	.....	....MYILGI	GIG.ALIVAF	IIIVVVWTIV	YLEYRKLVKQ
1592	ADK_CD_MAL	.....	..IQPLVILA	IVA..LVVTL	IIAIVVWTIV	FIEIRKIRRRQ
1593	AG_BE_VI11	.....	..MQSLEIAA	VVG..LIVAF	IIAIVVWTIV	FIEYRKIRKQ
1594	AG_NG_92NG	.....	..MQSLEIAA	IAG..LVVAA	IIAIVVWTI.	.....KIKKQ
1595	AGHU_GA_VI	.....	....MYILGI	GIG.ALVVAF	IIAIVVWTIA	YIEYRKLLRQ
1596	AGU_CD_Z32	.....	..MQFLEIAS	IVG..LIVAV	LAAIVVW...	..IEYRKIRKE
1597	AJ_BW_BW21	.....	..MRPLQIAA	IVG..VIVAI	FLAIVVWTIV	YIEYKRLVRQ
1598	B_AU_VH_AF	.....	..MQSLQIVA	IVA..LVVVT	IIAIVVWTIV	FIEYRRILRQ
1599	B_CN_RL42_	.....	..MQALTILA	IVA..LVVVA	IIAIVVWTIV	LLEYRKILRQ
1600	B_DE_D31_U	.....	..MQSLQVAA	IVA..LVVVA	IIAIVVWTIV	FIEYRKILRQ
1601	B_DE_HAN_U	.....	..MLSLQIAA	IVA..LVVAA	IIIVVVWTIV	VIEYRKLLRQ
1602	B_FR_HXB2_	.....	..TQPIPIVA	IVA..LVVAI	IIAIVVWSIV	IIIEYRKILRQ
1603	B_GA_OYI_M	.....	..IYSLQILA	IVA..LVVVT	IIAIVVWTIV	LLEYRKILRQ
1604	B_GB_CAM1_	.....	....MLPLQIA	IVA..LVVVA	IIAIVVWTIV	FIEYRKIRRRQ
1605	B_GB_GB8_A	.....	.....IQILT	IVA..LVVAG	IVAIVVWIIIV	FIEYRKILKK
1606	B_GB_MANC_	.....	..IVSLQIVA	IVA..LVVVT	IIAIVVWTIV	FIEYRKILRQ
1607	B_KR_WK_AF	.....	..MQLLAILA	IVG..LVVAA	IIAIVVWFIV	FIEYKKILKQ
1608	B_NL_3202A	.....	..MQPLVVAA	IVA..LVVVA	IIAIVVWSIV	FIEYRKILRQ
1609	B_TW_TWCYS	.....	..MQPLHILA	IVA..LVVAA	IIAIVVWTIV	LLEYRKILRQ
1610	B_US_BC_L0	.....	..MQPIQIAA	IVA..LVVVG	IIAIVVW...	.....KILRQ
1611	B_US_DH123	.....	..MQPLVILA	IVA..LVVAL	IIIVVVWSIV	LIEYRKILRQ
1612	B_US_JRCFS	.....	..MQPLQILA	IVA..LVVAG	IIAIVVWSIV	LIEYRKILRQ
1613	B_US_MNCG_	.....	..MQPLVIAA	IVA..LVVAG	IIAIVVS.IV	FIEYRKIRRRQ
1614	B_US_P896_	.....	..MLSLQILA	IVA..LVVAA	IIAIVVWSIV	FIEYRKILRQ
1615	B_US_RF_M1	.....	..MQSLEILA	IVA..LVVAA	IIAIVVWTIV	GIEIRKTLRQ
1616	B_US_SF2_K	.....	..MQSLQILA	IVS..LVVVA	IIAIVVWTIV	LIEYRKILRQ
1617	B_US_WEAU1	.....	..MQSLQILA	IVA..LVVAG	IIAIVVWSIV	LIEYRKILRQ
1618	B_US_WR27_	.....	....MPLYILA	VVA..LVLA	IIAIVVWTIV	FIEYRKILRQ
1619	B_US_YU2_M	.....	..LQSLQVLA	IVA..LVVAT	IIAIVVWTIV	FIEYRKILRQ

1620	BF1_BR_93B	.....	....MSYLLV	IGLAALIAAL	IIAIVVWTIA	YIEYRELVRQ
1621	C_BR_92BR0	.....	ML	ELIGRIDYRL	GVG.ALIVAL	IIVIIVWTIA
1622	C_BW_96BW0	.....	MI	SLAARVDYRI	GVG.AFIVAL	IIAIIVWTIV
1623	C_BW_96BW1	.....	MVD	LLA.KVDYKI	AVA.AFIIAL	IIAIVVWIIV
1624	C_BW_96BW1	.....	ML	YLLEKVDYRL	GVG.ALIIAL	IIAIIVWTIA
1625	C_BW_96BW1	.....	MVN	FLAAKVDYRL	GVG.ALIVAL	IIAIVVWSIV
1626	C_ET_ETH22	.....	MV	DLAKVDYRI	VIV.AFIVAL	IIAIVVWTIA
1627	C_IN_93IN1	.....	...	MIDLYRL	GVG.ALIVAL	IIAIVVWTIV
1628	C_IN_93IN9	.....	...	MLDLDYKL	AVG.ALIVAL	IIAIVVWIIA
1629	C_IN_93IN9	.....	...	IIDL DYRL	GVG.ALIVAF	IIAIVVWTIV
1630	C_IN_94IN1	.....	...	MLDLKL	AVG.ALIVAL	IIAIVVWTIV
1631	C_IN_95IN2	.....	...	MVNLDYKL	GVG.ALIVAL	IIAIVVWTIV
1632	CRF01_AE_C	.....	...	MSALQIA	IVG..LIVAL	IIAIVVWTIV
1633	CRF01_AE_C	.....	...	RLPLHICA	IVG..LIVAL	IIAIVVWTIV
1634	CRF01_AE_C	.....	...	MLPLQISA	IVR..LIVAL	IIAIVVWTLV
1635	CRF01_AE_T	.....	...	MSPLEISA	IVG..LIVAI	IIAIVVWTIV
1636	CRF01_AE_T	.....	...	MSPLEISA	IVG..LIVAL	IIAIVVWTIV
1637	CRF01_AE_T	.....	...	MHLWKLA	IVG..LLVAL	IIAIVVWTIV
1638	CRF01_AE_T	.....	...	MTPLEISA	VVG..LIVVL	IIAIVVWTIV
1639	CRF01_AE_T	.....	...	MTPLEISA	IVG..LIVAL	IIAIVVT.IV
1640	CRF01_AE_T	.....	...	MTPLEISA	IVG..LIVAL	IIAIVVT.IV
1641	CRF02_AG_F	.....	...	MQSLEITA	IVG..LVVAF	IIAIVVWAI
1642	CRF02_AG_F	.....	...	MKSLEIAA	IVG..LVVAI	IIAIVVWAI
1643	CRF02_AG_G	.....	...	MQSLEIAA	IVG..LVVAF	IIAIVVWAI
1644	CRF02_AG_N	.....	...	MQPLTITA	IVG..LVVAF	IIAIVVWSIV
1645	CRF02_AG_S	.....	...	MNSLDIVA	IVG..LVVAF	IIAIVVWTIV
1646	CRF02_AG_S	.....	...	MQPLAVAA	IVG..LVVAF	IIAIVVWTIV
1647	CRF03_AB_R	.....	...	MQSLAIAA	IVA..LVVVG	IIAIVVGSIV
1648	CRF03_AB_R	.....	...	MQFLVIAA	IVA..LVVGG	IIAIVVWSIV
1649	CRF04_cpx_	.....	...	MLFWEIWA	IVG..LVVAL	IIAIVVWTLV
1650	CRF04_cpx_	.....	M	SSLSSLEIWT	IVA..LIVAL	IIAIVVWTIV
1651	CRF04_cpx_	.....	M	SSMSSLQVWA	ITA..LIVAL	IIAIIVWTIA
1652	CRF05_DF_B	.....	....	MSDLLT	IAVVALIVAL	IIAIVVWIIV
1653	CRF05_DF_B	.....	....	MSDLLA	VAIAAFIVAL	IIAIVVWTIV
1654	CRF06_cpx_	.....	...	MQALEIAA	IVG..LVVAF	IIAIVVWTIV
1655	CRF06_cpx_	.....	...	MQSLEISA	IVG..LVVAF	IIAIVVWTIV
1656	CRF06_cpx_	.....	...	MQPLEISA	VVG..LIVAF	IIAIVVWTIV
1657	CRF06_cpx_	.....	...	MQPLEISA	IVG..LIVAF	IIAIVVWTIV
1658	CRF11_cpx_	.....	...	MIPLQIAG	IVA..LIVAA	IIAIVVWTIV
1659	CRF11_cpx_	.....	...	MITLRTVK	HSS..ISQHL	IIAIIVWTIA
1660	D_CD_84ZR0	.....	...	MQSLQILA	IVA..LVLAL	IIAIVVWTIV
1661	D_CD_ELI_K	.....	...	MQPLGIIA	IAA..LVVAI	IIAIVVWTIV
1662	D_CD_NDK_M	.....	...	MQPLVIAA	IAA..LVVAI	IIAIVVWTIV
1663	D_UG_94UG1	.....	...	MQPLEILA	IVA..LVVAL	IIAIVVWTIV
1664	F1_BE_VI85	.....	....	MSYLLA	IGIAALIVAL	IIAIVVWTIV
1665	F1_BR_93BR	.....	....	MSNLLA	IGIAALIVAL	IIAIVVWTIV
1666	F1_FI_FIN9	.....	....	MSDLLA	ITIVAFIVAL	IIAIVVWTIV

1667	F1_FR_MP41	.....	....MSNLYV	LSIVAFIIAL	IIAIVVWTIV	FIEYKKLLRQ
1668	F2_CM_MP25	.....	....MSLSLI	VVIAAYIVVL	ILAIIVWTIV	YIEYKKILRQ
1669	F2KU_BE_VI	.....	....MNL.LL	VGIGALIVAF	LLAIVVWTIA	YLEYRKVLKQ
1670	G_BE_DRCBL	.....	..MQPLEISA	IVG..LIVAS	IAAIVVWTIV	FIEYRKIRKQ
1671	G_NG_92NG0	.....	..MQALEIS.	.....LIVAF	IAATIVWSIV	FIEYRKIRKQ
1672	G_SE_SE616	.....	..MQSLVILA	IVG..LIVAF	IAAIVVWTIV	FIEYREIRKQ
1673	H_BE_VI991	.....	....MNILGI	GIG.ALVVAF	IIAIVVWTIA	YIEYRKLK.Q
1674	H_BE_VI997	.....	....MYIIGI	GIG.ALIVAF	IIAIVVWTIV	YIEYRKLVKQ
1675	H_CF_90CF0	.....	....MYILGL	GIG.ALVVTF	IIAIVVWTIV	YIEYKKLVQR
1676	J_SE_SE702	.....	..MVSLQIVA	IVA..LIVAF	FLAICVWTIV	YIEYKKLLRQ
1677	J_SE_SE788	.....	..MIPLQIAA	IVA..FIVAI	FLAIGMWTIV	YIEYKKLLRQ
1678	K_CD_EQTB1	.....	.....MVPLT	VGIIALVAAL	ILAIIVWTIA	YLEYRKVVVRQ
1679	K_CM_MP535	.....	.....MVSLA	ISIVALVVAL	ILAIIVWTIV	YIEYRKLVKQ
1680	N_CM_YBF30	.....	.....MLS	LGFIALGAAV	SIATIVWALL	YREYKKIKLQ
1681	O_CM_ANT70	.....	..MHHRDLLA	III..ISALL	FINVILWGFI	LRKYLEQKEQ
1682	O_CM_MVP51	.....	..MHQENLLA	LIA..LSALC	LINVLWLWLN	LRIYLVQRKQ
1683	O_SN_99SE	.....	..MHHRDLLA	LIT..TSALL	LTNVVLWTFI	LRQYLKQKKQ
1684	O_SN_99SE	.....	..MHHRDLLT	LII..ISALL	LTNVILWAFI	LRQYLRQKKQ
1685	U_CD_83C	.....	..MSILQIVA	IVA..IIVAL	ILAIIVVWTIV	YIEYKRLLRQ

	51					100
00BW0762_1	KKIDR....L	IKRIIERAED	SGNESDGD.H	EEL....STM	VDMGHLRLLD	
00BW0768_2	RKIDW....L	IKRIRERAED	SGNESEGD.T	EEL....STM	VDMGQLRLLD	
00BW0874_2	RKID....L	IKRIRERAED	SGNESDGD.T	EEL....STM	VDMGNLRLLD	
00BW1471_2	KKIDQ....L	VKRIREREED	SGNESDGD.I	EEL....STM	VDMGHLRLLD	
00BW1616_2	KRIDN....L	IKRIRERAED	SGNESDGD.T	EEL....STL	VDMGNLRLLD	
00BW1686_8	RKIDR....L	IERIKEREED	SGNESEGD.T	EEL....ATM	VDMGQLRLLD	
00BW1759_3	RKINW....L	IERIRERAED	SGNESEGD.T	EEL....ATM	VDMGHLRLLH	
00BW1773_2	KKIDR....V	LEKIRERAED	SGNESEGD.L	EEL....STL	VDVEHLRLVD	
00BW1783_5	RKIDR....L	IERIRERAED	SGNESDGD.Q	EEL....STM	VDMGHLRLLD	
00BW1795_6	RKINW....L	IERIRERAED	SGNESDGD.Q	EEL....ATM	VDMGHLRLLD	
00BW1811_3	AKIDK....I	IKRIRERAED	SGNESEGD.I	EEL....STM	VDMGHLRLMD	
00BW1859_5	RKIDW....L	IKRIRERAED	SGNESEGD.T	EEL....ATM	VDMGHLRLLD	
00BW1880_2	KKIDW....L	IERIRERAED	SGNESDGD.H	EEL....STM	VDMGHLRLLD	
00BW1921_1	RKIDR....L	IKRIRERAED	SGNESEGD.T	EEL....ATM	VDMGQLRLLG	
00BW2036_1	RKIDW....L	IKRIRERAED	SGNESEGD.I	EEL....ATM	VDMGHLRLLD	
00BW2063_6	RKIDW....L	IKRIRERAED	SGNESDGD.H	EEL....ATM	VDLGHLRLLD	
00BW2087_2	RKLDW....L	VKRIRERAED	SGNESDGD.V	EEL....STM	VDMGHLRLLD	
00BW2127_2	RKIDW....L	IKRIGERAED	SGNESEGD.T	EEL....ATM	VDMGHLRLLD	
00BW2276_7	RKIDW....L	VKRIRERAED	SGNESEGD.T	EEL....ATM	VDMGHIRLLD	
00BW3819_3	RKIDW....L	IKRIREREED	SGNESEGD.T	EEL....AAM	VDMGHLELLG	
00BW3842_8	KKIDW....L	IERIRERAED	NGNESEGD.T	EEL....ATM	VDMGHLRLLD	
00BW3871_3	RKIDW....L	IKRIRERAED	SGNESEGD.T	EEL....ATM	VDMGQLRLLD	
00BW3876_9	RKIDR....L	IKRIRERAED	SGNESEGD.I	EEL....EAI	VDMGHLRLLG	
00BW3886_8	RKIDW....L	IKRIRERAED	SGNESEGD.I	EDL....AMV	VDMGQLRLLD	
00BW3891_6	KRIDR....L	IERIRERAED	SGNESEGD.I	EEL....STM	VDMGHLRLLD	
00BW3970_2	RRLDW....L	VKRIRERAED	SGNESEGD.N	EEL....STV	VDLGHLRLLD	
00BW5031_1	RRIDQ....L	VKRIRERAED	SGNESDGD.T	EEL....STM	VDMGHLRLLD	
96BW01B21	RRINW....L	IERIRERAED	SGNESEGD.T	EEL....STM	VDMGHLRLLD	
96BW0407	RKIDW....L	VKRIRERAED	SGNESDGD.T	EEL....STM	VDMGHLRLLD	
96BW0502	RKIDR....L	IRKIRERAED	SGNESDGD.I	EEL....SAM	VDVGHLRLLD	
96BW06_J4	RKIDW....L	IKRIRERAED	SGNESEGD.T	EEL....ATM	VDMGQLRLLD	
96BW11_06	RKIDW....L	IERIRERAED	SGNESDGD.H	EEL....STM	VDMGHLRLLD	
96BW1210	RRIDR....L	VERIREREED	SGNESEGD.I	EEL....STM	VDMGHLRLLD	
96BW15B03	KNIDW....L	IKRIRERAED	SGNESEGD.T	EEL....ATM	VDMGHLRLLD	



96BW16_26	KKIDR....L	IERIRERAED	SGNDSEGD.I	EDL....STM	VDM DHLRLLLD
96BW17A09	RKLDE....L	VKRIRERAED	SGNESDGD.I	EEL....STM	VDMGHLRLLLD
96BWM01_5	RKIDC....L	IKRIRERAED	SGNESDGD.Q	EEL....ATM	VDMGRRLRLLLD
96BWM03_2	RKINW....L	VKRIRERAED	SGNESEGD.T	EEL....ATM	VDLEHFGLLLD
98BWM12_2	RRIDQ....L	IKRIGERAED	SGNESDGD.T	EEL....STL	VDMGHLRLLLD
98BWM13_4	RKIDR....L	IKRIRERAED	SGNESDGD.Q	DEL....ATM	VDMGHLRLLLD
98BWM14_a	RKIDW....L	IERIRERAED	SGNESEGD.T	EEL....ATM	VDMGQLRLLLD
98BWM14_1	RKIDC....L	IKRIRERAED	SGNESDGD.T	EEL....STM	VDMGNLRLLLD
98BWM18_d	RKIDW....L	IKRIRERVED	SGNESDGD.T	EEL....STL	VDMGNLRLLLD
98BWM036_a	KKIDR....L	IERIRERAED	SGNESEGD.T	EEL....STM	VDMGHLRLLLD
98BWM037_d	RKIDQ....L	VKRIRERAED	SGNESEGD.I	EEL....STM	VDMGNLRLLLD
99BW3932_1	RKIDW....L	IKRIRERAED	SGNESEGD.T	EEL....ATM	VDM EHLRLLL
99BW4642_4	RRIDW....L	IKRIRERAED	SGNESEGD.T	EEL....ATM	VDMGHLRLLLD
99BW4745_8	RKIDW....L	IKRIRERAED	SGNESEGD.T	EGL....STM	VDM EHLRLLLD
99BW4754_7	RKIDR....L	IERIRERAED	SGNESDGD.Q	EEL....SAM	VDMGHLRLLLD
99BWM16_8	RKINE....I	IKRIRERAED	SGNESDGD.M	EEL....STM	VDLGHLGLLLD
A2_CD_97CD	RKIDW....L	LERISERAED	SGNESDGD.T	EEL....SKM	VGMGNLGFWD
A2_CY_94CY	RKIDW....L	IKRISERAED	SGNESDGD.T	EEL....SAL	VERGHLDFGD
A2D___97KR	NKIDW....L	IKRISERAED	SGNESEGD.T	EEL....STL	MEMGNLDFGD
A2G_CD_97C	KRIER....L	LDRIGERAED	SGNESEGD.A	EEL....AKL	VEMGGFDPWV
A_BY_97BL0	RKIDR....L	XERXXXRAED	SGNESEGD.A	XEL....STL	MEVXNYALLD
A_KE_Q23_A	RKIDR....L	IERIRERAED	SGNESDGD.T	EEL....STL	IDMGDYDLGD
A_SE_SE659	R_KDR....L	IERIRERAED	SGNESDGD.T	EEL....SAL	IEMGNYNLGF
A_SE_SE725	RKIDK....L	VERIRERAED	SGNESDGD.T	NEL....AAL	IEMGNYNLGD
A_SE_SE753	KEIDG....L	VERIAERAED	SGNESDGD.T	EEL....STL	IEMGNYDLGV
A_SE_SE853	RKIDR....L	IERIRERAED	SGNESEGD.T	EEL....SAL	IEMGNYDLGN
A_SE_SE889	RKIDR....L	IRRISERAED	SGNESDGD.T	DEL....AKL	VEMGNYDLGD
A_SE_UGSE8	RKIDR....L	IERIRERAED	SGNESDGD.T	EEL....STL	IELGDYDLGD
A_UG_92UG0	RKIDR....L	VDRIRERAED	SGNESDGD.R	EEL....SLL	VDMGDYDLGD
A_UG_U455_	KKIDR....L	LNRIRERAED	SGNESDGD.T	EEL....SLL	VEMGNYDLGV
AC_IN_2130	RKIDR....L	IKRIRERAED	SGNESEGD.T	EEL....STM	VDMGQLRLLLD
AC_RW_92RW	RKIDR....L	IKKIRERAED	SGNESDGD.I	DEL....SKL	VGVGNYDLGD
AC_SE_SE94	RKIDW....L	IKRIRERAED	SGNESDGD.T	EEL....STM	VDMGHLRLLLD
ACD_SE_SE8	KKIDR....L	IERIRERAED	SGNESDGD.T	EEL....AAL	VEMGNYDPGD
ACG_BE_VI1	RKIDW....L	VKRIRERAED	SGNESEGD.T	EEL....STM	VDMGELRLMD
AD_SE_SE69	KRIDW....L	IDRIRERAED	SGNESEGDRD	ELS....EL	VEMGHPAPWD
AD_SE_SE71	RKIDR....I	LDRIRVRAED	SGNESDGD.T	EEL....SKL	IDMGNYDLGD
ADHK_NO_97	KRIDQ....L	IERIRERAED	SGNESDGD.T	EEL....SEL	VEMGRNLNGY
ADK_CD_MAL	RKIDR....L	IDRIRERAED	SGNESEGDTE	ELS....KL	VEMGHDAPWD
AG_BE_VI11	KKIEK....L	PDRIRERAED	SGNESEGD.T	DEL....ATL	VERGNFDPWV
AG_NG_92NG	EKIDR....L	LDRIRERAED	SGNESEGD.T	EEL....ATL	VDMVDFDPWV
AGHU_GA_VI	RKIDW....L	IRRISERAED	SGNESDGD.T	EEL....STL	VEMGNHNPGY
AGU_CD_Z32	KKIEY....L	IDRIRKRAED	SGNESEGD.T	EEL....STL	MEMGDFHPWV
AJ_BW_BW21	KKIDR....I	IDRIGERAED	SGNESDGD.T	DEL....HKL	VEMGPHDLWN
B_AU_VH_AF	RKIDR....L	IDRIAERAED	SGNESEGD.Q	EEL....AAL	VEMGHHAPWD
B_CN_RL42_	RKIDR....L	IDRIRERAED	SGNESDGD.Q	EEL....SAF	MEMGHHAPWD
B_DE_D31_U	RKIDR....L	IDRIIERAED	SGNESEGD.Q	EEL....SAL	VEMGHHAPWD
B_DE_HAN_U	RKINR....L	IDRLTERAED	SGNESEGD.Q	EEL....SAL	VERGHLAPWD
B_FR_HXB2_	RKIDR....L	IDRLIERAED	SGNESEGEIS	ALV....EMG	VEMGHHAPWD
B_GA_OYI_M	RKIDR....L	IDRIRERAED	SGNDSEGD.Q	EEL....SAL	VEMGHHAPWD
B_GB_CAM1_	KQVDR....L	IDRIIERAED	SGNESEGD.Q	EEL....SAL	MEMGHNAPWD
B_GB_GB8_A	KKIDR....L	IDRIIERAED	SDNESEGD.Q	EEL....SAL	VEMGHHAPWD
B_GB_MANC_	RKIDR....L	IDRIRERAED	SGNESEGD.Q	EEL....SEL	VEMGHLVPWD
B_KR_WK_AF	KKIDR....L	IDRIRERAED	SGNESEGD.Q	EEL....SAL	VEMGHHAPWD
B_NL_3202A	RKIDR....L	IDRIAERAED	SGNESEGD.Q	EEL....SAL	VEMGHHAPWD
B_TW_TWCYS	RKIDR....L	IDRIRERAED	SGNESEGD.Q	DEL....SAL	VEMGYHAPWD
B_US_BC_L0	RKIDR....L	IKRISKRAED	SGNESEGD.Q	EEL....SAL	VEMGHHALWD
B_US_DH123	KKIDR....L	IDRIRERAED	SGNESDGD.Q	EEL....SAL	VERGHLAPWD
B_US_JRCSE	RKIDR....L	IDKIRERAED	SGNESEGD.Q	EEL....SAL	VERGHLAPWD
B_US_MNCG_	RKIDR....L	IDRISERAED	SGNESEGD.Q	EEL....SAL	VGMGHDAPWV

B_US_P896_	RKIDR....L	IDRIREREED	SGNESEGD.Q	EEL....AAL	ERG.HLAPWD
B_US_RF_M1	KKIDR....L	IDRIRERAED	SGNESDGD.E	EEL....SAL	VEMGHHAPWD
B_US_SF2_K	R.IDR....L	IDRIREKAED	SGNESEGD.Q	EEL....SAL	VEMGHLAPWD
B_US_WEAU1	RKIDR....L	IDRIDRAED	SGNESEGD.Q	EEL....SAL	VEMGHHAPWD
B_US_WR27_	RKIDR....L	IDRIRERAED	SGNESEGD.Q	EEL....SAL	MEMGHHAPWD
B_US_YU2_M	RKIDR....L	INRITERAED	SGNESDGD.Q	EEL....SAL	VERGHLAPWD
BF1_BR_93B	RKINR....L	YKRIRERAED	SGNESEGD.A	EEL....AAL	GEMGPFIPGD
C_BR_92BR0	RRIDW....L	VKRIRERAED	SGNESGGD.T	EEL....ETM	VDMGHLRLLD
C_BW_96BW0	RKIDW....L	VKRIRERAED	SGNESDGD.T	EEL....STM	VDMGHLRLLD
C_BW_96BW1	RKIDW....L	IERIRERAED	SGNESDGD.H	EEL....STM	VDMGHLRLLD
C_BW_96BW1	RRIDR....L	VERIREREED	SGNESEGD.I	EEL....STM	VDMGHLRLLD
C_BW_96BW1	KNIDW....L	IKRIRERAED	SGNESEGD.T	EEL....ATM	VDMGHLRLLD
C_ET_ETH22	RRIDR....L	IKRTRERAED	SGNESDGD.T	EEL....STM	VDMGNLRLLD
C_IN_93IN1	SKINW....L	IKRIRERAED	SGNESEGD.T	EEL....STM	VDMGRLRLLD
C_IN_93IN9	RKIDW....L	IKRIRERAED	SGNESEGD.T	EEL....STM	VDMGRLRLLD
C_IN_93IN9	RRIDW....L	IKRIRERAED	SGNESEGD.T	EEL....STM	VDMGHLRLLD
C_IN_94IN1	RKIDW....L	IKRIRERAED	SGNESEGD.T	EEL....STM	VDMGRLRLLD
C_IN_95IN2	RKIDW....L	IKRIRERAED	SGNESEGD.T	EEL....STM	VDMGRLRLLD
CRF01_AE_C	RKIDR....L	IERIRERAED	SGNGSEGD.T	NEL....ATL	VEVGDFDPWV
CRF01_AE_C	RKIDR....L	VQRISERAED	SGNESEGD.T	EEL....AKL	VEMGDFDPWV
CRF01_AE_C	RKIDR....L	IERIRERAED	SGNESEGD.T	DEL....AKL	VEMGDFDPWV
CRF01_AE_T	RKIDR....L	VKRIRERAED	SGNESEGD.T	DEL....AKL	VEMGDFDPWV
CRF01_AE_T	RKIDR....L	VKRIRERAED	SGNESEGD.T	DEL....AKL	VEMGDFDPWV
CRF01_AE_T	RKIDR....L	VKRIREREED	SGNESEGD.T	DKL....AKL	VEMGDFDPWV
CRF01_AE_T	RKIDR....L	VKRIRERAED	SGNESEGD.T	DEL....AQL	VEMEDFDPWV
CRF01_AE_T	RKIDR....L	VKRIRERAED	SGNESEGD.T	DEL....AKL	VEMGDFDPWV
CRF01_AE_T	RKIDR....L	IKRIGERAED	SGNESEGD.T	DEL....AKL	VEMGDFDPWV
CRF02_AG_F	KKIDK....L	LDRIRERAED	SGNESDGD.A	EEL....STL	MEMGYD.HIL
CRF02_AG_F	KKIDK....L	LDRIRERAED	SGNESDGD.T	EEL....STL	LEMGYD.NIL
CRF02_AG_G	KKIDK....L	LDRIREREED	SGNESEGD.A	EEL....SKL	MEMGHD.FWI
CRF02_AG_N	KKIDR....L	LDRIRERAED	SGNESDGD.T	EEL....STL	MEMGYE.YIL
CRF02_AG_S	KKIDR....L	LDRIRERAED	SGNESDGD.T	EEL....STL	MEMGYD.NIL
CRF02_AG_S	GKIDK....L	LDRIRERAED	SGNESDGD.T	EEL....STL	LEMGYDNAAL
CRF03_AB_R	RKIDR....L	IDRIRERAED	SGNESEGD.Q	E.....AL	MEMGHLVPWD
CRF03_AB_R	RKIDR....L	IDRIRERAED	SGNESEGD.Q	E.....AL	MEMGHLAPWD
CRF04_cpx_	RRIDS....L	YNRIRERAED	SGNESDGD.A	EEL....STL	VGMGNFDPWV
CRF04_cpx_	RKIDR....L	YKRIRERAED	SGNESDGD.T	EEL....STL	VGMGDFDPWV
CRF04_cpx_	RKIDR....L	CKRIIERAED	SGNDSGD.T	EEL....STL	VDMGDFHPLV
CRF05_DF_B	RKINR....L	YKRIRERAED	SGNESEGD.A	EEL....AAL	GEVGPFIPGD
CRF05_DF_B	RKINR....L	YKRIRERAED	SGNESEGD.A	EEL....AAL	GEMGPFIPGN
CRF06_cpx_	KKIEK....L	LDRIRERAED	SGNESEGD.T	DEL....ATL	MEMGDFDPWV
CRF06_cpx_	RKIEK....L	LNRIERAED	SGNESEGD.T	EEL....AAF	MEMGNFDPWV
CRF06_cpx_	KKIEK....L	LDRIRERAED	SGNESEGD.T	DEL....ATL	MEMGNFDPWV
CRF06_cpx_	KKIEK....L	LDRIREREED	SGNDSEGD.T	EEL....ATL	MEMGNFDPWV
CRF11_cpx_	KKIDR....L	IDRIRERAED	SGNESEGD.T	EEL....ARL	VEMGPHDQWN
CRF11_cpx_	R.....K	DRLRIRRAED	SGNESEGD.T	EEL....AQL	VEMGPHDLWN
D_CD_84ZR0	RKIDW....L	IDRIREREED	SGNESEGDKE	ELS....TL	VEMGHHAPWD
D_CD_ELI_K	RRIDC....L	LDRITERAED	SGNESEGDRE	KLS....KL	VEMGHHAPWD
D_CD_NDK_M	RKIDC....L	IDRIRERAED	SGNESEGERE	ELS....KL	VEMGHHAPWD
D_UG_94UG1	RKIDW....L	IDRIRERAED	SGNESEGDKE	ELS....AL	VEMGHDAPWD
F1_BE_VI85	RKINK....L	YKRIRERAED	SGNESEGD.A	EEL....AAL	GEMGPFIPGD
F1_BR_93BR	RKINR....L	YKRISERAED	SGNESEGD.A	EEL....AAL	GEVGPFIPGD
F1_FI_FIN9	RKINR....L	YIRIRERAED	SGNESEGD.A	EEL....AAL	GKMGPFIIPGD
F1_FR_MP41	RKINR....L	YERIRERAED	SGNESEGD.A	EEL....AAL	GEMGSFISGD
F2_CM_MP25	KRINR....L	YERIIERAED	SGNESEGD.A	EEL....AAL	GEVGPLIPGD
F2KU_BE_VI	ERINQ....L	YNRLIERAED	SGNESEGE.A	EEL....AAL	GEVGHLVLGN
G_BE_DRCBL	KRIEK....L	LDRIRERAED	SGNESEGD.T	EEL....ATL	MELGDFDPWV
G_NG_92NG0	KKIEK....L	LDRIRERAED	SGNESEGD.T	EEL....ATL	MEMGDFDPWV
G_SE_SE616	KRIGK....L	LDRIRERAED	SGNESDGD.T	EEL....VTL	VEMGDFDPWV
H_BE_VI991	RKIDR....L	IERIRERAED	SGNESDGD.T	EEL....SKL	VEMGHLNLGY

H_BE_VI997	KKIDR....L	IQRIIEGAED	SGNESD....	EEL....STM	VERGHLTFGY
H_CF_90CF0	KKIDR....L	IERIGERAED	SGNESDGD.T	EEL....SKL	MEMGHLNLGY
J_SE_SE702	RKIDK....L	INRIRERAED	SGNESDGD.T	DEL....AEL	VEMGPHDLWN
J_SE_SE788	RKIDK....L	IDRIRERAED	SGNESDGD.T	EEL....ADL	VERGPHDLWN
K_CD_EQTB1	KRINW....L	FDRIRERAED	SGNESEGD.T	EEL....AAL	GETGHLILGD
K_CM_MP535	KRINW....L	IDRIRERAED	SGNESEGD.A	EEL....ADI	GELGHLILGN
N_CM_YBF30	EKIKH....I	RQRIREREED	SGNESDGD.A	EWLDGDEEWL	VTLLSSSKLD
O_CM_ANT70	DRKEREILER	LRRIREIRDD	SDYESNGE..	EEQ.....EV	MDLVLSHGFD
O_CM_MVP51	DRREQEILER	LRRIKEIRDD	SDYESNEE..	EQQ.....EV	MELIHSYGFA
O_SN_99SE_	DKREREILER	LRRIRQIEDD	SDYESDGT..	EEQ.....EV	RDLVHSYGFD
O_SN_99SE_	DRREREILER	LRRIRQIEDD	SDYESDGK..	EEQ.....EV	RDLVHGYGFD
U_CD___83C	RKIDW....L	IDRIRERAED	SGNESEGD.T	EEL....STL	VEMEPDNFRN

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00BW0762_1	ANGL..
00BW0768_2	GNDL..
00BW0874_2	VNDL..
00BW1471_2	VNDL..
00BW1616_2	DL....
00BW1686_8	VNVL..
00BW1759_3	DNNL..
00BW1773_2	INH...
00BW1783_5	AHDL..
00BW1795_6	ANNL..
00BW1811_3	IINY..
00BW1859_5	INDL..
00BW1880_2	ANDL..
00BW1921_1	HGL...
00BW2036_1	VHDL..
00BW2063_6	ANDL..
00BW2087_2	VNDL..
00BW2127_2	DL....
00BW2276_7	GNDL..
00BW3819_3	AHDL..
00BW3842_8	L.....
00BW3871_3	VNDI..
00BW3876_9	INN...
00BW3886_8	VNNL..
00BW3891_6	VNDV..
00BW3970_2	VTDL..
00BW5031_1	VNDL..
96BW01B21	DNAL..
96BW0407	DI....
96BW0502	VNN...
96BW06_J4	NL....
96BW11_06	ANDL..
96BW1210	ADGL..
96BW15B03	L.....
96BW16_26	INN...
96BW17A09	VNDL..
96BWMO1_5	TNDL..
96BWMO3_2	INL...
98BWMC12_2	DNEL..
98BWMC13_4	VNDL..
98BWMC14_a	VM....
98BWMO14_1	ANDL..
98BWMO18_d	ANDL..
98BWMO36_a	AHDL..
98BWMO37_d	ANDL..
99BW3932_1	.....

99BW4642_4	VNDL..
99BW4745_8	DL....
99BW4754_7	VNDL..
99BWMC16_8	ANDL..
A2_CD_97CD	DNDV..
A2_CY_94CY	VNNV..
A2D___97KR	AND...
A2G_CD_97C	GDNL..
A_BY_97BL0	DNNV..
A_KE_Q23_A	NNIL..
A_SE_SE659	DNNL..
A_SE_SE725	DNDL..
A_SE_SE753	GNNL..
A_SE_SE853	DNNL..
A_SE_SE889	NNNL..
A_SE_UGSE8	DNNL..
A_UG_92UG0	DNNL..
A_UG_U455_	DNNL..
AC_IN_2130	VNGL..
AC_RW_92RW	VNNL..
AC_SE_SE94	VNNL..
ACD_SE_SE8	DINL..
ACG_BE_VI1	AIDL..
AD_SE_SE69	VDDM..
AD_SE_SE71	DNNL..
ADHK_NO_97	VADL..
ADK_CD_MAL	VDDL..
AG_BE_VI11	GDNL..
AG_NG_92NG	GDNL..
AGHU_GA_VI	VNDL..
AGU_CD_Z32	GDNL..
AJ_BW_BW21	VNDL..
B_AU_VH_AF	VDDL..
B_CN_RL42_	VDDL..
B_DE_D31_U	VDDL..
B_DE_HAN_U	VNDQ..
B_FR_HXB2_	VDDL..
B_GA_OYI_M	VDDM..
B_GB_CAM1_	VNDL..
B_GB_GB8_A	VDDL..
B_GB_MANC_	VDDL..
B_KR_WK_AF	VDDL..
B_NL_3202A	VDDL..
B_TW_TWCYS	VNDQ..
B_US_BC_L0	IDDL..
B_US_DH123	IDDL..
B_US_JRCSE	INDL..
B_US_MNCG_	INDL..
B_US_P896_	VDDL..
B_US_RF_M1	VDDL..
B_US_SF2_K	VDDL..
B_US_WEAU1	IDDL..
B_US_WR27_	VDDL..
B_US_YU2_M	VDDL..
BF1_BR_93B	IDNL..
C_BR_92BR0	GNDL..
C_BW_96BW0	DN....
C_BW_96BW1	ANDL..
C_BW_96BW1	ADGL..
C_BW_96BW1	L.....

C_ET_ETH22	VNDL..
C_IN_93IN1	VNDL..
C_IN_93IN9	VNDL..
C_IN_93IN9	VNDM..
C_IN_94IN1	VNDL..
C_IN_95IN2	VNDL..
CRF01_AE_C	GDNL..
CRF01_AE_C	GDNL..
CRF01_AE_C	GDNV..
CRF01_AE_T	GDNL..
CRF01_AE_T	GDNL..
CRF01_AE_T	GDNV..
CRF01_AE_T	GDNL..
CRF01_AE_T	GDNL..
CRF01_AE_T	GDNL..
CRF02_AG_F	DNDNL.
CRF02_AG_F	DNDNL.
CRF02_AG_G	DNL...
CRF02_AG_N	DNDNL.
CRF02_AG_S	DNDNL.
CRF02_AG_S	DIDNL.
CRF03_AB_R	ADDL..
CRF03_AB_R	ADDL..
CRF04_cpx_	GDNL..
CRF04_cpx_	GNNV..
CRF04_cpx_	GNNL..
CRF05_DF_B	INNLL..
CRF05_DF_B	INNLL..
CRF06_cpx_	GDNL..
CRF06_cpx_	GDNL..
CRF06_cpx_	GDNL..
CRF06_cpx_	GDNL..
CRF11_cpx_	VNDL..
CRF11_cpx_	VNDL..
D_CD_84ZR0	VDDDL.
D_CD_ELI_K	IDDL..
D_CD_NDK_M	VDDL..
D_UG_94UG1	ADDM..
F1_BE_VI85	INNLL..
F1_BR_93BR	INNLL..
F1_FI_FIN9	VNNL..
F1_FR_MP41	INNLL..
F2_CM_MP25	INNLL..
F2KU_BE_VI	IHNLL..
G_BE_DRCBL	GDNL..
G_NG_92NG0	GNNL..
G_SE_SE616	GDNL..
H_BE_VI991	VADL..
H_BE_VI997	VADL..
H_CF_90CF0	VADL..
J_SE_SE702	VNDL..
J_SE_SE788	VNDL..
K_CD_EQTB1	INNLL..
K_CM_MP535	IDNL..
N_CM_YBF30	QGNWV.
O_CM_ANT70	NPMFEP
O_CM_MVP51	NPMFEL
O_SN_99SE_	NPMFEL
O_SN_99SE_	NPMFEP
U_CD___83C	DNDM..

Table 20. BLASTP Sequences producing significant alignments with S20757 (HBV Polymerase subtype ayw)

			Score (bits)	E: Value
gi	93080 pir	S20757 DNA-directed DNA polymerase (EC 2.7.7....	1553	0.0
gi	8925755 gb	AAF81607.1  DNA polymerase/reverse transcript...	1489	0.0
gi	1514497 emb	CAA68864.1  P [Hepatitis B virus]	1488	0.0
gi	27466573 gb	AAO12632.1  polymerase [Hepatitis B virus]	1482	0.0
gi	5257489 gb	AAD41360.1  polymerase [Hepatitis B virus]	1482	0.0
gi	118876 sp	P03156 DPOL_HPBVY P protein [Includes: DNA-dir...	1482	0.0
gi	27466565 gb	AAO12625.1  polymerase [Hepatitis B virus]	1481	0.0
gi	67003 pir	JDVLVB DNA-directed DNA polymerase (EC 2.7.7....	1480	0.0
gi	59433 emb	CAA46352.1  polymerase ORF [Hepatitis B virus]	1480	0.0
gi	6692498 gb	AAF24666.1  polymerase [Hepatitis B virus]	1479	0.0
gi	6692505 gb	AAF24673.1  polymerase [Hepatitis B virus]	1479	0.0
gi	2117935 pir	S71785 DNA-directed DNA polymerase (EC 2.7....	1477	0.0
gi	28436101 dbj	BAC57445.1  polymerase [Hepatitis B virus]	1476	0.0
gi	631984 pir	S47406 DNA-directed DNA polymerase (EC 2.7.7...	1475	0.0
gi	1359687 emb	CAA66431.1  polymerase [Hepatitis B virus]	1474	0.0
gi	18621117 emb	CAC87021.1  polymerase [Hepatitis B virus]	1474	0.0
gi	28436091 dbj	BAC57437.1  polymerase [Hepatitis B virus]	1473	0.0
gi	6692512 gb	AAF24680.1  polymerase [Hepatitis B virus]	1472	0.0
gi	22135695 gb	AAM09037.1  polymerase [Hepatitis B virus]	1471	0.0
gi	18621125 emb	CAC87015.1  polymerase [Hepatitis B virus]	1471	0.0
gi	1359679 emb	CAA66424.1  polymerase [Hepatitis B virus]	1470	0.0
gi	6692492 gb	AAF24660.1  polymerase [Hepatitis B virus]	1468	0.0
gi	2182121 gb	AAB59972.1  DNA polymerase [Hepatitis B virus]	1467	0.0
gi	4140295 emb	CAA10539.1  polymerase [Hepatitis B virus]	1467	0.0
gi	28436096 dbj	BAC57441.1  polymerase [Hepatitis B virus]	1466	0.0
gi	2829156 gb	AAC40810.1  polymerase [Hepatitis B virus]	1464	0.0
gi	27466519 gb	AAO12604.1  polymerase [Hepatitis B virus] >...	1463	0.0
gi	118869 sp	P24024 DPOL_HPBVA P protein [Includes: DNA-dir...	1462	0.0
gi	27466525 gb	AAO12672.1  polymerase [Hepatitis B virus]	1461	0.0
gi	762933 emb	CAA59514.1  polymerase [Hepatitis B virus]	1461	0.0
gi	22135690 gb	AAM09033.1  polymerase [Hepatitis B virus]	1459	0.0
gi	6063470 dbj	BAA85377.1  DNA polymerase/reverse transcrip...	1455	0.0
gi	6063465 dbj	BAA85373.1  DNA polymerase/reverse transcrip...	1454	0.0
gi	27466605 gb	AAO12660.1  polymerase [Hepatitis B virus]	1451	0.0
gi	2829149 gb	AAC40804.1  polymerase [Hepatitis B virus]	1451	0.0
gi	475987 gb	AAA18583.1  polymerase [Hepatitis B virus]	1450	0.0
gi	313784 emb	CAA42466.1  polymerase [Hepatitis B virus]	1446	0.0
gi	27466597 gb	AAO12653.1  polymerase [Hepatitis B virus]	1444	0.0
gi	15419833 gb	AAK97182.1 AF297620_3 polymerase [Hepatitis ...	1442	0.0
gi	93082 pir	S20752 DNA-directed DNA polymerase (EC 2.7.7....	1441	0.0
gi	27466613 gb	AAO12667.1  polymerase [Hepatitis B virus]	1435	0.0
gi	27466589 gb	AAO12646.1  polymerase [Hepatitis B virus]	1434	0.0
gi	27466538 gb	AAO12618.1  polymerase [Hepatitis B virus]	1432	0.0
gi	27466581 gb	AAO12639.1  polymerase [Hepatitis B virus]	1431	0.0
gi	15419828 gb	AAK97178.1 AF297619_3 polymerase [Hepatitis ...	1429	0.0
gi	27466544 gb	AAO12681.1  polymerase [Hepatitis B virus]	1427	0.0
gi	27466557 gb	AAO12692.1  polymerase [Hepatitis B virus]	1423	0.0
gi	16751312 gb	AAL25951.1  polymerase protein [Hepatitis B ...	1382	0.0
gi	11935073 gb	AAG41955.1 AF305327_2 polymerase [Hepatitis ...	1379	0.0
gi	13491150 gb	AAK27856.1 AF330110_3 polymerase [Hepatitis ...	1368	0.0
gi	6116700 dbj	BAA32859.2  pol protein [Hepatitis B virus]	1368	0.0
gi	3551332 dbj	BAA32886.1  pol protein [Hepatitis B virus]	1368	0.0
gi	28812222 dbj	BAC65108.1  polymerase protein [Hepatitis B...	1368	0.0
gi	6691505 dbj	BAA89330.1  polymerase protein [Hepatitis B ...	1368	0.0
gi	118872 sp	P12900 DPOL_HPBVL P protein [Includes: DNA-dir...	1368	0.0

gi	560084	dbj	BAA04927.1	DNA polymerase [Hepatitis B virus]	1367	0.0
gi	560089	dbj	BAA04931.1	DNA polymerase [Hepatitis B virus]	1367	0.0
gi	6116731	dbj	BAA32957.2	pol protein [Hepatitis B virus]	1366	0.0
gi	6691495	dbj	BAA89322.1	polymerase protein [Hepatitis B ...]	1365	0.0
gi	7188655	gb	AAF37833.1	AF222323_2 polymerase [Hepatitis B ...]	1365	0.0
gi	6063460	dbj	BAA85369.1	DNA polymerase/reverse transcrip...	1364	0.0
gi	3551347	dbj	BAA32898.1	pol protein [Hepatitis B virus]	1364	0.0
gi	6691500	dbj	BAA89326.1	polymerase protein [Hepatitis B ...]	1363	0.0
gi	28812217	dbj	BAC65104.1	polymerase protein [Hepatitis B ...]	1363	0.0
gi	3551342	dbj	BAA32894.1	pol protein [Hepatitis B virus]	1363	0.0
gi	628080	pir	S43491	DNA-directed DNA polymerase (EC 2.7.7...	1363	0.0
gi	12246972	gb	AAG49670.1	AF223956_3 polymerase [Hepatitis ...]	1362	0.0
gi	3551293	dbj	BAA32852.1	pol protein [Hepatitis B virus]	1362	0.0
gi	12246964	gb	AAG49663.1	AF223955_3 polymerase [Hepatitis ...]	1362	0.0
gi	21624231	dbj	BAC01103.1	polymerase protein [Hepatitis B ...]	1362	0.0
gi	118874	sp	P03157	DPOL_HPBVR P protein [Includes: DNA-dir...	1361	0.0
gi	6009784	dbj	BAA85065.1	polymerase [Hepatitis B virus]	1361	0.0
gi	22651880	gb	AAN03491.1	AF286594_3 DNA polymerase [Hepati...	1360	0.0
gi	18252591	gb	AAL66348.1	AF461043_2 P protein [Hepatitis B ...]	1360	0.0
gi	15778326	gb	AAL07381.1	AF411409_4 polymerase [Hepatitis ...]	1360	0.0
gi	3551268	dbj	BAA32832.1	pol protein [Hepatitis B virus]	1360	0.0
gi	14290241	gb	AAK59316.1	AF384371_2 polymerase [Hepatitis ...]	1358	0.0
gi	6063435	dbj	BAA85353.1	DNA polymerase/reverse transcrip...	1358	0.0
gi	6063440	dbj	BAA85357.1	DNA polymerase/reverse transcrip...	1358	0.0
gi	3551283	dbj	BAA32844.1	pol protein [Hepatitis B virus]	1358	0.0
gi	18252536	gb	AAL66307.1	AF458664_3 polymerase [Hepatitis ...]	1358	0.0
gi	6009769	dbj	BAA85053.1	polymerase [Hepatitis B virus]	1358	0.0
gi	13991865	gb	AAK51533.1	AF363961_2 polymerase [Hepatitis ...]	1357	0.0
gi	6063425	dbj	BAA85382.1	DNA polymerase/reverse transcrip...	1357	0.0
gi	2626986	dbj	BAA23435.1	DNA polymerase [Hepatitis B viru...	1357	0.0
gi	4490402	emb	CAB38767.1	P protein [Hepatitis B virus]	1357	0.0
gi	22415735	gb	AAM95242.1	DNA polymerase/reverse transcrip...	1357	0.0
gi	10934057	dbj	BAB16885.1	polymerase [Hepatitis B virus]	1356	0.0
gi	18252556	gb	AAL66323.1	AF461359_3 polymerase [Hepatitis ...]	1356	0.0
gi	2627009	dbj	BAA23455.1	DNA polymerase [Hepatitis B virus]	1356	0.0
gi	560074	dbj	BAA04919.1	DNA polymerase [Hepatitis B virus]	1356	0.0
gi	479847	pir	S35527	DNA-directed DNA polymerase (EC 2.7.7...	1356	0.0
gi	18252545	gb	AAL66314.1	AF461357_2 polymerase [Hepatitis ...]	1356	0.0
gi	1742906	dbj	BAA09083.1	DNA polymerase [Hepatitis B virus]	1355	0.0
gi	6009764	dbj	BAA85049.1	polymerase [Hepatitis B virus] >...	1355	0.0
gi	2627002	dbj	BAA23449.1	DNA polymerase [Hepatitis B virus]	1355	0.0
gi	6063455	dbj	BAA85365.1	DNA polymerase/reverse transcrip...	1355	0.0
gi	10441115	gb	AAG16953.1	AF182804_4 polymerase [Hepatitis ...]	1354	0.0
gi	6009774	dbj	BAA85057.1	polymerase [Hepatitis B virus]	1353	0.0
gi	4490407	emb	CAB38771.1	P protein [Hepatitis B virus]	1353	0.0
gi	3582359	dbj	BAA32913.1	pol protein [Hepatitis B virus]	1353	0.0
gi	3582355	dbj	BAA32874.1	pol protein [Hepatitis B virus]	1353	0.0
gi	12246980	gb	AAG49677.1	AF223957_3 polymerase [Hepatitis ...]	1352	0.0
gi	16751307	gb	AAL25947.1	polymerase protein [Hepatitis B ...]	1352	0.0
gi	3582375	dbj	BAA32925.1	pol protein [Hepatitis B virus]	1352	0.0
gi	15778340	gb	AAL07392.1	AF411412_4 polymerase [Hepatitis ...]	1352	0.0
gi	4206637	gb	AAD11755.1	DNA polymerase [Hepatitis B virus]	1352	0.0
gi	15425690	dbj	BAB64319.1	polymerase [Hepatitis B virus]	1352	0.0
gi	3551352	dbj	BAA32902.1	pol protein [Hepatitis B virus]	1352	0.0
gi	3582395	dbj	BAA32963.1	pol protein [Hepatitis B virus]	1352	0.0
gi	5114071	gb	AAD40205.1	AF090839_2 polymerase [Hepatitis B ...]	1352	0.0
gi	9082085	gb	AAF82723.1	AF233236_2 pol [Hepatitis B virus]	1352	0.0
gi	6983935	gb	AAF34734.1	AF160501_2 polymerase [Hepatitis B ...]	1351	0.0
gi	560094	dbj	BAA04935.1	DNA polymerase [Hepatitis B virus]	1351	0.0
gi	18032033	gb	AAL49990.1	polymerase [Hepatitis B virus]	1351	0.0

gi	18146671	dbj	BAB82392.1	polymerase [Hepatitis B virus]	1351	0.0
gi	6006322	dbj	BAA84819.1	polymerase protein [Hepatitis B ...]	1350	0.0
gi	18252551	gb	AAL66319.1	AF461358_3 polymerase [Hepatitis ...]	1350	0.0
gi	7188649	gb	AAF37828.1	AF223222_2 polymerase [Hepatitis B...]	1350	0.0
gi	12060441	dbj	BAB20611.1	DNA polymerase [Hepatitis B virus]	1350	0.0
gi	18845085	gb	AAL79545.1	AF473543_4 P protein [Hepatitis B...]	1350	0.0
gi	3551322	dbj	BAA32878.1	pol protein [Hepatitis B virus]	1350	0.0
gi	12246956	gb	AAG49656.1	AF223954_4 polymerase [Hepatitis ...]	1350	0.0
gi	6063430	dbj	BAA85349.1	DNA polymerase/reverse transcrip...	1350	0.0
gi	2288872	dbj	BAA21665.1	DNA polymerase [Hepatitis B virus]	1350	0.0
gi	1220111	dbj	BAA04072.1	DNA polymerase [Hepatitis B virus]	1349	0.0
gi	9454168	gb	AAF87689.1	polymerase protein [Hepatitis B v...]	1349	0.0
gi	18146683	dbj	BAB82402.1	polymerase [Hepatitis B virus]	1349	0.0
gi	3551278	dbj	BAA32840.1	pol protein [Hepatitis B virus]	1349	0.0
gi	3551372	dbj	BAA32939.1	pol protein [Hepatitis B virus]	1349	0.0
gi	19849035	gb	AAL99437.1	AF405706_3 polymerase [Hepatitis ...]	1349	0.0
gi	3551357	dbj	BAA32906.1	pol protein [Hepatitis B virus]	1349	0.0
gi	15778321	gb	AAL07377.1	AF411408_4 polymerase [Hepatitis ...]	1348	0.0
gi	15072542	gb	AAK81690.1	polymerase protein [Hepatitis B ...]	1348	0.0
gi	21624238	dbj	BAC01109.1	polymerase protein [Hepatitis B...]	1348	0.0
gi	12247012	gb	AAG49705.1	AF223961_3 polymerase [Hepatitis ...]	1348	0.0
gi	5114086	gb	AAD40217.1	AF090842_2 polymerase [Hepatitis B...]	1348	0.0
gi	3582407	dbj	BAA32972.1	pol protein [Hepatitis B virus]	1347	0.0
gi	15425698	dbj	BAB64325.1	polymerase [Hepatitis B virus]	1347	0.0
gi	18146665	dbj	BAB82387.1	polymerase [Hepatitis B virus]	1347	0.0
gi	23194252	gb	AAN15074.1	P protein [Hepatitis B virus]	1347	0.0
gi	560079	dbj	BAA04923.1	DNA polymerase [Hepatitis B virus]	1347	0.0
gi	10443833	gb	AAG17595.1	AF241410_3 polymerase [Hepatitis ...]	1346	0.0
gi	13991870	gb	AAK51537.1	AF363962_2 polymerase [Hepatitis ...]	1346	0.0
gi	4007054	emb	CAA10426.1	DNA polymerase [Hepatitis B virus]	1346	0.0
gi	3551362	dbj	BAA32910.1	pol protein [Hepatitis B virus]	1346	0.0
gi	18146677	dbj	BAB82397.1	polymerase [Hepatitis B virus]	1346	0.0
gi	12246988	gb	AAG49684.1	AF223958_3 polymerase [Hepatitis ...]	1346	0.0
gi	15211897	emb	CAC51286.1	polymerase [Hepatitis B virus]	1345	0.0
gi	18389989	gb	AAL68823.1	polymerase [Hepatitis B virus]	1345	0.0
gi	3582363	dbj	BAA32916.1	pol protein [Hepatitis B virus]	1345	0.0
gi	10441110	gb	AAG16949.1	AF182803_4 polymerase [Hepatitis ...]	1345	0.0
gi	10443841	gb	AAG17602.1	AF241411_3 polymerase [Hepatitis ...]	1345	0.0
gi	3551382	dbj	BAA32947.1	pol protein [Hepatitis B virus]	1345	0.0
gi	3582387	dbj	BAA32950.1	pol protein [Hepatitis B virus]	1344	0.0
gi	3551317	dbj	BAA32871.1	pol protein [Hepatitis B virus]	1344	0.0
gi	10441104	gb	AAG16944.1	AF182802_3 polymerase [Hepatitis ...]	1343	0.0
gi	118866	sp	P03159	DPOL_HP BV2 P protein [Includes: DNA-dir...]	1343	0.0
gi	15425694	dbj	BAB64322.1	polymerase [Hepatitis B virus]	1343	0.0
gi	4007049	emb	CAA10422.1	DNA polymerase [Hepatitis B virus]	1343	0.0
gi	29123239	gb	AAO62971.1	pol protein [Hepatitis B virus]	1343	0.0
gi	4007064	emb	CAA10438.1	DNA polymerase [Hepatitis B virus]	1342	0.0
gi	452623	emb	CAA53358.1	polymerase [Hepatitis B virus]	1342	0.0
gi	18252541	gb	AAL66311.1	AF458665_3 polymerase [Hepatitis ...]	1342	0.0
gi	527443	emb	CAA84791.1	DNA polymerase [Hepatitis B virus]	1342	0.0
gi	15211890	emb	CAC51280.1	polymerase [Hepatitis B virus]	1342	0.0
gi	329617	gb	AAA62812.1	DNA polymerase	1341	0.0
gi	4007079	emb	CAA10454.1	DNA polymerase [Hepatitis B virus]	1341	0.0
gi	9454173	gb	AAF87693.1	polymerase protein [Hepatitis B v...]	1341	0.0
gi	452628	emb	CAA53354.1	polymerase [Hepatitis B virus]	1341	0.0
gi	3582367	dbj	BAA32919.1	pol protein [Hepatitis B virus]	1340	0.0
gi	5114066	gb	AAD40201.1	AF090838_2 polymerase [Hepatitis B...]	1340	0.0
gi	15419860	gb	AAK97203.1	AF297625_3 polymerase [Hepatitis ...]	1340	0.0
gi	4490412	emb	CAB38775.1	P protein [Hepatitis B virus]	1340	0.0
gi	18252566	gb	AAL66331.1	AF461361_3 polymerase [Hepatitis ...]	1340	0.0



gi	4007059	emb	CAA10430.1	DNA polymerase [Hepatitis B virus]	1340	0.0
gi	5114081	gb	AAD40213.1	AF090841_2 polymerase [Hepatitis B...	1339	0.0
gi	3582371	dbj	BAA32922.1	pol protein [Hepatitis B virus]	1339	0.0
gi	12247003	gb	AAG49697.1	AF223960_4 polymerase [Hepatitis ...	1339	0.0
gi	4033548	emb	CAA10450.1	DNA polymerase [Hepatitis B virus]	1339	0.0
gi	3892581	emb	CAA09962.1	polymerase [Hepatitis B virus]	1339	0.0
gi	5114076	gb	AAD40209.1	AF090840_2 polymerase [Hepatitis B...	1338	0.0
gi	12060436	dbj	BAB20607.1	DNA polymerase [Hepatitis B virus]	1338	0.0
gi	118868	sp	P17100	DPOL_HPBV9 P protein [Includes: DNA-dir...	1337	0.0
gi	27466434	gb	AAO12555.1	polymerase [Hepatitis B virus]	1337	0.0
gi	3582399	dbj	BAA32966.1	pol protein [Hepatitis B virus]	1337	0.0
gi	3551273	dbj	BAA32836.1	pol protein [Hepatitis B virus]	1337	0.0
gi	14285168	gb	AAK58873.1	polymerase [synthetic construct]...	1337	0.0
gi	3582391	dbj	BAA32953.1	pol protein [Hepatitis B virus]	1337	0.0
gi	15419845	gb	AAK97191.1	AF297622_3 polymerase [Hepatitis ...	1337	0.0
gi	118870	sp	P17393	DPOL_HPBVI P protein [Includes: DNA-dir...	1336	0.0
gi	3551377	dbj	BAA32943.1	pol protein [Hepatitis B virus]	1336	0.0
gi	10443825	gb	AAG17588.1	AF241409_3 polymerase [Hepatitis ...	1336	0.0
gi	10443817	gb	AAG17581.1	AF241408_3 polymerase [Hepatitis ...	1336	0.0
gi	29124889	gb	AAO63519.1	pol protein [Hepatitis B virus]	1335	0.0
gi	399401	sp	P31870	DPOL_HPBVM P protein [Includes: DNA-dir...	1335	0.0
gi	6063445	dbj	BAA85339.1	DNA polymerase/reverse transcrip...	1335	0.0
gi	19568078	gb	AAL89566.1	polymerase [Hepatitis B virus]	1334	0.0
gi	27466426	gb	AAO12548.1	polymerase [Hepatitis B virus]	1334	0.0
gi	22655601	gb	AAN04128.1	polymerase [Hepatitis B virus]	1334	0.0
gi	8161369	gb	AAA69721.2	polymerase [Hepatitis B virus]	1334	0.0
gi	10441120	gb	AAG16957.1	AF182805_4 polymerase [Hepatitis ...	1334	0.0
gi	10443809	gb	AAG17574.1	AF241407_3 polymerase [Hepatitis ...	1333	0.0
gi	18146689	dbj	BAB82407.1	polymerase [Hepatitis B virus]	1333	0.0
gi	4007069	emb	CAA10442.1	DNA polymerase [Hepatitis B virus]	1333	0.0
gi	18031709	gb	AAK57744.1	polymerase [Hepatitis B virus]	1333	0.0
gi	18252561	gb	AAL66327.1	AF461360_3 polymerase [Hepatitis ...	1332	0.0
gi	6959503	gb	AAF33121.1	polymerase protein [orangutan hep...	1332	0.0
gi	26224721	gb	AAN76318.1	polymerase [Hepatitis B virus]	1332	0.0
gi	4007074	emb	CAA10446.1	DNA polymerase [Hepatitis B virus]	1332	0.0
gi	18031714	gb	AAK57745.1	polymerase [Hepatitis B virus]	1332	0.0
gi	7434791	pir	S67505	DNA-directed DNA polymerase (EC 2.7....	1332	0.0
gi	15419855	gb	AAK97199.1	AF297624_3 polymerase [Hepatitis ...	1332	0.0
gi	7434793	pir	T13468	DNA-directed DNA polymerase (EC 2.7....	1331	0.0
gi	4323205	gb	AAD16257.1	polymerase [Hepatitis B virus]	1331	0.0
gi	12060194	dbj	BAB20451.1	DNA polymerase [Hepatitis B virus]	1331	0.0
gi	23194347	gb	AAN15122.1	polymerase [Hepatitis B virus]	1330	0.0
gi	20151228	gb	AAM12945.1	DNA polymerase/reverse transcrip...	1330	0.0
gi	23884547	gb	AAN40009.1	pol protein [Hepatitis B virus]	1330	0.0
gi	21431681	gb	AAM53414.1	U87747_3 DNA polymerase/reverse t...	1330	0.0
gi	3551337	dbj	BAA32890.1	pol protein [Hepatitis B virus]	1329	0.0
gi	5019933	gb	AAD37919.1	P protein [Hepatitis B virus]	1329	0.0
gi	15419840	gb	AAK97187.1	AF297621_3 polymerase [Hepatitis ...	1329	0.0
gi	6006331	dbj	BAA84825.1	polymerase protein [Hepatitis B ...	1329	0.0
gi	19568073	gb	AAL89569.1	polymerase [Hepatitis B virus]	1329	0.0
gi	29124918	gb	AAO63539.1	pol protein [Hepatitis B virus]	1328	0.0
gi	329630	gb	AAA45483.1	P protein [Hepatitis B virus]	1328	0.0
gi	15778331	gb	AAL07385.1	AF411410_4 polymerase [Hepatitis ...	1328	0.0
gi	6566410	dbj	BAA88275.1	P protein [Hepatitis B virus]	1328	0.0
gi	4490397	emb	CAB38763.1	P protein [Hepatitis B virus]	1328	0.0
gi	12060187	dbj	BAB20445.1	DNA polymerase [Hepatitis B virus]	1327	0.0
gi	6063450	dbj	BAA85343.1	DNA polymerase/reverse transcrip...	1327	0.0
gi	118877	sp	P03155	DPOL_HPBVZ P protein [Includes: DNA-dir...	1327	0.0
gi	29124883	gb	AAO63514.1	pol protein [Hepatitis B virus]	1325	0.0
gi	4033543	emb	CAA10434.1	DNA polymerase [Hepatitis B virus]	1325	0.0

gi	6692525	gb	AAF24693.1	polymerase [Hepatitis B virus]	1325	0.0
gi	6692559	gb	AAF24727.1	polymerase [Hepatitis B virus]	1325	0.0
gi	23194340	gb	AAN15116.1	polymerase [Hepatitis B virus]	1325	0.0
gi	560064	dbj	BAA04911.1	DNA polymerase [Hepatitis B virus]	1324	0.0
gi	29124898	gb	AAO63526.1	pol protein [Hepatitis B virus]	1324	0.0
gi	29124927	gb	AAO63545.1	pol protein [Hepatitis B virus]	1323	0.0
gi	6692566	gb	AAF24734.1	polymerase [Hepatitis B virus]	1323	0.0
gi	6692553	gb	AAF24721.1	polymerase [Hepatitis B virus]	1323	0.0
gi	6692518	gb	AAF24686.1	polymerase [Hepatitis B virus] >g...	1323	0.0
gi	1359702	emb	CAA66444.1	polymerase [Hepatitis B virus] >...	1323	0.0
gi	29124867	gb	AAO63501.1	pol protein [Hepatitis B virus]	1323	0.0
gi	29124872	gb	AAO63505.1	pol protein [Hepatitis B virus] ...	1323	0.0
gi	27466479	gb	AAO12576.1	polymerase [Hepatitis B virus]	1322	0.0
gi	6692546	gb	AAF24714.1	polymerase [Hepatitis B virus]	1322	0.0
gi	3551312	dbj	BAA32867.1	pol protein [Hepatitis B virus]	1322	0.0
gi	27466487	gb	AAO12611.1	polymerase [Hepatitis B virus]	1322	0.0
gi	118871	sp	P17394 DPOL_HPBVJ	P protein [Includes: DNA-dir...	1321	0.0
gi	9454473	gb	AAF87833.1 AF282917_3	DNA polymerase [Hepatitis B virus]	1321	0.0
gi	19224214	gb	AAL86445.1 AF479684_3	P gene product [Hepatitis B virus]	1321	0.0
gi	6692572	gb	AAF24740.1	polymerase [Hepatitis B virus]	1321	0.0
gi	3551297	dbj	BAA32855.1	pol protein [Hepatitis B virus]	1321	0.0
gi	3551327	dbj	BAA32882.1	pol protein [Hepatitis B virus]	1320	0.0
gi	1359695	emb	CAA66434.1	polymerase [Hepatitis B virus]	1320	0.0
gi	3551367	dbj	BAA32932.1	pol protein [Hepatitis B virus]	1320	0.0
gi	118873	sp	P17395 DPOL_HPBVO	P protein [Includes: DNA-dir...	1319	0.0
gi	29124862	gb	AAO63497.1	pol protein [Hepatitis B virus]	1319	0.0
gi	18621110	emb	CAC87028.1	polymerase [Hepatitis B virus]	1319	0.0
gi	3582403	dbj	BAA32969.1	pol protein [Hepatitis B virus]	1318	0.0
gi	27261550	gb	AAN85925.1	DNA polymerase [Hepatitis B virus]...	1318	0.0
gi	1914703	emb	CAA66699.1	polymerase [Hepatitis B virus]	1318	0.0
gi	4323200	gb	AAD16253.1	polymerase [Hepatitis B virus]	1318	0.0
gi	6573293	dbj	BAA88291.1	P protein [Hepatitis B virus]	1318	0.0
gi	6006341	dbj	BAA84833.1	polymerase protein [Hepatitis B virus] ...	1316	0.0
gi	6566440	dbj	BAA88286.1	P protein [Hepatitis B virus]	1315	0.0
gi	560059	dbj	BAA04907.1	DNA polymerase [Hepatitis B virus]	1315	0.0
gi	14334410	gb	AAK59391.1	polymerase [Hepatitis B virus]	1315	0.0
gi	5019954	gb	AAD37936.1	P protein [Hepatitis B virus]	1315	0.0
gi	16117323	dbj	BAB69785.1	polymerase [Hepatitis B virus]	1315	0.0
gi	7434792	pir	T13473	DNA-directed DNA polymerase (EC 2.7....	1315	0.0
gi	5019965	gb	AAD37945.1	P protein [Hepatitis B virus]	1314	0.0
gi	29124908	gb	AAO63533.1	pol protein [Hepatitis B virus]	1314	0.0
gi	6566428	dbj	BAA88281.1	P protein [Hepatitis B virus]	1313	0.0
gi	29124894	gb	AAO63523.1	pol protein [Hepatitis B virus]	1311	0.0
gi	22135730	gb	AAM09065.1	polymerase [Hepatitis B virus]	1311	0.0
gi	560069	dbj	BAA04915.1	DNA polymerase [Hepatitis B virus]	1311	0.0
gi	15419850	gb	AAK97195.1 AF297623_3	polymerase [Hepatitis B virus] ...	1311	0.0
gi	9634217	ref	NP_037757.1	polymerase protein [orangutan h...	1310	0.0
gi	16117333	dbj	BAB69793.1	polymerase [Hepatitis B virus]	1309	0.0
gi	9971630	dbj	BAB12582.1	polymerase protein [Hepatitis B virus] ...	1308	0.0
gi	27466450	gb	AAO12569.1	polymerase [Hepatitis B virus]	1306	0.0
gi	12247036	gb	AAG49726.1 AF223964_3	polymerase [Hepatitis B virus] ...	1306	0.0
gi	12247028	gb	AAG49719.1 AF223963_3	polymerase [Hepatitis B virus] ...	1305	0.0
gi	5019945	gb	AAD37929.1	P protein [Hepatitis B virus]	1305	0.0
gi	18146701	dbj	BAB82417.1	polymerase [Hepatitis B virus]	1305	0.0
gi	12247020	gb	AAG49712.1 AF223962_3	polymerase [Hepatitis B virus] ...	1304	0.0
gi	5019981	gb	AAD37958.1	P protein [Hepatitis B virus]	1304	0.0
gi	3892582	emb	CAA53343.1	polymerase [Hepatitis B virus]	1304	0.0
gi	27466442	gb	AAO12562.1	polymerase [Hepatitis B virus]	1304	0.0
gi	22135715	gb	AAM09053.1	polymerase [Hepatitis B virus]	1301	0.0
gi	12247044	gb	AAG49733.1 AF223965_3	polymerase [Hepatitis B virus] ...	1301	0.0

gi	22135725	gb	AAM09061.1	polymerase [Hepatitis B virus]	1301	0.0
gi	11191880	dbj	BAB17962.1	polymerase [Hepatitis B virus]	1300	0.0
gi	3551392	dbj	BAA32961.1	pol protein [Hepatitis B virus]	1300	0.0
gi	6006336	dbj	BAA84829.1	polymerase protein [Hepatitis B ...]	1299	0.0
gi	2627021	dbj	BAA23467.1	DNA polymerase [Hepatitis B virus]	1298	0.0
gi	2627015	dbj	BAA23461.1	DNA polymerase [Hepatitis B virus]	1297	0.0
gi	16117328	dbj	BAB69789.1	polymerase [Hepatitis B virus]	1297	0.0
gi	22135735	gb	AAM09069.1	polymerase [Hepatitis B virus]	1297	0.0
gi	14485226	gb	AAK62976.1	AF384372_2 polymerase [Hepatitis ...]	1296	0.0
gi	3551288	dbj	BAA32848.1	pol protein [Hepatitis B virus]	1295	0.0
gi	11191960	dbj	BAB18032.1	polymerase [Hepatitis B virus]	1294	0.0
gi	11191888	dbj	BAB17969.1	polymerase [Hepatitis B virus] ...	1293	0.0
gi	11191840	dbj	BAB17927.1	polymerase [Hepatitis B virus] ...	1293	0.0
gi	11191920	dbj	BAB17997.1	polymerase [Hepatitis B virus]	1293	0.0
gi	11191904	dbj	BAB17983.1	polymerase [Hepatitis B virus]	1291	0.0
gi	11191952	dbj	BAB18025.1	polymerase [Hepatitis B virus]	1291	0.0
gi	1169410	sp	Q05486	DPOL_HPBVT P protein [Includes: DNA-di...]	1289	0.0
gi	22135705	gb	AAM09045.1	polymerase [Hepatitis B virus]	1288	0.0
gi	452633	emb	CAA53350.1	polymerase [Hepatitis B virus]	1288	0.0
gi	18146695	dbj	BAB82412.1	polymerase [Hepatitis B virus]	1287	0.0
gi	22135710	gb	AAM09049.1	polymerase [Hepatitis B virus]	1287	0.0
gi	11191864	dbj	BAB17948.1	polymerase [Hepatitis B virus]	1286	0.0
gi	59451	emb	CAA48354.1	HBV polymerase [Hepatitis B virus]	1286	0.0
gi	11191848	dbj	BAB17934.1	polymerase [Hepatitis B virus] ...	1286	0.0
gi	22135700	gb	AAM09041.1	polymerase [Hepatitis B virus]	1285	0.0
gi	5019976	gb	AAD37954.1	P protein [Hepatitis B virus]	1281	0.0
gi	22135720	gb	AAM09057.1	polymerase [Hepatitis B virus]	1279	0.0
gi	5019939	gb	AAD37924.1	P protein [Hepatitis B virus]	1276	0.0
gi	1914697	emb	CAA66674.1	polymerase [Hepatitis B virus]	1273	0.0
gi	1914691	emb	CAA66679.1	polymerase [Hepatitis B virus]	1271	0.0
gi	5019970	gb	AAD37949.1	P protein [Hepatitis B virus]	1263	0.0
gi	15425702	dbj	BAB64328.1	polymerase [Hepatitis B virus]	1258	0.0
gi	29124905	gb	AAO63531.1	pol protein [Hepatitis B virus]	1253	0.0
gi	27466464	gb	AAO12704.1	polymerase [Hepatitis B virus]	1248	0.0
gi	27466471	gb	AAO12710.1	polymerase [Hepatitis B virus]	1244	0.0
gi	18252571	gb	AAL66335.1	AF461362_3 polymerase [Hepatitis ...]	1243	0.0
gi	27466511	gb	AAO12597.1	polymerase [Hepatitis B virus]	1239	0.0
gi	27466457	gb	AAO12698.1	polymerase [Hepatitis B virus]	1238	0.0
gi	15211905	emb	CAC51293.1	polymerase [Hepatitis B virus]	1227	0.0
gi	399402	sp	Q02314	DPOL_HPBVP P protein [Includes: DNA-dir...]	1224	0.0
gi	1914708	emb	CAA66684.1	polymerase [Hepatitis B virus]	1220	0.0
gi	27466503	gb	AAO12583.1	polymerase [Hepatitis B virus]	1184	0.0
gi	118867	sp	P12933	DPOL_HPBV4 P protein [Includes: DNA-dir...]	1157	0.0
gi	4468850	emb	CAB38229.1	polymerase [Hepatitis B virus]	1122	0.0
gi	1914719	emb	CAA66694.1	polymerase [Hepatitis B virus]	1101	0.0
gi	9630375	ref	NP_046799.1	polymerase [woolly monkey hepat...]	1049	0.0
gi	1185115	emb	CAA51254.1	DNA polymerase [Hepatitis B virus]	922	0.0
gi	20800461	gb	AAM28642.1	U87746_4 DNA polymerase/reverse t...	910	0.0
gi	21326585	ref	NP_647604.1	P gene product (AA 304-843); c...	907	0.0
gi	4377612	emb	CAA53339.1	polymerase [Hepatitis B virus]	904	0.0
gi	4377613	emb	CAA53338.1	polymerase [Hepatitis B virus]	901	0.0
gi	1549226	dbj	BAA04073.1	ORF [Hepatitis B virus]	898	0.0
gi	9454414	gb	AAF87797.1	polymerase [Hepatitis B virus]	895	0.0
gi	1550614	dbj	BAA04075.1	ORF [Hepatitis B virus]	893	0.0
gi	59409	emb	CAA32399.1	DNA polymerase [Hepatitis B virus]	879	0.0
gi	118894	sp	P03160	DPOL_WHV1 P protein [Includes: DNA-dire...]	727	0.0
gi	9626716	ref	NP_040994.1	A protein [Ground squirrel hepa...]	727	0.0
gi	22256032	ref	NP_671813.1	DNA polymerase [Woodchuck hepa...]	725	0.0
gi	15637595	gb	AAL04547.1	AF410859_1 polymerase [Woodchuck ...]	725	0.0
gi	15637587	gb	AAL04543.1	AF410855_1 type II mutant polymer...	725	0.0

gi	118895	sp	P12899	DPOL_WHV59	P protein [Includes: DNA-dir...	724	0.0
gi	15637597	gb	AAL04548.1	AF410860_1	polymerase [Woodchuck ...	724	0.0
gi	15637599	gb	AAL04549.1	AF410861_1	polymerase [Woodchuck ...	722	0.0
gi	15637593	gb	AAL04546.1	AF410858_1	defective polymerase [...	721	0.0
gi	118898	sp	P17396	DPOL_WHV8I	P protein [Includes: DNA-dir...	721	0.0
gi	15637591	gb	AAL04545.1	AF410857_1	type I mutant polymera...	721	0.0
gi	15637589	gb	AAL04544.1	AF410856_1	type IV mutant polymer...	717	0.0
gi	118897	sp	P06275	DPOL_WHV8	P protein [Includes: DNA-dire...	706	0.0
gi	3582379	dbj	BAA32928.1		pol protein [Hepatitis B virus]	692	0.0
gi	9885813	gb	AAG01539.1	AF291830_2	polymerase [Hepatitis B...	692	0.0
gi	118875	sp	P03158	DPOL_HPBWV	DNA polymerase	680	0.0
gi	9628830	ref	NP_043864.1		polymerase [Arctic ground squir...	669	0.0
gi	8926931	dbj	BAA98025.1		pol protein [Hepatitis B virus]	669	0.0
gi	8926928	dbj	BAA98023.1		pol protein [Hepatitis B virus]	667	0.0
gi	8926925	dbj	BAA98021.1		pol protein [Hepatitis B virus]	667	0.0
gi	8926934	dbj	BAA98027.1		pol protein [Hepatitis B virus]	655	0.0
gi	13345982	gb	AAK19538.1	AF335734_2	polymerase [Hepatitis ...	583	e-166
gi	12083172	gb	AAG48743.1	AF329861_2	polymerase [Hepatitis ...	583	e-166
gi	13345979	gb	AAK19536.1	AF335733_2	polymerase [Hepatitis ...	583	e-166
gi	12083181	gb	AAG48749.1	AF329864_2	polymerase [Hepatitis ...	582	e-166
gi	12083178	gb	AAG48747.1	AF329863_2	polymerase [Hepatitis ...	582	e-165
gi	12083163	gb	AAG48737.1	AF329858_1	polymerase [Hepatitis ...	581	e-165
gi	12083167	gb	AAG48740.1	AF329859_2	polymerase [Hepatitis ...	581	e-165
gi	13345988	gb	AAK19542.1	AF335736_2	polymerase [Hepatitis ...	580	e-165
gi	13345985	gb	AAK19540.1	AF335735_2	polymerase [Hepatitis ...	578	e-164
gi	2982339	gb	AAC06361.1		DNA polymerase [Hepatitis B virus]	568	e-161
gi	336159	gb	AAA46774.1		polymerase protein	566	e-161
gi	118899	sp	P11292	DPOL_WHVW6	P protein [Includes: DNA-dir...	560	e-159
gi	225532	prf		1305266C	gene P	555	e-157
gi	1107586	emb	CAA56892.1		polymerase [Hepatitis B virus]	540	e-153
gi	1107579	emb	CAA56878.1		polymerase [Hepatitis B virus]	538	e-152
gi	1185116	emb	CAA51255.1		HBsAg [Hepatitis B virus]	465	e-130
gi	59414	emb	CAA32405.1		DNA polymerase [Hepatitis B virus]	459	e-129
gi	21326589	ref	NP_647608.1		P gene product, put.DNA polyme...	458	e-128
gi	1321828	emb	CAA96556.1		polymerase [Hepatitis B virus]	441	e-123
gi	5019960	gb	AAD37941.1		P protein [Hepatitis B virus]	440	e-123
gi	329652	gb	AAA69719.1		coat protein [Hepatitis B virus]	433	e-121
gi	329651	gb	AAA69720.1		coat protein [Hepatitis B virus]	429	e-120
gi	27466495	gb	AAO12590.1		polymerase [Hepatitis B virus]	429	e-120
gi	21218028	dbj	BAB96528.1		large S protein [Hepatitis B vi...	413	e-115
gi	1321832	emb	CAA96561.1		polymerase [Hepatitis B virus]	410	e-114
gi	27450190	gb	AAO14552.1	AF460225_1	polymerase [Hepatitis ...	385	e-106
gi	27450188	gb	AAO14551.1	AF460224_1	polymerase [Hepatitis ...	384	e-106
gi	27450192	gb	AAO14553.1	AF460226_1	polymerase [Hepatitis ...	383	e-106
gi	27450198	gb	AAO14556.1	AF460229_1	polymerase [Hepatitis ...	382	e-105
gi	27450196	gb	AAO14555.1	AF460228_1	polymerase [Hepatitis ...	382	e-105
gi	27450194	gb	AAO14554.1	AF460227_1	polymerase [Hepatitis ...	382	e-105
gi	27450200	gb	AAO14557.1	AF460230_1	polymerase [Hepatitis ...	375	e-103
gi	27450202	gb	AAO14558.1	AF460231_1	polymerase [Hepatitis ...	375	e-103
gi	3328370	gb	AAC26832.1		DNA polymerase [Hepatitis B virus]	374	e-103
gi	23380174	gb	AAM83022.1		polymerase [Hepatitis B virus]	373	e-103
gi	23380081	gb	AAM82960.1		polymerase [Hepatitis B virus]	373	e-103
gi	23380171	gb	AAM83020.1		polymerase [Hepatitis B virus]	372	e-102
gi	23380180	gb	AAM83026.1		polymerase [Hepatitis B virus]	370	e-102
gi	23380177	gb	AAM83024.1		polymerase [Hepatitis B virus]	369	e-102
gi	23380072	gb	AAM82954.1		polymerase [Hepatitis B virus]	369	e-101
gi	23380084	gb	AAM82962.1		polymerase [Hepatitis B virus] >...	368	e-101
gi	23380078	gb	AAM82958.1		polymerase [Hepatitis B virus]	368	e-101
gi	23380066	gb	AAM82950.1		polymerase [Hepatitis B virus]	368	e-101
gi	23380111	gb	AAM82980.1		polymerase [Hepatitis B virus]	368	e-101

gi	23380063	gb	AAM82948.1	polymerase [Hepatitis B virus]	367	e-101
gi	23380087	gb	AAM82964.1	polymerase [Hepatitis B virus]	367	e-101
gi	3335627	gb	AAD13662.1	DNA polymerase [Hepatitis B virus]	366	e-101
gi	23380069	gb	AAM82952.1	polymerase [Hepatitis B virus]	366	e-101
gi	23380090	gb	AAM82966.1	polymerase [Hepatitis B virus]	366	e-101
gi	23380060	gb	AAM82946.1	polymerase [Hepatitis B virus]	366	e-101
gi	23380105	gb	AAM82976.1	polymerase [Hepatitis B virus]	365	e-100
gi	23380132	gb	AAM82994.1	polymerase [Hepatitis B virus]	365	e-100
gi	23380093	gb	AAM82968.1	polymerase [Hepatitis B virus]	365	e-100
gi	23380183	gb	AAM83028.1	polymerase [Hepatitis B virus]	>...	365 e-100
gi	23380120	gb	AAM82986.1	polymerase [Hepatitis B virus]	365	e-100
gi	13991875	gb	AAK51541.1	AF363963_2 truncated polymerase [...	365	e-100
gi	23380129	gb	AAM82992.1	polymerase [Hepatitis B virus]	363	e-100
gi	23380186	gb	AAM83030.1	polymerase [Hepatitis B virus]	363	e-100
gi	23380168	gb	AAM83018.1	polymerase [Hepatitis B virus]	363	e-100
gi	23380075	gb	AAM82956.1	polymerase [Hepatitis B virus]	363	e-100
gi	23380123	gb	AAM82988.1	polymerase [Hepatitis B virus]	361	3e-99
gi	23380135	gb	AAM82996.1	polymerase [Hepatitis B virus]	357	4e-98
gi	23380030	gb	AAM82926.1	polymerase [Hepatitis B virus]	351	3e-96
gi	23380021	gb	AAM82920.1	polymerase [Hepatitis B virus]	351	3e-96
gi	23379934	gb	AAM82862.1	polymerase [Hepatitis B virus]	>...	350 8e-96
gi	23380036	gb	AAM82930.1	polymerase [Hepatitis B virus]	349	1e-95
gi	23380156	gb	AAM83010.1	polymerase [Hepatitis B virus]	349	1e-95
gi	23379922	gb	AAM82854.1	polymerase [Hepatitis B virus]	349	1e-95
gi	23379943	gb	AAM82868.1	polymerase [Hepatitis B virus]	349	1e-95
gi	23379967	gb	AAM82884.1	polymerase [Hepatitis B virus]	349	1e-95
gi	23379928	gb	AAM82858.1	polymerase [Hepatitis B virus]	349	1e-95
gi	23380057	gb	AAM82944.1	polymerase [Hepatitis B virus]	348	2e-95
gi	23379925	gb	AAM82856.1	polymerase [Hepatitis B virus]	>...	348 2e-95
gi	23380141	gb	AAM83000.1	polymerase [Hepatitis B virus]	348	2e-95
gi	23380165	gb	AAM83016.1	polymerase [Hepatitis B virus]	348	2e-95
gi	23379997	gb	AAM82904.1	polymerase [Hepatitis B virus]	348	3e-95
gi	23380147	gb	AAM83004.1	polymerase [Hepatitis B virus]	>...	348 3e-95
gi	23379868	gb	AAM82818.1	polymerase [Hepatitis B virus]	>...	348 3e-95
gi	23379958	gb	AAM82878.1	polymerase [Hepatitis B virus]	>...	348 3e-95
gi	23379904	gb	AAM82842.1	polymerase [Hepatitis B virus]	347	3e-95
gi	23379931	gb	AAM82860.1	polymerase [Hepatitis B virus]	347	3e-95
gi	23380159	gb	AAM83012.1	polymerase [Hepatitis B virus]	347	3e-95
gi	23380144	gb	AAM83002.1	polymerase [Hepatitis B virus]	347	3e-95
gi	23379892	gb	AAM82834.1	polymerase [Hepatitis B virus]	347	4e-95
gi	23380000	gb	AAM82906.1	polymerase [Hepatitis B virus]	347	4e-95
gi	23380042	gb	AAM82934.1	polymerase [Hepatitis B virus]	347	4e-95
gi	23380003	gb	AAM82908.1	polymerase [Hepatitis B virus]	347	5e-95
gi	23379886	gb	AAM82830.1	polymerase [Hepatitis B virus]	347	5e-95
gi	23380009	gb	AAM82912.1	polymerase [Hepatitis B virus]	>...	347 6e-95
gi	23380153	gb	AAM83008.1	polymerase [Hepatitis B virus]	347	6e-95
gi	23379973	gb	AAM82888.1	polymerase [Hepatitis B virus]	>...	347 6e-95
gi	23380045	gb	AAM82936.1	polymerase [Hepatitis B virus]	346	7e-95
gi	23379877	gb	AAM82824.1	polymerase [Hepatitis B virus]	>...	346 8e-95
gi	23380138	gb	AAM82998.1	polymerase [Hepatitis B virus]	346	9e-95
gi	23379871	gb	AAM82820.1	polymerase [Hepatitis B virus]	346	9e-95
gi	23380162	gb	AAM83014.1	polymerase [Hepatitis B virus]	346	9e-95
gi	23379946	gb	AAM82870.1	polymerase [Hepatitis B virus]	>...	346 9e-95
gi	23379895	gb	AAM82836.1	polymerase [Hepatitis B virus]	346	1e-94
gi	23379913	gb	AAM82848.1	polymerase [Hepatitis B virus]	345	1e-94
gi	23379916	gb	AAM82850.1	polymerase [Hepatitis B virus]	345	1e-94
gi	23379991	gb	AAM82900.1	polymerase [Hepatitis B virus]	345	1e-94
gi	23380012	gb	AAM82914.1	polymerase [Hepatitis B virus]	345	1e-94
gi	23379889	gb	AAM82832.1	polymerase [Hepatitis B virus]	345	1e-94
gi	23379949	gb	AAM82872.1	polymerase [Hepatitis B virus]	345	1e-94

gi 23380039 gb AAM82932.1	polymerase [Hepatitis B virus]	345	1e-94
gi 23379898 gb AAM82838.1	polymerase [Hepatitis B virus]	345	2e-94
gi 23379880 gb AAM82826.1	polymerase [Hepatitis B virus]	345	2e-94
gi 23380033 gb AAM82928.1	polymerase [Hepatitis B virus]	345	2e-94
gi 23379874 gb AAM82822.1	polymerase [Hepatitis B virus]	344	3e-94
gi 23379979 gb AAM82892.1	polymerase [Hepatitis B virus]	344	3e-94
gi 23380015 gb AAM82916.1	polymerase [Hepatitis B virus]	344	4e-94
gi 23379937 gb AAM82864.1	polymerase [Hepatitis B virus]	344	4e-94
gi 23379940 gb AAM82866.1	polymerase [Hepatitis B virus] >...	343	5e-94
gi 23380054 gb AAM82942.1	polymerase [Hepatitis B virus]	343	7e-94
gi 23379910 gb AAM82846.1	polymerase [Hepatitis B virus]	343	7e-94
gi 23379901 gb AAM82840.1	polymerase [Hepatitis B virus]	343	8e-94
gi 23380018 gb AAM82918.1	polymerase [Hepatitis B virus]	343	9e-94
gi 23380027 gb AAM82924.1	polymerase [Hepatitis B virus]	342	1e-93
gi 1914714 emb CAA66689.1	polymerase [Hepatitis B virus]	342	1e-93
gi 23379982 gb AAM82894.1	polymerase [Hepatitis B virus]	342	2e-93
gi 5019986 gb AAD37962.1	P protein [Hepatitis B virus]	341	2e-93
gi 23380051 gb AAM82940.1	polymerase [Hepatitis B virus]	341	2e-93
gi 27450186 gb AAO14550.1	AF460223_1 polymerase [Hepatitis ...]	341	3e-93
gi 5019949 gb AAD37932.1	P protein [Hepatitis B virus]	341	4e-93
gi 27450210 gb AAO14562.1	AF460235_1 polymerase [Hepatitis ...]	338	2e-92
gi 27450206 gb AAO14560.1	AF460233_1 polymerase [Hepatitis ...]	337	4e-92
gi 1107593 emb CAA56885.1	polymerase [Hepatitis B virus]	336	7e-92
gi 27450208 gb AAO14561.1	AF460234_1 polymerase [Hepatitis ...]	336	8e-92
gi 27450182 gb AAO14548.1	AF460221_1 polymerase [Hepatitis ...]	336	8e-92
gi 27450184 gb AAO14549.1	AF460222_1 polymerase [Hepatitis ...]	335	2e-91
gi 3820918 emb CAA08937.1	polymerase [Hepatitis B virus] >...	332	2e-90
gi 3820942 emb CAA08951.1	polymerase [Hepatitis B virus]	330	5e-90
gi 3820933 emb CAA08947.1	polymerase [Hepatitis B virus]	326	8e-89
gi 3820945 emb CAA08953.1	polymerase [Hepatitis B virus]	326	9e-89
gi 3820930 emb CAA08945.1	polymerase [Hepatitis B virus]	325	3e-88

Query= gi|93080|pir|S20757 DNA-directed DNA polymerase (EC 2.7.7.7) - hepatitis B virus (subtype ayw, patient E)  
 (832 letters)  
 cutoff = 3e-88  
 Database: All non-redundant GenBank CDS  
 translations+PDB+SwissProt+PIR+PRF  
 1,376,942 sequences; 442,405,847 total letters

BLASTP 2.2.5 (Nov-16-2002) (Altschul, S.F., et al., "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402 (1997)) against HBV subtype sequence S20757, cutoff = 3e-88 (to select human sequences).

Table 21: CLUSTALW alignment of 19 HBV polymerase sequences

		10	20	30	40	50	60
1686							
1687							
1688							
1679	S71785						
1680	S47406						
1681	JDVLA1						
1682	S20752						
1693	S67505						
1694	JQ2229						
1695	UNK_494016	-----	-----	-----	-----	-----	-----
1696	UNK_494017	-----	-----	-----	-----	-----	-----
1697	UNK_494015						
1698	UNK_494018						
1699	JDVLVS						
1700	JDVLVR						
1701	T13468						
1702	T13473						
1703	S43491						
1704	S35527						

Prim.cons. MPLSYQHFRKLLLLDDGTEAGPLEEEELPRLADEGLNRRVAEDLNLGNLNVSIPTWTHKVG

		70	80	90	100	110	120
JDVLKS							
JDVLVD							
JDVLJ3							
S71785							
S47406							
JDVLA1							
S20752							
S67505							
JQ2229							
UNK_494016		-----	-----	-----	-----	-----	-----
UNK_494017		-----	-----	-----	-----	-----	-----
UNK_494015							
UNK_494018							
JDVLVS							
JDVLVR							
T13468							
T13473							
S43491							
S35527							

Prim.cons. FTGLYSSTVPVFNPEWQTPSFPHIHLQEDIINRCQQYVGPLTVNEKRRLKLIMPARFYPN

		130	140	150	160	170	180
JDVLKS							
JDVLVD							
JDVLJ3							
S71785							
S47406							
JDVLA1							
S20752							
S67505							

JQ2229 VTKYFPMDKGIKPYYPEHAVNHYFKTRHYLHTLWKAGILYKRESTRSASFCGSPYSWEQE  
 UNK\_494016 -----  
 UNK\_494017 -----  
 UNK\_494015 LTKYLPLDKGIKPYYPEYAVNHYFKTRHYLHTLWKAGILYKRETTTRSASFCGSPYSWEQE  
 UNK\_494018 LTKYLPLDKGIKPYYPEYAVNHYFKTRHYLHTLWKAGILYKRETTTRSASFCGSPYSWEQE  
 JDVLVS LTKYLPLDKGIKPYYPEHAVNHYFKTRHYLHTLWKAGILYKRETTTRSASFCGSPYSWEQE  
 JDVLVR LTKYLPLDKGIKPYYPEHAVNHYFKTRHYLHTLWKAGILYKRETTTRSASFCGSPYSWEQE  
 T13468 LTKYLPLDKGIKPYYPEHAVNHYFKTRHYLHTLWKAGILYKRETTTRSASFCGSPYSWEQE  
 T13473 LTKYLPLDKGIKPYYPEHAVNHYFKTRHYLHTLWKAGILYKRETTTRSASFCGSPYSWEQE  
 S43491 LTKYLPLDKGIKPYYPEHAVNHYFQTRHYLHTLWKAGILYKRETTTRSASFCGSPYSWEQE  
 S35527 LTKYLPLDKGIKPYYPEHAVNHYFKTRHYLHTLWKAGILYKRETTTRSASFCGSPYSWEQE

Prim.cons. LTKYLPLDKGIKPYYPEHAVNHYFQTRHYLHTLWKAGILYKRETTTRSASFCGSPYSWEQE

	190	200	210	220	230	240
JDVLKS	LQHGR	LVIKTSQRHG	DESFC	SQPSG	ILSRSS	VGPCIRSQLKQSR
JDVLVD	LQHGR	LVIKTSQRHG	DESFC	SQSSG	ILSRSS	VGPCIRSQLKQSR
JDVLJ3	LQHGR	LVLQTSTRHG	DKSFRP	QSSGIL	SRSPV	GPCIQSQLRQSR
S71785	LQHG	-----	AESFH	QQSSG	ILSRPP	VGSSSLQSKHRKS
S47406	LQHG	-----	AESFH	QQSSG	ILSRPP	VGSSSLQSKHKS
JDVLA1	LQHG	-----	AESFH	QQSSG	ILSRPP	VGSSSLQSKHKS
S20752	LQHG	-----	AESI	HQQSS	GILSRPP	VGSSSLQSKHRKS
S67505	LQHG	-----	AEPVC	QQSLG	ILPRAS	VGSPVQSQLKQSR
JQ2229	LQHG	STSLNDTKRH	GTESL	CAQSS	GILSRP	SAGSAIQSKFQQSR
UNK_494016	-----	-----	-----	-----	-----	-----
UNK_494017	-----	-----	-----	-----	-----	-----
UNK_494015	LQHGR	LVFQTSTRHG	DESFC	SQSSG	ILSRSP	VGPCVRSQKQSR
UNK_494018	LQHGR	LVFQTSTRHG	DESFC	SQSSG	ILSRSP	VGPCVRSQKQSR
JDVLVS	LQHGR	LVFQTSTRHG	DESFC	SQSSG	ILSRSP	VGPCVRSQKQSR
JDVLVR	LQHGR	LVFQTSTRHG	DESFC	SQSSG	ILSRSP	VGPCVRSQKQSR
T13468	LQHGR	LVFQTSTRHG	DESFC	SQSSG	ILSRSP	VGPCVRSQKQSR
T13473	LQHGR	LVFQTSTRHG	DKSFC	SQSSG	ILSRSP	VGPCVRSQKQSR
S43491	LQHGR	LVFQTSTRHG	DESFC	SQSSG	ILSRSP	VGPCVRSQKQSR
S35527	LQHGR	LVFQTSTRHG	DESFC	SQSSG	ILSRSP	VGPCVRSQKQSR

Prim.cons. LQHGRLVFQTSTRHGDESFCSSGILSRSPVGPCVRSQKQSRGLQPQQGSLARGQQG

	250	260	270	280	290	300
JDVLKS	RSGS	IRARVHPSTR	RCFG	VEPSG	SGHVD	PSVNNSSSCL
JDVLVD	RSGS	IRAKAHPSTR	RYFG	VEPSG	SGHIDH	SVNNSSSCL
JDVLJ3	SGS	IRAGIHSTP	WGT	VGVEP	SSSGH	TNCANSSSCL
S71785	RSWS	IRAGIHPTA	RRPFG	VEPSG	SGHNTN	LASKSASCIYQ
S47406	RSWS	IRAGIHPTA	RRPFG	VEPSG	SGHNTN	LASKSASCLYQ
JDVLA1	RSWS	IRAGIHPTA	RRPFG	VEPSG	SGHTTN	LASKSASCLH
S20752	WSWS	IRAGTHPTA	RRPFG	VEPSG	SGHTTH	RASKSASCLYQ
S67505	RSGS	IRARVHSTT	RRSFR	VELSG	SGSNH	IASTSSSCRH
JQ2229	RSGR	LSRVHTPTR	WPAG	VEPS	SSTRCV	NNLASRSASCF
UNK_494016	-----	-----	-----	-----	-----	-----
UNK_494017	-----	-----	-----	-----	-----	-----
UNK_494015	RSGS	IWSRVHPTT	RRPFG	VEPSG	SGHIDN	TASSTSSCLH
UNK_494018	RSGS	IWSRVHPTT	RRPFG	VEPSG	SGHIDN	TASSTSSCLH
JDVLVS	RSGS	IRARVPPTT	RRSFG	VEPSG	SGHIDN	RASSTSSCLH
JDVLVR	RSGS	IRARVHPTT	RRSFG	VEPSG	SGHIDN	SASSTSSCLH
T13468	RSGS	IRARVHPTT	RRSFG	VEPSG	SGHIDN	SARSASSCLH
T13473	RIGS	IRARVHPTT	RRSFG	VEPSG	SGHIDN	SASSPSSCLH
S43491	RSGS	IRARVHPTT	RRPFG	VEPSG	SGHIDN	SASSASSCFH
S35527	RSGR	LRARVHPTT	RRSFG	VEPSG	SGHIDN	SASSSSSCLH



Prim.cons. RSGSIRARVHPTTRRPFQVPEPSGSGHIDNSASSSSSCLHQSAVRKTAYSHLSTSKRQSSS

	310	320	330	340	350	360
JDVLKS	G	H	A	V	E	F
JDVLVD	G	H	A	V	E	F
JDVLJ3	G	N	A	V	E	L
S71785	G	H	A	V	E	L
S47406	G	H	A	V	E	L
JDVLA1	G	H	A	V	E	L
S20752	G	R	A	V	E	L
S67505	G	H	E	V	E	L
JQ2229	G	N	A	V	E	L
UNK_494016	----	L	H	N	I	P
UNK_494017	----	L	H	N	I	P
UNK_494015	G	H	A	V	E	-----
UNK_494018	G	H	A	V	E	-----
JDVLVS	G	H	A	V	E	L
JDVLVR	G	H	A	V	E	L
T13468	G	H	A	V	E	L
T13473	G	H	A	V	E	L
S43491	G	H	A	V	E	L
S35527	G	H	A	V	E	L

Prim.cons. GHAVELHNIPPSSARSQSEGP2FSCWWLQFRNSKPCSDYCLSHIVNLLEDWGPCTEHGEH

	370	380	390	400	410	420
JDVLKS	H	I	R	I	P	R
JDVLVD	H	I	R	I	P	R
JDVLJ3	R	I	R	T	P	R
S71785	H	I	R	I	P	R
S47406	H	I	R	I	P	R
JDVLA1	H	I	R	I	P	R
S20752	H	I	R	I	P	R
S67505	H	I	R	I	P	R
JQ2229	Y	I	R	T	P	R
UNK_494016	N	I	R	I	P	R
UNK_494017	N	I	R	I	P	R
UNK_494015	-----	-----	-----	-----	-----	-----
UNK_494018	-----	-----	-----	-----	-----	-----
JDVLVS	N	I	R	I	P	R
JDVLVR	N	I	R	I	P	R
T13468	L	V	D	K	N	P
T13473	D	K	N	P	H	N
S43491	N	I	R	I	P	R
S35527	N	I	R	I	P	R

Prim.cons. HIRIPRTPARVTGGVFLVDKNPHNTTESRLVVDFSQFSRGSTRVSWPKFAVPNLQSLTNL

	430	440	450	460	470	480
JDVLKS	L	S	S	N	L	S
JDVLVD	L	S	S	N	L	S
JDVLJ3	L	S	S	D	L	S
S71785	L	S	S	N	L	S
S47406	L	S	S	N	L	S
JDVLA1	L	S	S	N	L	S
S20752	L	S	S	N	L	S
S67505	L	S	S	N	L	S

JQ2229	LSSNLSWLSLDVSAAFYHPLHPAAMPHELLVGSSGLSRYVARLSSTSRIHQHGHTLQNL
UNK_494016	LSSNLSWLSLDVSAAFYHIPLHPAAMPHELLVGSSGLPRYVARLSSTSRNINYQHGTMQNL
UNK_494017	LSSNLSWLSLDVSAAFYHIPLHPAAMPHELLVGSSGLPRYVARLSSTSRNINYQHGTMQNL
UNK_494015	-----
UNK_494018	-----
JDVLVS	LSSNLSWLSLDVSAAFYHIPLHPAAMPHELLVGSSGLPRYVARLSSTSRNINHQHGTMQDL
JDVLVR	LSSNLSWLSLDVSAAFYHIPLHPAAMPHELLVGSSGLPRYVARLSSTSRNINHQHGTMQDL
T13468	LSSNLSWLSLDVSAAFYHIPLHPAAMPHELLVGSSGLPRYVARLSSTSRNINXQHGTMQDL
T13473	LSSNLSWLSLDVSAAFYHIPLHPAAMPHELLVGSSGLPRYVARLSSTSRNINXQHGTMQDL
S43491	LSSNLSWLSLDVSAAFYHIPLHPAAMPHELLVGSSGLQRYVARLSSTSRNINYQHGTMQDL
S35527	LSSNLSWLSLDVSAAFYHIPLHPAAMPHELLVGSSGLPRYVARLSSTSRNINYQHGTMQDL

Prim.cons. LSSNLSWLSLDVSAAFYHIPLHPAAMPHELLVGSSGLSRYVARLSSTSRNINHQHGTMQNL

	490	500	510	520	530	540
JDVLKS	HDSCSRQLYVSLMMLLYKTYGWLHLHYSHPIVLGFRKIPMGVGLSPFLLAQFTSAICSVVR					
JDVLVD	HDSCSRQLYVSLMMLLYKTYGWLHLHYSHPIVLGFRKIPMGVGLSPFLLAQFTSAICSVVR					
JDVLJ3	HDSCSRNLYVSLMMLLYKTYGRKLHLHYSHPIILGFRKIPMGVGLSPFLLAQFTSAICSVVR					
S71785	HDYCSRNLVSLLLLLYQTFGRKLHLHYSHPIILGFRKIPMGVGLSPFLLAQFTSAICSVVR					
S47406	HDYCSRNLVSLLLLLYQTFGRKLHLHYSHPIILGFRKIPMGVGLSPFLLAQFTSAICSVVR					
JDVLA1	HDSCSRNLYVSLLLLLYQTFGRKLHLHYSHPIILGFRKIPMGVGLSPFLLAQFTSAICSVVR					
S20752	HDSCSRQLYVSLMMLLYQNFQWLHLHYSHPIVLGFRKIPMGVGLSPFLLAQFTSAICSVVR					
S67505	HDHCSRNLVSLMMLLYKTFGRKLHLHYSHPIVLGFRKIPMGVGLSPFLLAQFTSSICSVVR					
JQ2229	HNSCTRNLVSLLLLLYQTLGRKLHLHYSHPIILGFRKIPMGVGLSPFLLAQFTSAICSVVR					
UNK_494016	HDSCSRNLYVSLLLLLYKTFGRKLHLHYSHPIILGFRKIPMGVGLSPFLLAQFTSAICSVVR					
UNK_494017	HDSCSRNLYVSLLLLLYKTFGRKLHLHYSHPIILGFRKIPMGVGLSPFLLAQFTSAICSVVR					
UNK_494015	-----					
UNK_494018	-----					
JDVLVS	HDSCSRNLYVSLLLLLYKTFGRKLHLHYSHPIILGFRKIPMGVGLSPFLLAQFTSAICSVVR					
JDVLVR	HDSCSRNLYVSLLLLLYKTFGRKLHLHYSHPIILGFRKIPMGVGLSPFLLAQFTSAICSVVR					
T13468	HESCSRNLVSLLLLLYKTFGRKLHLHYSHPIILGFRKIPMGVGLSPFLLAQFTSAICSVVR					
T13473	HDSCSKHLYVSLLLLLYKTFGRKLHLHYSHPIIXLGFRKIPMGVGLSPFLLAQFTSAICSVVR					
S43491	HDSCSKHLYVSLLLLLYKTFGRKLHLHYSHPIILGFRKIPMGVGLSPFLLAQFTSAICSVVR					
S35527	HDSCSRNLYVSLLLVYKTFGRKLHLHYSHPIILGFRKIPMGVGLSPFLLAQFTSAICSVVR					

Prim.cons. HDSCSRNLYVSLLLLLYKTFGRKLHLHYSHPIILGFRKIPMGVGLSPFLLAQFTSAICSVVR

	550	560	570	580	590	600
JDVLKS	RAFPHCLAFSYMDDVVLGAKSVQHREFLYTAVTNFLLSLGIHLNPNKTKRWGYSLNFMGY					
JDVLVD	RAFPHCLAFSYMDDVVLGAKSVQHRESLYTAVTNFLLSLGIHLNPNKTKRWGYSLNFMGY					
JDVLJ3	RAFPHCLAFSYMDDVVLGAKSVQHLESLEYAAVTNFLLSLGIHLNPNKTKRWGYSLNFMGY					
S71785	RAFPHCLAFSYMDDVVLGAKSVQHLESLEYAAVTNFLLSLGIHLNPNKTKRWGYSLNFMGY					
S47406	RAFPHCLAFSYMDDVVLGAKSVQHLESLEYAAVTNFLLSLGIHLNPNKTKRWGYSLNFMGY					
JDVLA1	RAFPHCLAFSYMDDVVLGAKTVHHLESLEYAAVTNFLLSLGIHLNPNKTKRWGYSLNFMGY					
S20752	RAFPHCLAFSYMDDVVLGAKSVQHLESLEYAAVTNFLLSLGIHLNPNKTKRWGYSLNFMGY					
S67505	RAFPHCLAFSYMDDLVLGAKSVQHLESLEYAAVTNFLLSLGIHLNPNKTKRWGYSLNFMGY					
JQ2229	RAFPHCLAFSYMDDLVLGAKSVQHLESLEYAAVTNFLLSVGIHLNNTSKTKRWGYSLNFMGY					
UNK_494016	RAFPHCLAFSYMDDVVLGAKSVQHLESLEYAAVTNFLLSLGIHLNPNKTKRWGYSLNFMGY					
UNK_494017	RAFPHCLAFSYMDDVVLGAKSVQHLESLEYAAVTNFLLSLGIHLNPNKTKRWGYSLNFMGY					
UNK_494015	-----					
UNK_494018	-----					
JDVLVS	RAFPHCLAFSYMDDVVLGAKSVQHLESLEYAAVTNFLLSLGIHLNPNKTKRWGYSLNFMGY					
JDVLVR	RAFPHCLAFSYMDDVVLGAKSVQHLESLEYAAVTNFLLSLGIHLNPNKTKRWGYSLNFMGY					
T13468	RAFPHCLAFSYMDDVVLGAKSVQHLESLEYAAVTNFLLSLGIHLNPNKTKRWGYSLNFMGY					
T13473	RAFPHCLAFSYMDDVVLGAKSVQHLESLEYAAVTNFLLSLGIHLNPNKTKRWGYSLNFMGY					
S43491	RAFPHCLAFSYMDDVVLGAKSVQHLESLEYAAVTNFLLSLGIHLNPNKTKRWGYSLNFMGY					
S35527	RAFPHCLAFSYMDDVVLGAKSVQHLESLEYAAVTNFLLSLGIHLNPNKTKRWGYSLNFMGY					

Prim.cons.      RAFPHCLAFSYMDDVVLGAKSVQHLESFLTAVTNFLLSLGIHLNPNKTKRWGYSLNFMGY

	610	620	630	640	650	660
JDVLKS	VIGSWGTL	PQDHIVQKIKHC	FRKLPVNR	PIDWKVCQ	RIVGLLGFA	APFTQCGYPALMPLY
JDVLVD	IIGSWGTL	PQDHIVQKIKHC	FRKLPVNR	PIDWKVCQ	RIVGLLGFA	APFTQCGYPALMPLY
JDVLJ3	VIGSWGTL	PQEHIVLKIKQC	FRKLPVNR	PIDWKVCQ	RIVGLLGFA	APFTQCGYPALMPLY
S71785	VIGSYGSL	PQDHIIQKIKEC	FRKLPINR	PIDWKVCQ	RIVGLLGFA	APFTQCGYPALMPLY
S47406	VIGCYGSL	PQDHIIQKIKEC	FRKLPVNR	PIDWKVCQ	RIVGLLGFA	APFTQCGYPALKPLY
JDVLA1	VIGCYGSL	PQDHIIQKIKEC	FRKLPVNR	PIDWKVCQ	RIVGLLGFA	APFTQCGYPALMPLY
S20752	VIGCYGSL	PQEHIIQKIKEC	FRKVPVNR	PIDWKVCQ	RIVGLLGFA	APFTQCGYPALMPLY
S67505	IIGSWGSL	PQDHIVQKIKQC	FRKLPVNR	PIDWKVCQ	RIVGLLGFA	APFTQCGYPALMPLY
JQ2229	VIGSWGSL	PQDHIVHKIKEC	FRKLPVNR	PIDWKVCQ	RIVGLLGFA	APFTQCGYPALMPLY
UNK_494016	VIGSWGTL	PQEHIVQKLKQC	FRKLPVNR	PIDWKVCQ	RIVGLLGFA	APFTQCGYPALMPLY
UNK_494017	VIGSWGTL	PQEHIVQKLKQC	FRKLPVNR	PIDWKVCQ	RIVGLLGFA	APFTQCGYPALMPLY
UNK_494015	-----	-----	-----	-----	-----	-----
UNK_494018	-----	-----	-----	-----	-----	-----
JDVLVS	VIGSWGTL	PQEHIVLKIKQC	FRKLPVNR	PIDWKVCQ	RIVGLLGFA	APFTQCGYPALMPLY
JDVLVR	VIGSWGTL	PQEHIVLKLKQC	FRKLPVNS	PIDWKVCQ	RIVGLLGFA	APFTQCGYPALMPLY
T13468	VIGSWGTL	PQEHIVQKIKQC	FRKLPVNR	PIDWKVCQ	XIVGLLGFA	APFTQCGYPALMPLY
T13473	VIGSWGTL	PQDHIVQKLKQC	FRKLPVNR	PIDWKVCQ	RIVGLLGFA	APFTQCGYPALMPLY
S43491	VIGSWGTL	PQEHIVQKLKQC	FRKLPVNR	PIDWKVCQ	RIVGLLGFA	APFTQCGYPALMPLY
S35527	VIGSWGTL	PQEHIVLKLKQC	FRKLPVNR	PIDWKVCQ	RIVGLLGFA	APFTQCGYPALMPLY

Prim.cons.      VIGSWGTLPQEHIVQKIKQCFRKLPVNRPIDWKVCQRIVGLLGFAAPFTQCGYPALMPLY

	670	680	690	700	710	720
JDVLKS	ACIQAKQA	FTFSPTYKA	FLSKQYMN	LYPVARQR	PGLCQVFAD	ATPTGWGLAIGHQRM
JDVLVD	ACIQAKQA	FTFSPTYKA	FLSKQYMN	LYPVARQR	PGLCQVFAD	ATPTGWGLAIGHQRM
JDVLJ3	ACIQAKQA	FTFSPTYKA	FLNKQYLN	LYPVARQR	PGLCQVFAD	ATPTGWGLAIGHQRM
S71785	ACIQSKQA	FTFSPTYKA	FLCKQYLN	LYPVARQR	PGLCQVFAD	ATPTGWGLVMGHQRM
S47406	ACIQSKQA	FTFSPTYKA	FLCKQYLN	LYPVARQR	PGLCQVFAD	ATPTGWGLVMGHQRM
JDVLA1	ACIQSKQA	FTFSPTYKA	FLCKQYLN	LYPVARQR	PGLCQVFAD	ATPTGWGLVMGHQRM
S20752	ACIQFKQA	FTFSPTYKA	FLCKQYLN	LYPVARQR	PGLCQVFAD	ATPTGWGLGMGHQRM
S67505	ACIQAKQA	FTFSPTYKA	FLRTQYLT	LYPVARQR	PGLCQVFAD	ATPTGWGLAIGHQRM
JQ2229	ACITAKQA	AFVFSPTYK	AFCKQYMN	LYPVARQR	PGLCQVFAD	ATPTGWGLAIGHQRM
UNK_494016	ACIQSKQA	FTFSPTYKA	FLCKQYLN	LYPVARQR	SGLCQVFAD	ATPTGWGLAIGHRRM
UNK_494017	ACIQSKQA	FTFSPTYKA	FLCKQYLN	LYPVARQR	SGLCQVFAD	ATPTGWGLAIGHRRM
UNK_494015	-----	-----	-----	-----	-----	-----
UNK_494018	-----	-----	-----	-----	-----	-----
JDVLVS	ACIQSKQA	FTFSPTYKA	FLCKQYLN	LYPVARRT	ALCQVFAD	ATPTGWGLAIGHRRM
JDVLVR	ACIQSKQA	FTFSPTYKA	FLCKQYLN	LYPVARQR	SGLCQVFAD	ATPTGWGLAIGHRRM
T13468	ACIQAKQA	FTFSPTYKA	FLCKQYLN	LYPVARQR	SGLCQVFAD	ATPTGWGLAIGHRRM
T13473	ACIQSKQA	FTFSPTYKA	FLCKQYLN	LYPVARQR	SGLCQVFAD	ATPTGWGLAIGHRRM
S43491	ACIQSKQA	FTFSPTYKA	FLCKQYLN	LYPVARQR	SGLCQVFAD	ATPTGWGLAIGHQRM
S35527	ACIQSKQA	FTFSPTYKA	FLCQYLN	LYPVARQR	SGLCQVFGD	ATPTGWGLAIGHRRM

Prim.cons.      ACIQSKQAFTFSPTYKAFLCKQYLNLYPVARQRPGLCQVFADATPTGWGLAIGHQRM

	730	740	750	760	770	780
JDVLKS	FVAPLP	PIHTAELLA	ACFARS	SRGAKL	IGTDNS	VVLSRKYTSFPWLLG
JDVLVD	FVAPLP	PIHTAELLA	ACFARS	SRGAKL	IGTDNS	VVLSRKYTSFPWLLG
JDVLJ3	FVSPLP	PIHTVELLA	ACFARS	SRGAKL	IGTDNS	VVLSRKYTSFPWLLG
S71785	FLAPLP	PIHTAELLA	ACFARS	SGANIL	IGTDNS	VVLSRKYTSFPWLLG
S47406	FLAPLP	PIHTAELLA	ACFARS	SGANIL	IGTDNS	VVLSRKYTSFPWLLG
JDVLA1	FQAPLP	PIHTAELLA	ACFARS	SGANIL	IGTDNS	VVLSRKYTSFPWLLG
S20752	FSAPLP	PIHTAELLA	ACFARS	SGANIL	IGTDNS	VVLSRKYTSFPWLLG
S67505	FVAPLP	PIHTAELLA	ACFARS	SGANI	IGTDNS	VVLSPKYTSFPWLLG

JQ2229	FVAPLPIHTAELLAACFARSRSRGATLIGTDNSVVLSRKYTSFPWLLGCAANWILRGTSFV
UNK_494016	FVAPLPIHTAELLAACFARSRSRGAKLIGTDNSVVLSRKYTSFPWLLGCAANWILRGTSFV
UNK_494017	FVAPLPIHTAELLAACFARSRSRGAKLIGTDNSVVLSRKYTSFPWLLGCAANWILRGTSFV
UNK_494015	-----
UNK_494018	-----
JDVLVS	VAPLPIHTAELLAACFARSRSRGAKLIGTDNSVVLSRKYTSFPWLLGCAANWILRGTYFVY
JDVLVR	FVAPLPIHTAELLAACFARSRSRGAKLIGTDNSVVLSRKYTSFPWLLGCAANWILRGTSFV
T13468	FVAPLPIHTAELLAACFARSRSRGAKLIGTDNSVVLSRKYTSFPWLLGCAANWILRGTSFV
T13473	FVAPLPIHTAELLAACFARSRSRGAKLIGTDNSVVLSRKYTSFPWLLGCAANWILRGTSFV
S43491	FVAPLPIHTAELLAACFARSRSRGATLIGTDNSVVLSRKYTSFPWLLGCAANWILRGTSFV
S35527	FVAPLPIHTAELLAACFARSRSRGAKLIGTDNSVVLSRKYTSFPWLLGCAANWILRGTSFV

Prim.cons. FVAPLPIHTAELLAACFARSRSRGAKLIGTDNSVVLSRKYTSFPWLLGCAANWILRGTSFV

	790	800	810	820	830	840
JDVLKS	YVPSALNPADDPSRGRLGLSRPLLRLPFQPTTGRTSLYAVSPSVPSHLPVRVHFASPLHV					
JDVLVD	YVPSALNPADDPSRGRLGLSRPLLRLPFQPTTGRTSLYAVSPSVPSHLPVRVHFASPLHV					
JDVLJ3	YVPSALNPADDPSRGRLGLYRPLLRLPYRPTTGRTSLYADSPSVPSHLPDRVHFASPLHV					
S71785	YVPSALNPADDPSRGRLGIFRPLLRLPFRPTTGRTSLYADSPSVPSHLPVRVHFASPLHV					
S47406	YVPSALNPADDPSRGRLGLSRPLLRLPFRPTTGRTSLYADSPSVPSHLPDRVHFASPLHV					
JDVLA1	YVPSALNPADDPSRGRLGLSRPLLRLPFRPTTGRTSLYADSPSVPSHLPDRVHFASPLHV					
S20752	YVPSALNPADDPSRGRLGLSRPLLCLPFRPTTGRTSLYADSPSVPSHLPDRVHFASPLHV					
S67505	YVPSALNPADDPSRGRLGLYRPLLRLPFRPTTGRTSLYAVSPSVPSHLPVRVHFASPLHV					
JQ2229	YVPSALNPADDPSRGRLGLYRPLLRLPFQPTTGRTSLYADSPSVPSHLPDRVHFASPLHV					
UNK_494016	YVPSALNPADDPSRGRLGLYRPLLHLRPFRTTGRTSLYAVSPSVPSHLPDRVHFASPLHV					
UNK_494017	YVPSALNPADDPSRGRLGLYRPLLHLRPFRTTGRTSLYAVSPSVPSHLPDRVHFASPLHV					
UNK_494015	-----					
UNK_494018	-----					
JDVLVS	VPSALNPADDPSRGRLGLIRPLLHLRFRPTTGRTSLYAVSPSVPSHLPDRVHFASPLHVA					
JDVLVR	YVPSALNPADDPSRGRLGLYRPLLRLPFRPTTGRTSLYAVSPSVPSHLPDRVHFASPLHV					
T13468	YVPSALNPADDPSRGRLGLYRPLLHLRPFRTTGRTSLYAVSPSVPSHLPDRVHFASPLHV					
T13473	YVPSALNPADDPSRGRLGLYRPLLHLRPFRTTGRTSLYAVSPSVPSHLPDRVHFASPLHV					
S43491	YVPSALNPADDPSRGRLGLYRPLLRLSFRPTTGRTSLYAVSPSVPSHLPDRVHFASPLHV					
S35527	YVPSALNPADDPSRGRLGLYRPLLHLRPFQPTTGRTSLYAVSPSVPSHLPVRVHFASPLHV					

Prim.cons. YVPSALNPADDPSRGRLGLYRPLLRLPFRPTTGRTSLYAVSPSVPSHLPDRVHFASPLHV

JDVLKS	AWRPP
JDVLVD	AWRPP
JDVLJ3	AWRPP
S71785	AWRPP
S47406	AWRPP
JDVLA1	AWRPP
S20752	AWRPP
S67505	AWRPP
JQ2229	AWRPP
UNK_494016	AWRPP
UNK_494017	AWRPP
UNK_494015	-----
UNK_494018	-----
JDVLVS	WRPP-
JDVLVR	AWRPP
T13468	AWRPP
T13473	AWRPP
S43491	AWRPP
S35527	AWRPP

Prim.cons. AWRPP

CLUSTALW alignment of 19 HBV polymerase sequences representing the sybtypes adw (4), ayw (5), ayr (4) and adr (6) (NPS@: Network Protein Sequence Analysis, TIBS Vol. 25, No 3 (291):147-150, Combet C., Blanchet C., Geourjon C. and Deléage G. (March 2000))

CLUSTALW options used :

```
endgaps=1
gapdist=8
gapext=0.2
gapopen=10.0
hgapresidues=GPSNDQERK
ktuple=1
matrix=gonnet
maxdiv=30
outorder=aligned
pairgap=3
score=percent
topdiags=5
type=PROTEIN
window=5
```

Table 22. HCV Multiple Sequence Alignment  
GCG Multiple Sequence File.  
Written by Omiga 1.1

Name: BEBE1	SEQ ID NO: 1706	Len: 3052	Check: 2605	Weight: 1.00
Name: D89815	SEQ ID NO: 1707	Len: 3052	Check: 9655	Weight: 1.00
Name: ED43type_4	SEQ ID NO: 1708	Len: 3052	Check: 4987	Weight: 1.00
Name: HC_C2	SEQ ID NO: 1710	Len: 3052	Check: 6273	Weight: 1.00
Name: HC_G9	SEQ ID NO: 1709	Len: 3052	Check: 217	Weight: 1.00
Name: HCU16326	SEQ ID NO: 1711	Len: 3052	Check: 5854	Weight: 1.00
Name: HCV_H_CMR	SEQ ID NO: 1712	Len: 3052	Check: 4932	Weight: 1.00
Name: HCV_J1	SEQ ID NO: 1713	Len: 3052	Check: 4947	Weight: 1.00
Name: HCV_J483	SEQ ID NO: 1714	Len: 3052	Check: 2553	Weight: 1.00
Name: HCV_J8	SEQ ID NO: 1715	Len: 3052	Check: 9778	Weight: 1.00
Name: HCV_JK1	SEQ ID NO: 1716	Len: 3052	Check: 4917	Weight: 1.00
Name: HCV_JS	SEQ ID NO: 1717	Len: 3052	Check: 3982	Weight: 1.00
Name: HCV_K1_R1	SEQ ID NO: 1718	Len: 3052	Check: 9084	Weight: 1.00
Name: HCV_K1_R2	SEQ ID NO: 1719	Len: 3052	Check: 47	Weight: 1.00
Name: HCV_K1_R3	SEQ ID NO: 1720	Len: 3052	Check: 1630	Weight: 1.00
Name: HCV_K1_S1	SEQ ID NO: 1721	Len: 3052	Check: 3578	Weight: 1.00
Name: HCV_K1_S2	SEQ ID NO: 1722	Len: 3052	Check: 9909	Weight: 1.00
Name: HCV_K1_S3	SEQ ID NO: 1723	Len: 3052	Check: 9508	Weight: 1.00
Name: HCV_L2	SEQ ID NO: 1724	Len: 3052	Check: 4175	Weight: 1.00
Name: HCV_N	SEQ ID NO: 1725	Len: 3052	Check: 1702	Weight: 1.00
Name: HCV12083	SEQ ID NO: 1726	Len: 3052	Check: 7564	Weight: 1.00
Name: HCV1480	SEQ ID NO: 1727	Len: 3052	Check: 5620	Weight: 1.00
Name: HCVPOLYP	SEQ ID NO: 1728	Len: 3052	Check: 2663	Weight: 1.00
Name: HD_1	SEQ ID NO: 1729	Len: 3052	Check: 4040	Weight: 1.00
Name: HPCCGAA	SEQ ID NO: 1730	Len: 3052	Check: 5414	Weight: 1.00
Name: HPCFG	SEQ ID NO: 1731	Len: 3052	Check: 7119	Weight: 1.00
Name: HPCGENANTI	SEQ ID NO: 1732	Len: 3052	Check: 9591	Weight: 1.00
Name: HPCGENOM	SEQ ID NO: 1733	Len: 3052	Check: 2009	Weight: 1.00
Name: HPCHUMR	SEQ ID NO: 1734	Len: 3052	Check: 4863	Weight: 1.00
Name: HPCJ	SEQ ID NO: 1735	Len: 3052	Check: 3553	Weight: 1.00
Name: HPCJCG	SEQ ID NO: 1736	Len: 3052	Check: 6658	Weight: 1.00
Name: HPCJK046	SEQ ID NO: 1737	Len: 3052	Check: 436	Weight: 1.00
Name: HPCJK049	SEQ ID NO: 1738	Len: 3052	Check: 9796	Weight: 1.00
Name: HPCJTA	SEQ ID NO: 1739	Len: 3052	Check: 2902	Weight: 1.00
Name: HPCJTB	SEQ ID NO: 1740	Len: 3052	Check: 4237	Weight: 1.00
Name: HPCK3A	SEQ ID NO: 1741	Len: 3052	Check: 2180	Weight: 1.00
Name: HPCPLYPRE	SEQ ID NO: 1742	Len: 3052	Check: 6557	Weight: 1.00
Name: HPCPOLP	SEQ ID NO: 1743	Len: 3052	Check: 1218	Weight: 1.00
Name: HPCPP	SEQ ID NO: 1744	Len: 3052	Check: 3845	Weight: 1.00
Name: HPCUNKCD	SEQ ID NO: 1745	Len: 3052	Check: 6214	Weight: 1.00
Name: MKC1A	SEQ ID NO: 1746	Len: 3052	Check: 1615	Weight: 1.00
Name: NDM59	SEQ ID NO: 1747	Len: 3052	Check: 9717	Weight: 1.00
Name: NZLI	SEQ ID NO: 1748	Len: 3052	Check: 2255	Weight: 1.00
Name: SA13	SEQ ID NO: 1749	Len: 3052	Check: 9158	Weight: 1.00
Name: Th580	SEQ ID NO: 1750	Len: 3052	Check: 37	Weight: 1.00
Name: Type_3a_CB	SEQ ID NO: 1751	Len: 3052	Check: 7958	Weight: 1.00
Name: TypeV_D	SEQ ID NO: 1752	Len: 3052	Check: 303	Weight: 1.00
Name: VN004	SEQ ID NO: 1753	Len: 3052	Check: 3873	Weight: 1.00
Name: VN235	SEQ ID NO: 1754	Len: 3052	Check: 7756	Weight: 1.00
Name: VN405	SEQ ID NO: 1755	Len: 3052	Check: 7249	Weight: 1.00

SEQ ID NO		1			50
1706	BEBE1	MSTNPKPQRK	TKRNTNRRPQ	DVKFPGGGQI	VGGVYLLPRR GPRLGVRRAAR
1707	D89815	MSTNPKPQRK	TKRNTNRRPQ	DVKFPGGGQI	VGGVYLLPRR GPRLGVRATR
1708	ED43type_4	MSTNPKPQRK	TKRNTNRRPM	DVKFPGGGQI	VGGVYLLPRR GPRLGVRATR

<u>1709</u>	HC_C2	MSTNPKPQRK	TKRNTNRRPQ	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
<u>1710</u>	HC_G9	MSTNPKPQRK	TKRNTNRRPQ	DVKFPGGGQI	VGGVYLLPRR	GPRVGVRATR
<u>1711</u>	HCU16326	MSTNPKPQRK	TKRNTNRRPQ	DIKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
<u>1712</u>	HCV_H_CMR	MSTNPKPQRK	TKRNTNRRPQ	DVEFPGGGQI	VGGVYLLPRR	GPRLGVRATR
<u>1713</u>	HCV_J1	MSTIPKPQRK	TKRNTNRRPQ	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
<u>1714</u>	HCV_J483	MSTNPKPQRK	TKRNTNRRPQ	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
<u>1715</u>	HCV_J8	MSTNPKPQRK	TKRNTNRRPQ	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
<u>1716</u>	HCV_JK1	MSTNPKPQRK	TKRNTNRRPQ	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
<u>1717</u>	HCV_JS	MSTNPKPQRK	TKRNTNRRPQ	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
<u>1718</u>	HCV_K1_R1	MSTNPKPQRK	TKRNTNRRPQ	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
<u>1719</u>	HCV_K1_R2	MSTNPKPQRK	TKRNTNRRPQ	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
<u>1720</u>	HCV_K1_R3	MSTNPKPQRK	TKRNTNRRPQ	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
<u>1721</u>	HCV_K1_S1	MSTNPKPQRK	TKRNTNRRPQ	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
<u>1722</u>	HCV_K1_S2	MSTNPKPQRK	TKRNTNRRPQ	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
<u>1723</u>	HCV_K1_S3	MSTNPKPQRK	TKRNTNRRPQ	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
<u>1724</u>	HCV_L2	MSTNPKPQRK	TKRNTNRRPQ	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
<u>1725</u>	HCV_N	MSTNPKPQRK	TKRNTNRRPQ	EVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
<u>1726</u>	HCV12083	MSTLPPKPQRK	TKRNTNRRPM	DVKFPGGGQI	VGGVYLLPRK	GPRLGVRATR
<u>1727</u>	HCV1480	MSTNPKPQRK	TKRNTNRRPQ	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
<u>1728</u>	HCVPOLYP	MSTNPKPQRK	TKRNTNRRPQ	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
<u>1729</u>	HD_1	MSTNPKPQRK	TKRNTNRRPQ	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
<u>1730</u>	HPCCGAA	MSTNPKPQRK	TKRNTNRRPQ	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
<u>1731</u>	HPCFG	MSTLPPKPQRK	TKRNTLRRPK	NVKFPAGGQI	VGGVYLLPRR	GPRLGVRATR
<u>1732</u>	HPCGENANTI	MSTNPKPQRK	TKRNTNRRPQ	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
<u>1733</u>	HPCGENOM	MSTNPKPQRK	TKRNTNRRPQ	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
<u>1734</u>	HPCHUMR	MSTNPKPQRK	TKRNTNRRPQ	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
<u>1735</u>	HPCJ	MSTNPKPQRK	TKRNTNRRPQ	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
<u>1736</u>	HPCJCG	MSTNPKPQRK	TKRNTNRRPQ	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
<u>1737</u>	HPCJK046	MSTNPKPQRK	TKRNTNRRPQ	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
<u>1738</u>	HPCJK049	MSTLPPKPQRI	TKRNTNRRPQ	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
<u>1739</u>	HPCJTA	MSTNPKPQRK	TKRNTYRRPQ	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
<u>1740</u>	HPCJTB	MSTNPKPQRK	TKRNTYRRPQ	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
<u>1741</u>	HPCK3A	MSTLPPKPQRK	TKRNTIIRRPQ	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
<u>1742</u>	HPCPLYPRE	MSTNPKPQKK	NKRNTNRRPQ	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
<u>1743</u>	HPCPOLP	MSTNPKPQRK	TKRNTNRRPQ	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
<u>1744</u>	HPCPP	MSTNPKPQRK	IKRNTNRRPQ	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
<u>1745</u>	HPCUNKCD	MSTNPKPQRK	TKRNTNRRPQ	DIKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
<u>1746</u>	MKC1A	MSTNPKPQRK	IKRNTNRRPQ	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
<u>1747</u>	NDM59	MSTNPKPQRK	TKRNTSRRPQ	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
<u>1748</u>	NZLI	MSTLPPKPQRK	TKRNTIIRRPQ	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
<u>1749</u>	SA13	MSTNPKPQRK	TKRNTNRRPQ	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
<u>1750</u>	Th580	MSTLPPKPQRK	TKRNTNRRPM	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
<u>1751</u>	Type_3a_CB	MSTLPPKPQRK	TKRNTIIRRPQ	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
<u>1752</u>	TypeV_D	MSTLPPKPQRK	TKRNTIIRRPQ	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
<u>1753</u>	VN004	MSTLPPKPQRK	TKRNTNRRPM	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
<u>1754</u>	VN235	MSTLPPKPQKR	NQRNTNRRPQ	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
<u>1755</u>	VN405	MSTLPPKPQRK	TKRNTNRRPM	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR

	51				100
BEBE1	KTSEERSQPRG	RRQPIPKDRR	STGKSWGRPG	YPWPLYRNEG	LGWAGWLLSP
D89815	KTSEERSQPRG	RRQPIPKARR	PEGRTWAQPG	YPWPLYGNEG	LGWAGWLLSP
ED43type_4	KTSEERSQPRG	RRQPIPKARR	PEGRSWAQPG	YPWPLYGNEG	CGWAGWLLSP
HC_C2	KTSEERSQPRG	RRQPIPKARR	PEGRAWAQPG	YPWPLYGNEG	MGWAGWLLSP
HC_G9	KTSEERSQPRG	RRQPIPKARR	PEGRSWAQPG	YPWPLYGNEG	CGWAGWLLSP
HCU16326	KTSEERSQPRG	RRQPIPKARR	PEGRAWAQPG	YPWPLYGNEG	LGWAGWLLSP
HCV_H_CMV	KTSEERSQPRG	RRQPIPKARR	PEGRTWAQPG	YPWPLYGNEG	CGWAGWLLSP
HCV_J1	KTSEERSQPRG	RRQPIPKVRR	PEGRTWAQPG	YPWPLYGNEG	CGWAGWLLSP
HCV_J483	KTSEERSQPRG	WRQPIPKARR	PEGRAWAQPG	YPWPLYGNEG	LGWAGWLLSP
HCV_J8	KTSEERSQPRG	RRQPIPKDRR	STGKSWGKPG	YPWPLYGNEG	CGWAGWLLSP
HCV_JK1	KTSEERSQPRG	RRQPIPKARQ	PEGRAWAQPG	YPWPLYGNEG	LGWAGWLLSP
HCV_JS	KTSEERSQPRG	RRQPIPKARR	PEGRTWAQPG	YPWPLYGNEG	MGWAGWLLSP
HCV_K1_R1	KTSEERSQPRG	RRQPIPKARR	PEGRAWAQPG	YPWPLYGNEG	LGWAGWLLSP
HCV_K1_R2	KTSEERSQPRG	RRQPIPKARQ	PEGRAWAQPG	YPWPLYGNEG	MGWAGWLLSP
HCV_K1_R3	KTSEERSQPRG	RRQPIPKVRR	SEGRTWAQPG	YPWPLYGNEG	LGWAGWLLSP
HCV_K1_S1	KTSEERSQPRG	RRQPIPKARR	PEGRAWAQPG	YPWPLYGNEG	LGWAGWLLSP
HCV_K1_S2	KTSEERSQPRG	RRQPIPKARQ	PEGRAWAQPG	YPWPLYGNEG	MGWAGWLLSP
HCV_K1_S3	KTSEERSQPRG	RRQPIPKVRR	SEGRTWAQPG	YPWPLYGNEG	LGWAGWLLSP
HCV_L2	KTSEERSQPRG	RRQPIPKARQ	PEGRAWAQPG	YPWPLYANEG	LGWAGWLLSP
HCV_N	KTSEERSQPRG	RRQPIPKARR	PEGRAWAQPG	YPWPLYGNEG	MGWAGWLLSP
HCV12083	KTSEERSQPRG	RRQPIPKARQ	PQGRHWAQPG	YPWPLYGSEG	CGWAGWLLSP
HCV1480	KNSERSQPRG	RRQPIPKARR	PTGRSWGQPG	YPWPLYANEG	LGWAGWLLSP
HCVPOLYP	KTSEERSQPRG	RRQPIPKARR	PEGRAWAQPG	YPWPLYGNEG	MGWAGWLLSP
HD_1	KTSEERSQPRG	RRQLIPKARQ	PEGRSWAQPG	YPWPLYGNEG	MGWAGWLLSP
HPCCGAA	KTSEERSQPRG	RRQPIPKARR	PEGRTWAQPG	YPWPLYGNEG	CGWAGWLLSP
HPCFG	KTSEERSQPRG	RRQPTPKARP	REGRSWAQPG	YPWPLYGNEG	CGWAGWLLPP
HPCGENANTI	KTWERSQPRG	RRQPIPKARQ	PEGRAWAQPG	YPWPLYGNEG	LGWAGWLVSP
HPCGENOM	KTSEERSQPRG	RRQPIPKARR	PEGRTWAQPG	YPWPLYGNEG	FGWAGWLLSP
HPCHUMR	KTSEERSQPRG	RRQPIPKARR	PEGRTWAQPG	YPWPLYGNEG	LGWAGWLLSP
HPCJ	KTSEERSQPRG	RRQPIPKARR	PEGRTWAQPG	YPWPLYGNEG	MGWAGWLLSP
HPCJCG	KTSEERSQPRG	RRQPIPKARR	PEGRTWAQPG	YPWPLYGNEG	MGWAGWLLSP
HPCJK046	KTSEERSQPRG	RRQPIPKARR	QTGRAWGQPG	YAWPLYGNEG	CGWAGWLLSP
HPCJK049	KTSEERSQPRS	RRQPIPRARR	TEGRSWAQPG	YPWPLYGNEG	CGWAGWLLSP
HPCJTA	KTSEERSQPRG	RRQPIPKARR	PEGRAWAQPG	YPWPLYGNEG	LGWAGWLLSP
HPCJTB	KTSEERSQPRG	RRQPIPKARR	PEGRAWAQPG	YPWPLYGNEG	LGWAGWLLSP
HPCK3A	KTSEERSQPRG	RRKPIPKARR	SEGRSWAQPG	YPWPLYGNEG	CGWAGWLLSP
HPCPLYPRE	KTSEERSQPRG	RRQPIPKARR	PEGRTWAQPG	YPWPLYGNEG	CGWAGWLLSP
HPCPOLP	KTSEERSQPRG	RRQPIPKDRR	STGKSWGKPG	YPWPLYGNEG	LGWAGWLLSP
HPCPP	KTSEERSQPRG	RRQPIPKARQ	PEGRAWAQPG	YPWPLYGNEG	LGWAGWLLSP
HPCUNKCD	KTSEERSQPRG	RRQPIPKARR	PEGRAWAQPG	YPWPLYGNEG	LGWAGWLLSP
MKC1A	KTSEERSQPRG	RRQPIPKARQ	PEGRAWAQPG	YPWPLYGNEG	LGWAGWLLSP
NDM59	KTSEERSQPRG	RRQPIPKDRR	STGKSWGKPG	YPWPLYGNEG	LGWAGWLLSP
NZLI	KTSEERSQPRG	RRQPIPKARR	SEGRSWAQPG	YPWPLYGNEG	CGWAGWLLSP
SA13	KTSEERSQPRG	RRQPIPKARQ	PTGRSWGQPG	YPWPLYANEG	LGWAGWLLSP
Th580	KTSEERSQPRG	RRQPIPKARP	SQGRTWGQPG	YPWPLYGNEG	CGWAGWLMSP
Type_3a_CB	KTSEERSQPRR	RRQPIPKARQ	SGGRSWAQPG	YPWPLYGNEG	CGWAGWLLSP
TypeV_D	KTSEERSQPRG	RRQPIPKARR	SEGRSWAQPG	YPWPLYGNEG	CGWAGWLLSP
VN004	KTSEERSQPRG	RRQPIPKARQ	PIGRSWGQPG	YPWPLYGNEG	CGWAGWLLSP
VN235	KTSEERSQPRG	RRQPIPKARR	QTGRTWAQPG	YPWPLYGNEG	CGWMGWLLSP
VN405	KTSEERSQPRG	RRQPIPKARQ	SQGRHWAQPG	YPWPLYGNEG	CGWAGWLLSP
	101				150
BEBE1	RGSRPSWGGS	DPRHKSRNLG	KVIDTLTCGF	ADLMGYIPVV	GAPVGGVARA
D89815	RGSRPSWGPN	DPRRRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGGAARA
ED43type_4	RGSRPSWGPN	DPRGRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPVGSVARA
HC_C2	RGSRPSWGPN	DPRRRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGGAARA
HC_G9	RGSRPSWGGS	DPRRRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGGAARA
HCU16326	RGSRPSWGPT	DPRRKSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGVARA



HCV_H_CM	RGSRPSWGPT	DPRRRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGAARA
HCV_J1	RGSRPSWGPT	DPRRRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGAARA
HCV_J483	RGSRPSWGPT	DPRRRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGAARA
HCV_J8	RGSRPTWGPT	DPRHRSRNLG	RVIDTITCGF	ADLMGYIPVV	GAPVGGVARA
HCV_JK1	YGSRPRWGPT	DPRRRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGAARA
HCV_JS	RGSRPNWGPT	DPRRRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGAARA
HCV_K1_R1	RGSRPSWGPT	DPRRRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGAARA
HCV_K1_R2	RGSRPSWGPT	DPRRRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGAARA
HCV_K1_R3	RGSRSSWGPT	DPRRRSRNLG	KVIDTLTCGF	ADLMGYIPVV	GPPLGGVARA
HCV_K1_S1	RGSRPSWGPT	DPRRRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGAARA
HCV_K1_S2	RGSRPSWGPT	DPRRRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGAARA
HCV_K1_S3	RGSRSNWGPT	DPRRRSRNLG	KVIDTLTCGF	ADLMGYIPVV	GPPLGGVARA
HCV_L2	RGSRPSWGPT	DPRRRSRNLG	KVIDTPTCGF	ADLMGYIPLV	GAPLGGAARA
HCV_N	RGSRPSWGPT	DPRRRSRNLG	KVIDTLTCGL	ADLMGYVPLV	GGPLGGVARA
HCV12083	RGSRPHWGPN	DPRRRSRNLG	KVIDTLTCGF	ADLMWYIPVV	GAPLGGAARA
HCV1480	RSSRPNWGPN	DPRRKSPNLG	RVIHTLTCGF	PHLMGYIPLV	GGPVGGVSRA
HCVPOLYP	RGSRPSWGPT	DPRRRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGAARA
HD_1	RGSRPSWGPT	DPRRRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGAARA
HPCCGAA	RGSRPSWGPT	DPRRRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGAARA
HPCFG	RGSRPSWGQ	DPRRRSRNLG	KVIDTLTCGF	ADLMGYIPLI	GAPVGGVARA
HPCGENANTI	RGSRPNWGPT	DPRRRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGAARA
HPCGENOM	RGSRPSWGPT	DPRRRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGAARA
HPCJ	RGSRPSWGPT	DPRRRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGAARA
HPCJCG	RGSRPSWGPT	DPRRRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGAARA
HPCJK046	RGSRPTWGPN	DPRRRSRNLG	KVIDTLTCGL	ADLMGYIPVI	GGPLGGVAAA
HPCJK049	RGSRPSWGPN	DPRRRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPVGGVARA
HPCJTA	RGSRPSWGPT	DPRRRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGAARA
HPCJTB	RGSRPSWGPT	DPRRRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGAARA
HPCK3A	RGSRPNWAPN	DPRRRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGAARA
HPCPLYPRE	RGSRPSWGPT	DPRRRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGAARA
HPCPOLP	RGSRPSWGPN	DPRHRSRNLG	KVIDTLTCGF	ADLMGYIPVV	GAPLGGAARA
HPCPP	RGSRPSWGPT	DPRRRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGAARA
HPCUNKCD	RGSRPSWGPT	DPRRKSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGAARA
MKC1A	RGSRPSWGPT	DPRRRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGAARA
NDM59	RGSRPSWGPT	DPRHRSRNLG	KVIDTLTCGF	ADLMGYIPVV	GAPLGGAARA
NZLI	RGSRPSWGPN	DPRRRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPVGGVARA
SA13	RGSRPNWGPN	DPRRKSRNLG	KVIDTLTCGF	ADLMGYIPLV	GGPVGGVARA
Th580	RGSRPSWGPN	DPRRRSRNLG	KVIDTLTCGL	ADLMGYIPVV	GGPLGGVAAA
Type_3a_CB	RGSRPSWGPN	DPRRRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPVGGVARA
TypeV_D	RGSRPSWGQ	DPRRRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPVGGVARA
VN004	RGSRPNWGPN	DPRRRSRNLG	KVIDTLTCGL	ADLMGYIPVL	GGPLGGVAAA
VN235	RGSRPHWGPN	DPRRRSRNLG	KVIDTLTCGF	ADLMGYIPVV	GAPLGGAARA
VN405	RGSRPNWGPN	DPRRRSRNLG	KVIDTLTCGF	ADLMGYIPVV	GAPLGGAARA

	151			200	
BEBE1	LAHGVRVLED	GINYATGNLP	GCSFSIFLLA	LLSCISVPVS	AVEVRNTSSS
D89815	LAHGVRVLED	GVNYATGNLP	GCSFSIFLLA	LLSCLTIPAS	AYEVRNVSGI
ED43type_4	LAHGVRVLED	GINYATGNLP	GCSFSIFLLA	LLSCLTVPAS	AVNYRNVSGI
HC_C2	LAHGVRVLED	GVNYATGNLP	GCSFSIFLLA	LLSCLTIPAS	AYEVRNASGV
HC_G9	LAHGVRVLED	GVNYATGNLP	GCSFSIFLLA	LLSCLTVPAS	AVGVRNNSGV
HCU16326	LAHGVRVLED	GVNYATGNLP	GCSFSIFLLA	LLSCLTTPVS	AYEVRNASGM
HCV_H_CM	LAHGVRVLED	GVNYATGNLP	GCSFSIFLLA	LLSCLTVPAS	AYQVRNSSGL
HCV_J1	LAHGVRVLED	GVNYATGNLP	GCSFSIFLLA	LLSCLTVPAS	AYQVRNSTGL
HCV_J483	LAHGVRVLED	GVNYATGNLP	GCSFSIFLLA	LLSCLTIPAS	AYEVRNVSGI
HCV_J8	LAHGVRVLED	GINYATGNLP	GCSFSIFLLA	LLSCVTVPVS	AVEVRNISSS
HCV_JK1	LAHGVRVLED	GVNYATGNLP	GCSFSIFLLA	LLSCLTVPVS	TYEVRNVSGV
HCV_JS	LAHGVRVLED	GVNYATGNLP	GCSFSIFLLA	LLSCLTTPAS	AYEVRNVSGI
HCV_K1_R1	LAHGVRVLED	GVNYATGNLP	GCSFSIFLLA	LLSCLTIPAS	AYEVCNASGL
HCV_K1_R2	LAHGVRVLED	GVNYATGNLP	GCSFSIFLLA	LLSCLTIPAS	AYEVRNASGV

HCV_K1_R3	LAHGVRVLEV	GVNYATGNLP	GCSFSIFLLA	LLSCLTIPAS	AYEVRNVSGV
HCV_K1_S1	LAHGVRVLED	GVNYATGNLP	GCSFSIFLLA	LLPCLTIPAS	AYEVCNASGL
HCV_K1_S2	LAHGVRVLED	GVNYATGNLP	GCSFSIFLLA	LLSCLTIPAS	AYEVRNVASGV
HCV_K1_S3	LAHGVRVLEV	GVNYATGNLP	GCSFSIFLLA	LLSCLTIPAS	AYEVRNVSGV
HCV_L2	LAHGVRVLED	SVNYATGNLP	GCSFSIFLLA	LLSCLTVPAS	AYEVRNVSGI
HCV_N	LAHGVRVLED	GVNYATGNMP	GCSFSIFLLA	LLSCLTVPAS	AHEVRNVASGV
HCV12083	LAHGVRRAIED	GINYATGNLP	GCSFSIFLLA	LLSCLTTPAS	ALTYGNSSGL
HCV1480	LAHGVRVLED	GINYATGNLP	GCPFSIFVLA	LLWCLTVPAS	AVPYRNASGV
HCVPOLYP	LAHGVRVLED	GVNYATGNLP	GCSFSIFLLG	LLSCLTIPAS	AYEVRNVSGV
HD_1	LAHGVRVLEG	GVNYATGNLP	GCSFSIFLLA	LLSCLTIPAS	AYEVRNVSGV
HPCCGAA	LAHGVRVLED	GVNYATGNLP	GCSFSIFLLA	LLSCLTVPAS	AYQVRNSSGL
HPCFG	LAHGVRRALED	GVNYATGNLP	GCSFSIFLLA	LFSCLTCPAS	SLEYRNASGL
HPCGENANTI	LAHGVRVLED	GVNYATGNLP	GCSFSIFLLA	LLSCLTIPAS	AYEVHNVSGI
HPCGENOM	LAHGVRVLED	GVNYATGNLP	GCSFSIFLLA	LLSCLTTPAS	AYEVRNVSGI
HPCHUMR	LAHGVRVLED	GVNYATGNLP	GCSFSIFLLA	LLSCLTTPAS	AYEVHNVSGI
HPCJ	LAHGVRVLED	GVNYATGNLP	GCSFSIFLLA	LLSCLTVPVS	AYEVRNVSGG
HPCJCG	LAHGVRVLED	GVNYATGNLP	GCSFSIFLLA	LLSCLTIPAS	AYEVRNVSGI
HPCJK046	LAHGVRRAVED	GVNYATGNLP	GCSFSIFLLA	LLSCLTVPAS	AVNYANKSGI
HPCJK049	LAHGVRRALED	GINFATGNLP	GCSFSIFLLA	LLSCLLTPTA	GLEVRNASGL
HPCJTA	LAHGVRVLED	GVNYATGNLP	GCSFSIFLLA	LLSCLTIPAS	AYQVRNASGL
HPCJTB	LAHGVRVLED	GVNYATGNLP	GCSFSIFLLA	LLSCLTIPAS	AYQVRNRSGL
HPCK3A	LAHGVRRALED	GINFATGNLP	GCSFSIFLLA	LFSCLIHPAA	SLEWRNTSGL
HPCPLYPRE	LAHGVRVLED	GVNYATGNLP	GCSFSIFLLA	LLSCLTVPAS	AYQVRNSTGL
HPCPOLP	LAHGVRVLED	GVNFATGNLP	GCSFSIFLLA	LLSCITTPVS	AAEVKNISTG
HPCPP	LAHGVRVLED	GVNYATGNLP	GCSFSIFLLA	LLSCLTIPAS	AYQVRNASGV
HPCUNKCD	LAHGVRVLED	GVNYATGNLP	GCSFSIFLLA	LLSCLTTPVS	AYEVRNASGM
MKC1A	LAHGVRVLED	GVNYATGNLP	GCSFSIFLLA	LLSCLTIPAS	AYQVRNASGV
NDM59	LAHGVRVLED	GVNYATGNLP	GCSFSIFLLA	LLSCITVPVS	AVQVKNISDS
NZLI	LAHGVRRALED	GINFATGNLP	GCSFSIFLLA	LFSCLIHPAA	SLEWRNTSGL
SA13	LAHGVRVLED	GVNYATGNLP	GCSFSIFILA	LLSCLTVPTS	AVPYRNASGV
Th580	LAHGVRRAIED	GINYATGNLP	GCSFSIFILA	LLSCLTTPAS	ALTYGNSSGL
Type_3a_CB	LAHGVRRALED	GINFATGNLP	GCSFSIFLLA	LFSCLIHPAA	SLEWRNTSGL
TypeV_D	LAHGVRRALED	GINFATGNLP	GCSFSIFLLA	LFSCLIHPAA	SLEWRNTSGL
VN004	LAHGVRRAIED	GVNYATGNLP	GCSFSIFLLA	LLSCLTTPAS	AIQVRNASGI
VN235	LAHGVRRAVED	GINYATGNLP	GCSFSIFLLA	LLSCLTTPAS	AVHYANKSGI
VN405	LAHGVRRAIED	GINYATGNLP	GCSFSIFLLA	LLSCLTTPAS	AVHYRNISGI

	201			250	
BEBE1	YMATNDCSNS	SIVWQLEGAV	LHTPGCVPCV	KTGN.KSRCW	VPVTPNIAIN
D89815	YHVTNDCSNS	SIVYEAADVI	MHAPGCVPCV	RENN.SSRCW	VALTPTLAAR
ED43type_4	YHVTNDCPNS	SIVYEAADHMI	MHLPGCVPCV	REGN.QSRCW	VALTPTVAAP
HC_C2	YHVTNDCSNS	SIVYEAADMI	MHNPGCVPCV	RENN.SSRCW	VALTPTLAAR
HC_G9	YHVTNDCPNA	SVVYETENLI	MHLPGCVPYV	REGN.ASRCW	VSLSPTVAAR
HCU16326	YHVTNDCSNS	SIVYEAADMI	MHTPGCVPCV	REDN.SSRCW	VALTPTLAAR
HCV_H_CMR	YHVTNDCPNS	SIVYEAADAI	LHTPGCVPCV	REGN.ASRCW	VAVTPTVATR
HCV_J1	YHVTNDCPNS	SIVYEAADAI	LHTPGCVPCV	REGN.VSRCW	VAMTPTVATR
HCV_J483	YHVTNDCSNS	SIVYEAADMI	MHTPGCVPCV	REDN.SSRCW	VALTPTLAAR
HCV_J8	YYATNDCSNN	SITWQLTDAV	LHLPGCVPCV	NDNG.TLHCW	IQVTPNVAVK
HCV_JK1	YHVTNDCSNS	SIVYEAADMI	MHTPGCVPCV	REGN.SSRCW	VALTPTLAAR
HCV_JS	YHVTNDCSNS	SIVYEAADII	MHTPGCVPCV	REKN.ISRCW	VALTPTLAAR
HCV_K1_R1	YHVTNDCSNS	SIVYEAQDMI	MHTPGCVPCV	RENN.SSRCW	VALTPTLAAR
HCV_K1_R2	YHVTNDCSNA	SIVYEAADMI	MHTPGCVPCV	REAN.SSRCW	VALTPTLAAR
HCV_K1_R3	YHVTNDCSNS	SIVYEAEDVI	MHTPGCLPCV	RENN.SSRCW	VALTPTLAGR
HCV_K1_S1	YHVTNDCSNS	SIVYEAEDMI	MHTPGCVPCV	RENN.SSRCW	VALTPTLAAR
HCV_K1_S2	YHVTNDCSNA	SIVYEAADMI	MHTPGCVPCV	REAN.SSRCW	VALTPTLAAR
HCV_K1_S3	YHVTNDCSNS	SIVYEAEDVI	MHTPGCLPCV	RENN.SSRCW	VALTPTLAGR
HCV_L2	YHVTNDCSNS	SIVYEAADLI	MHTPGCVPCV	REAN.SSRCW	VALTPTLAAR
HCV_N	YHVTNDCSNS	SIVFEAADLI	MRTPGCVPCV	REGN.SSRCW	VALTPTLAAR
HCV12083	YHLTNDCSNS	SIVLEADAMI	LHLPGCLPCV	RVGN.QSTCW	HAVSPTLATP
HCV1480	YHVTNDCPNS	SIVYEAADNLI	LHAPGCVPCV	LEDN.VSRCW	VQITPTLSAP

HCVPOLYP	YHVTNDCSNA	SIVYEADMI	MHVPGCVPCV	RVDN.SSRCW	VALTPTLAAR
HD_1	YHVTNDCSNS	SIVYETADMI	MHTPGCVPCV	REDN.SSRCW	VALTPTLAAR
HPCCGAA	YHVTNDCPNS	SVVYEADAI	LHTPGCVPCV	REGN.ASRCW	VAVTPTVATR
HPCFG	YLLTNDCSNR	SIVYEADDVI	LHLPGCVPCV	ETDNNNTSCW	TPISPTVAVK
HPCGENANTI	YHVTNDCSNS	SIVYEADMI	MHTPGCVPCV	RENN.SSRCW	VALTPTLAAR
HPCGENOM	YHVTNDCSNS	SIVYEADLI	MHTPGCVPCV	REGN.SSRCW	VALTPTLAAR
HPCHUMR	YHVTNDCSNA	SIVYEADLI	MHTPGCVPCV	REGN.SSRCW	VALTPTLAAR
HPCJ	YHVTNDCSNS	SIVYEADVI	MHTPGCVPCV	RENN.SSRCW	VALTPTLAAR
HPCJCG	YHVTNDCSNS	SIVYEADMI	MHTPGCVPCV	RESN.FSRCW	VALTPTLAAR
HPCJK046	YHLTNDPCNS	SMVYEAEAI	LHLPGCVPCI	RTGN.QSRCW	TPATPTLAIP
HPCJK049	YTVTNDCSNG	SIVYEAGDVI	LHLPGCIPCV	RLNN.ASKCW	TPVSPTVAVS
HPCJTA	YHVTNDCSNS	SIVYEAGMI	MHTPGCVPCV	RENN.ASRCW	VALTPTLAAR
HPCJTB	YHVTNDCSNS	SIVYEAGMI	MHTPGCVPCV	RENN.VSRCW	VALTPTLAAR
HPCK3A	YVLTNDCSNS	SIVYEADDVI	LHTPGCIPCV	QDGN.TSTCW	TPVTPTVAVR
HPCPLYPRE	YHVTNDCPNS	SIVYEADAI	LHTPGCVPCV	REGN.ASRCW	VAMTPTVATR
HPCPOLP	YMTNDCNTD	SITWQLQAAV	LHVP GCVPCE	KVGN.TSRCW	IPVSPNVAVQ
HPCPP	YHVTNDCSNS	SIVYEADVI	MHTPGCVPCV	RENN.SSRCW	VALTPTLAAR
HPCUNKCD	YHVTNDCSNS	SIVYEADMI	MHTPGCVPCV	REDN.SSRCW	VALTPTLAAR
MKC1A	YHVTNDCSNS	SIVYEADVI	MHTPGCVPCV	RENN.SSRCW	VALTPTLAAR
NDM59	YMTNDCSND	SITWQLQAAV	LHVP GCVPCE	KMGN.ISRCW	IPVSPNVAVQ
NZLI	YVLTNDCSNS	SIVYEADDVI	LHTPGCVPCV	QDGN.TSTCW	TPVTPTVAVR
SA13	YHVTNDCPNS	SIVYEADLI	LHAPGCVPCE	RQGN.VSRCW	VQITPTLSAP
Th580	YHLTND CPRS	SIVLEAEAMI	LHLAGCVPCV	RAGN.ISRCW	HPVSPTLAVP
Type_3a_CB	YVLTNDCSNS	SIVYEADDVI	LHTPGCVPCV	QNDN.ISTCW	TPVTPTVAVR
TypeV_D	YVLTNDCSNS	SIVYEADDVI	LHTPGCVPCV	QDGN.TSTCW	TPVTPTVAVR
VN004	YHLTNDCSNN	SIVFEAETII	LHLPGCVPCI	KVGN.GSRCW	LSVSPTLAVP
VN235	YHLTND CPNS	SIVYEAEDFI	MHLPGCVPCI	KSGN.GSSCW	LPATLTIAVP
VN405	YHLTND CPNS	SIIYEADNII	MHTPGCVPCV	KTGN.KSQCW	VPVAPTLAVA

	251			300	
	BEBE1	QPGALTGLR	AHIDVIVMSA	TLCSALYVGD	VCGALMIAAQ
	D89815	NASVPTTTLR	RHVDLLVGTA	AFCSAMYVGD	LCGSVFLISQ
ED43type_4	YIGAPLESRL	SHVDLMVGAA	TVCSGLYIGD	LCGGLFLVGQ	MFSFRPRRHW
HC_C2	NASVPTTTLR	RHVDLLVGAA	ALCSAMYVGD	LCGSVFLVSQ	LFTFSPRRHE
HC_G9	DSRPVPSEVR	RRVDSIVGAA	AFCSAMYVGD	LCGSIFLVGQ	IFTFSPRRHW
HCU16326	NASVPTTTLR	RHVDLLVGVA	AFCSAMYVGD	LCGSVFLVSQ	LFTFSPRRHE
HCV_H_CMR	DGKLPTTQLR	RHIDLLVGS	TLCSALYVGD	LCGSVFLVGQ	LFTFSPRRHW
HCV_J1	DGKLPTTQLR	RHIDLLVGS	TLCSALYVGD	LCGSVFLIGQ	LFTFSPRRHW
HCV_J483	NASVPTTTLR	RHVDLLVGAA	AFCSAMYVGD	LCGSVFLVSQ	LFTFSPRRHE
HCV_J8	HRGALTRSLR	THVDMIVMAA	TACSALYVGD	VCGAVMILSQ	AFMVSPQRHN
HCV_JK1	NSSIPTTTLR	RHVDLLVGAA	ALCSAMYVGD	LCGSVFLVSQ	LFTFSPRRYE
HCV_JS	NISVPTATIR	RHVDLLVGTA	AFCSAMYVGD	LCGSVFLVSQ	LFTFSPRRHE
HCV_K1_R1	NASIPTTTLR	RHVDLLVGAA	AFCSAMYVGD	LCGSVFLVSQ	LFTFSPRRYE
HCV_K1_R2	NSSVPTTTLR	RHVDLLVGAA	AFCSAMYVGD	LCGSVFLVSQ	LFTFSPRRHE
HCV_K1_R3	NSSIPTTTLR	RHVDLLVGAA	AFCSAMYVGD	LCGSVFLVSQ	LFTFSPRRYE
HCV_K1_S1	NASIPTTTLR	RHVDLLVGAA	AFCSAMYVGD	LCGSVFLVSQ	LFTFSPRRYE
HCV_K1_S2	NSSVPTTTLR	RHVDLLVGAA	AFCSAMYVGD	LCGSVFLVSQ	LFTFSPRRHE
HCV_K1_S3	NSSIPTTTLR	RHVDLLVGAA	AFCSAMYVGD	LCGSVFLVSQ	LFAFSPRRYE
HCV_L2	DSSIPTATIR	RHVDLLVGAA	AFCSAMYVGD	LCGSVFLVSQ	LFTFSPRLHQ
HCV_N	NATIHTTTLR	HHVDLLVGAA	ALCSAMYVGD	LCGSVFLVSQ	LFTFSPRRHA
HCV12083	NASTPATGFR	RHVDLLAGAA	VVCSSLYIGD	LCGSLFLAGQ	LFAFQPRRHW
HCV1480	SFGAVTALLR	RAVDYLAGGA	AFCSALYVGD	ACGALSIVGQ	MFTYKPRQHT
HCVPOLYP	NASVPTTAIR	RHVDLLVGAA	TFCSAMYVGD	LCGSVFLVAQ	LFTFSPRRHE
HD_1	NASIPTTTLR	RHVDLLVGAA	AFCSAMYVGD	LCGSVFLVSQ	LFTFSPRRHA
HPCCGAA	DGKLPTTQLR	RHIDLLVGS	TLCSALYVGD	LCGSVFLVGQ	LFTFSPRRHW
HPCFG	HPGVTTASIR	NHVNMLVAPP	TLCSALYVED	AFGAVSLVGQ	AFTFRPRQHK
HPCGENANTI	NNSVPTATIR	RHVDLLVGAA	AFCSAMYVGD	LCGSVFLVSQ	LFTFSPRRYE
HPCGENOM	NATIPTATVR	RHVDLLVGAA	AFSSAMYVGD	LCGSVFLVSQ	LFTFSPRRYE
HPCHUMR	NVTIPTTTLR	RHVDLLVGAA	AFCSAMYVGD	LCGSVFLVSQ	LFTFSPRRHV
HPCJ	NTTVPTTTLR	RHVDLLVGTA	AFCSAMYVGD	LCGSVFLVSQ	LFTFSPRRHE

HPCJCG	NSSIPTTTIR	RHVDLLVGAA	ALCSAMYVGD	LCGSVFLVSQ	LFTFSPRRYE
HPCJK046	NSTVPASGFR	QHIDLMVGAA	ALCSAMYLG	LCGGVFLVGQ	LFTFRPRIHQ
HPCJK049	RPGAATASLR	THVDMMVGAA	TLCSALYVGD	LCGALFLVGQ	GFSWRHRQHW
HPCJTA	NTSIPTTTIR	RHVDLLVGAA	AFCSAMYVGD	LCGSVFLVSQ	LFTFSPRRYE
HPCJTB	NTSIPTTTIR	RHVDLLVGAA	AFCSAMYVGD	LCGSVFLVSQ	LFTFSPRRYE
HPCK3A	YVGATTASIR	SHVDLLVGAG	TMCSALYVGD	MCGPVFLVGQ	AFTFRPRRHR
HPCPLYPRE	DGKLPAQQLR	RHIDLLVGSA	TLCSALYVGD	LCGSVFLVGQ	LFTFSPRRHW
HPCPOLP	QPGALTQQLR	THIDMVVMSA	TLCSALYVGD	LCGGVMLAAQ	MFIVSPQHHW
HPCPP	NSSIPTTTIR	RHVDLLVGAA	ALCSAMYVGD	FCGSVFLVSQ	LFTFSPRRYE
HPCUNKCD	NASVPTTTLR	RHVDLLVGVA	AFCSAMYVGD	LCGSVFLVSQ	LFTFSPRRHE
MKC1A	NSSIPTTTIR	RHVDLLVGAA	ALCSAMYVGD	FCGSVFLVSQ	LFTFSPRRYE
NDM59	RPGALTQQLR	AHIDMVVMSA	TLCSALYVGD	LCGGVMLAAQ	MFIVSPQHHH
NZLI	YVGATTASIR	SHVDLLVGAA	TMCSALYVGD	MCGAVFLVGQ	AFTFRPRRHQ
SA13	SLGAVTAPLR	RAVDYLAGGA	ALCSALYVGD	ACGAVFLVGQ	MFTYSPRRHN
Th580	NASVPASGFR	KHVDLLAGAA	VVCSSMYIGD	LCGAVFLAGQ	LATFSPRIHD
Type_3a_CB	YVGATTASIR	SHVDLLVGAA	TMCSALYVGD	MCGAVFLVGQ	AFTFRPRRHQ
TypeV_D	YVGATTASIR	SHVDLLVGAA	TMCSALYVGD	MCGAVFLVGQ	AFTFRPRRHQ
VN004	NSSVPIHGFR	RHVDLLVGAA	AFCSAMYIGD	LCGSVFLVGQ	LFTFRPKHHQ
VN235	NASIPVRGFR	RHVDLMVGAA	AFCSAMYVGD	LCGGIFLVGQ	LFSFNPRRHW
VN405	NASVPIRGFR	SHVDLLVGSA	AACSALYIGD	LCGGVFLVGQ	LFTFRPRQHT

301			350		
BEBE1	FVQECNCSIY	PGKITGHRMA	WDMMMNWSPT	TTMLLAYLVR	IPEVLDIIT
D89815	TVQDCNCSIY	PGHVSghRMA	WDMMMNWSPT	AALVVSQLLR	IPQAVMDMVA
ED43type_4	TTQDCNCSIY	TGHITGHRMA	WDMMMNWSPT	TTLVLAQVMR	IPPTLVDLLS
HC_C2	TVQDCNCSIY	PGHITGHRMA	WDMMMNWSPT	TALVVSQLLR	IPQAVMDMVA
HC_G9	TTQDCNCSIY	PGHVTGHRMA	WDMMMNWSPT	GALVVAQLLR	IPQAIVDMIA
HCU16326	TVQDCNCSIY	PGRVSGHRMA	WDMMMNWSPT	TALVVSQLLR	IPQAVVDMVT
HCV_H_CM	TTQSCNCSIY	PGHITGHRMA	WDMMMNWSPT	AALVVAQLLR	IPQAIMDMIA
HCV_J1	TTQGCNCSIY	PGHITGHRMA	WDMMMNWSPT	AALVMAQLLR	IPQAILDMIA
HCV_J483	TVQDCNCSIY	PGHLSGHRMA	WDMMMNWSPT	TALVVSQLLR	IPQAVVDMVA
HCV_J8	FTQECNCSIY	QGHITGHRMA	WDMMLWSPT	LTMLAYAAR	VPELVLEIIF
HCV_JK1	TVQDCNCSLY	PGHVSghRMA	WDMMMNWSPT	TALVVSQLLR	IPQAVVDMV
HCV_JS	TVQDCNCSLY	PGHVSghRMA	WDMMMNWSPT	AALVVSQLLR	IPQAVVDMVA
HCV_K1_R1	TVQDCNCSIY	PGHVSghRMA	WDMMMNWSPT	TALVVSQLLR	IPQAVVDMVA
HCV_K1_R2	TVQDCNCSIY	PGHVSghRMA	WDMMMNWSPT	TALVVSQLLR	IPQAVMDMVA
HCV_K1_R3	TVQDCNCSLY	PGHITGHRMA	WDMMMNWSPT	TALVVSQLLR	IPQAVVDMVA
HCV_K1_S1	TVQDCNCSIY	PGHVSghRMA	WDMMMNWSPT	TALVVSQLLR	IPQAVVDMVA
HCV_K1_S2	TVQDCNCSIY	PGHVSghRMA	WDMMMNWSPT	TALVVSQLLR	IPQAVMDMVA
HCV_K1_S3	TVQDCNCSLY	PGHITGHRMA	WDMMMNWSPT	TALVVSQLLR	IPQAVMDMVA
HCV_L2	TVQDCNCSIY	PGHITGHRMA	WDMMMNWSPT	AALVVSQLLR	IPQAIVDMVA
HCV_N	TLQDCNCSIY	PGHASghRMA	WDMMMNWSPT	TALVVSQLLR	IPQAVDMVA
HCV12083	TVQDCNCSIY	TGHVTGhKMA	WDMMMNWSPT	TTLVLSSILR	VPEICASVIF
HCV1480	TVQDCNCSIY	SGHITGHRMA	WDMMMKWSPT	TALLMAQLLR	IPQVVIDIIA
HCVPOLYP	TVQDCNCSIY	PGHITGHRMA	WDMMMNWSPT	AALVVSQLLR	IPQAIVDMVA
HD_1	TVQDCNCSIY	PGHVSghRMA	WDMMMNWSPT	AALVVSQLLR	IPQAVVDMVA
HPCCGAA	TTQDCNCSIY	PGHITGHRMA	WDMMMNWSPT	AALVVAQLLR	IPQAIMDMIA
HPCFG	TVQTCNCSIY	PGHVSghRMA	WDMMMNWSPT	IGLVISHLMR	LPQTFFDLV
HPCGENANTI	TVQDCNCSIY	PGHVTGHRMA	WDMMMNWSPT	TALVVSQLLR	IPQAVVDMVG
HPCGENOM	TIQDCNCSIY	PGHVTGHRMA	WDMMMNWSPT	TALVVSQLLR	IPQAVMDMV
HPCHUMR	TLQDCNCSIY	PGHVSghRMA	WDMMMNWSPT	TALVVSQLLR	IPQAVVDMVA
HPCJ	TVQDCNCSIY	PGHLSGHRMA	WDMMMNWSPT	AALVVSQLLR	IPQAVVDMVA
HPCJCG	TVQDCNCSIY	PGHVSghRMA	WDMMMNWSPT	TALVVSQLLR	IPQAVVDMVA
HPCJK046	TVQDCNCSIY	TGHVTGHRMA	WDMMMNWSPT	ATFVVSSALR	APQVLFDFIFA
HPCJK049	TVQDCNCSIY	PGHITGHRMA	WDMMMNWSPT	MTLIVSQVLR	LPQTMFDLVI
HPCJTA	TVQDCNCSIY	PGHVSghRMA	WDMMMNWSPT	TALVVSQLLR	IPQAVVDMVA
HPCJTB	TVQDCNCSIY	PGHVSghRMA	WDMMMNWSPT	TALVVSQLLR	IPQAVVDMVA
HPCK3A	TVQTCNCSLY	PGHLSGQMA	WDMMMNWSPT	VGMVVAHILR	LPQTLFDVVA
HPCPLYPRE	TTQGCNCSIY	PGHITGHRMA	WDMMMNWSPT	TALVMAQLLR	IPQAILDMIA
HPCPOLP	FVQDCNCSIY	PGTITGHRMA	WDMMMNWSPT	ATMILAYAMR	VPEVIIDIIG

HPCPP	TVQDCNCSIY	PGHVSGHRMA	WDMIMNWSPT	TALVVSQLLR	IPQAVVDMVA
HPCUNKCD	TVQDCNCSIY	PGRVSGHRMA	WDMMMNWSPT	TALVVSQLLR	IPQAVVDMVT
MKC1A	TVQDCNCSIY	PGHVSGHRMA	WDMIMNWSPT	TALVVSQLLR	IPQAVVDMVA
NDM59	FVQECNCSIY	PGAITGHRMA	WDMMMNWSPT	ATMILAYAMR	VPEVIIDIIS
NZLI	TVQTCNCSLY	PGHLSGHRMA	WDMMMNWSPT	VGMVVAHVLR	LPQTLFDIMA
SA13	VVQDCNCSIY	SGHITGHRMA	WDMMMNWSPT	TALVMAQLLR	IPQVVIDIIA
Th580	ITQDCNCSVY	TGHVTGHRMA	WDMMMNWSPT	TTLVLSSILR	VPEIVLEVFA
Type_3a_CB	TVQTCNCSLY	PGHLSGHRMA	WDMMMNWSPT	LGMVAHVLR	VPQTLFDIIA
TypeV_D	TVQTCNCSLY	PGHLSGHRMA	WDMMMNWSPT	VGMVVSHVLR	LPQTLFDIIA
VN004	VTQDCNCSIY	AGHITGHRMA	WDMMLNWSPT	VSYVVSSALR	VPQLLLEVIT
VN235	VVQDCNCSIY	VGHITGHRMA	WDMMMNWSPT	ATLVLSYVMR	IPQVIMDIFT
VN405	TVQECNCSIY	TGHITGHRMA	WDMMMNWSPT	VTFITSSLLR	VPQLLLEIAL

		351			400	
	BEBE1	GGHWGVMFGL	AYFSMQGAWA	KVVVILLLLTA	GVEASTYTTG	AVVGRSTHFL
	D89815	GAHWGVLAGL	AYYSMVGNGA	KVLIVMLLLFA	GVDGHTRVTG	GVQGHVTSTL
ED43type_4	GGHWGVLVGV	AYFSMQANWA	KVILVLFLFA	GVDAETHVSG	AAVGRSTAGL	
	HC_C2	GAHWGVLAGL	AYYSMVGNGA	KVLIVLLLLFA	GVDGNTYVTG	GAAARGASGI
	HC_G9	GAHWGVLAGL	AYYSMVGNGA	KVVVVLLLLFA	GVDAETRVTG	GAAGHTAFGF
HCU16326	GSHWGILAGL	AYYSMVGNGA	KVLIAMLLFA	GVDGTTHTVG	GAQGRAASSL	
HCV_h_CMR	GAHWGVLAGI	AYFSMVGNGA	KVLVVLLLLFA	GVDAETHVTG	GSAGHTTAGL	
	HCV_J1	GAHWGVLAGI	AYFSMVGNGA	KVLVVLLLLFA	GVDAAETIVSG	GQAARAMSGI
HCV_J483	GAHWGVLAGL	AYYSMVGNGA	KVLIVALLFA	GVDGETYTSG	GAASHTTSTL	
	HCV_J8	GGHWGVVFG	AYFSMQGAWA	KVIAILLLLVA	GVDATTYSSG	QEAGRTVAGF
	HCV_JK1	GAHWGVLAGL	AYYSMVGNGA	KVLIVMLLLFA	GVDGTTYVSV	GHASQTTTRV
	HCV_JS	GAHWGVLAGL	AYYSMIGNWA	KVLIVMLLLFA	GADGTTHTVG	GVQAHGAYGL
HCV_K1_R1	GAHWGVLAGL	AYYSMVGNGA	KVLIVMLLLFA	GVDGNTYTTG	AAQGRTVSRL	
HCV_K1_R2	GAHWGVLAGL	AYYSMVGNGA	KVLIVMLLLFA	GVDGNTYVSG	GAKSHTTQGL	
HCV_K1_R3	GAHWGVLAGL	VYYSMVGNGA	KVLIVMLLLFV	GVDGSTHVSG	GTTAYNTRSF	
HCV_K1_S1	GAHWGVLAGL	AYYSMVGNGA	KVLIVMLLLFA	GVDGDTYTTG	GAQGHTTSRV	
HCV_K1_S2	GAHWGVLAGL	AYYSMVGNGA	KVLIVMLLLFA	GVDGRTTVTG	GAQGHTTQRL	
HCV_K1_S3	GAHWGVLAGL	VYYSMVGNGA	KVLIVMLLLFV	GVDGSTRVSG	GTTAYNTRGL	
	HCV_L2	GAHWGVLAGL	AYYPMVGNGA	KVLIVMLLLFA	GVDGTTVTMG	GTVARTTYGF
	HCV_N	GAHWGVLAGL	AYYSMAGNWA	KVLIVMLLLFA	GVDGHTLTG	GHAHLTSGF
HCV12083	GGHWGILLAV	AYFGMAGNWL	KVLAVLFLFA	GVEAQT.MIA	HGVSQTTSGF	
	HCV1480	GGHWGVLLAA	AYFASTANWA	KVILVLFLFA	GVDGRHTVTG	GTVGQGLKSL
HCVPOLYP	GAHWGVLAGL	AYYSMVGNGA	KVLIVMLLLFA	GVDGDTHTTG	GVAGRDLRF	
	HD_1	GAHWGVLAGL	AYYSMVGNGA	KVLIVMLLLFA	GVDGTTTVTG	GSQARTVYEL
	HPCCGAA	GAHWGVLAGI	KYFSMVGNGA	KVLVVLLLLFA	GVDAETHVTG	GNAGR'TTAGL
	HPCFG	GAHWGVMAGL	AYFSMQGNWA	KVVIVLIMFS	GVDATHTTTG	GSAAQATAGF
HPCGENANTI	GAHWGVLAGL	AYYSMVGNGA	KVLIVMLLLFA	GVDGSTIVSG	GTVARTTHSL	
HPCGENOM	GAHWGVLAGL	AYYAMVGNGA	KVLIVMLLLFA	GVDGDTYASG	GAQGRSTLGF	
HPCHUMR	GAHWGVLAGL	AYYSMAGNWA	KVLIVMLLLFA	GVDGDTHVTG	GAQAKTTNRL	
	HPCJ	GAHWGVLAGL	AYYSMVGNGA	KVLIVMLLLFA	GVDGQTYTTG	GAVARTTTGF
	HPCJCG	GAHWGVLAGL	AYYSMVGNGA	KVLIVMLLLFA	GVDGHTHTVG	GRVASSTQSL
HPCJK046	GGHWGIIGAL	LYYSTAANWA	KVIVLILLFA	GVDAST.YVA	SSVSQATSGL	
HPCJK049	GAHWGVMAGV	AYYSMQGNWA	KVFLVLCLFS	GVDASTTITG	GVAASGAFTI	
	HPCJTA	GAHWGVLAGL	AYYSMVGNGA	KVLIVMLLLFA	GVDGVTYTTG	GSQARHTQSV
	HPCJTB	GAHWGVLAGL	AYYSMVGNGA	KVLIVMLLLFA	GVDGVTYTTG	GSQARHTQGV
HPCK3A	GAHWGIAGL	AYYSMQGNWA	KVAIIMVMFS	GVDASTHVTA	GQAARNAYGI	
HPCPLYPRE	GAHWGVLAGI	AYFSMVGNGA	KVLVVLLLLFA	GVDAETHVTG	GSAGHTVSGF	
HPCPOLP	GAHWGVMFGL	AYFSMQGAWA	KVVVILLLAA	GVDAAQTHTVG	GSTAHNARTL	
	HPCPP	GAHWGVLAGL	AYYSMVGNGA	KVLIVMLLLFA	GVDGGTHVTG	GKVAYTTQGF
HPCUNKCD	GSHWGILAGL	AYYSMVGNGA	KVLIAMLLFA	GVDGTTHTVG	GAQGRAASSL	
	MKC1A	GAHWGVLAGL	AYYSMVGNGA	KVLVVMLLFA	GVDGGTHVTG	GKVAYTTQGF
NDM59	GAHWGVMFGL	AYFSMQGAWA	KVVVILLLLTA	GVDAHTRSIA	GSVAHATSGL	
	NZLI	GAHWGILAGL	AYYSMQGNWA	KVAIIMVMFS	GVDAHTYTTG	GTASRHTQAF
	SA13	GAHWGVLFAL	AYYASANWA	KVVLVLFLFA	GVDANTRTVG	GSAAQGARGL
Th580	GGHWGVLIAI	AYFGMSGNWL	KVIAVLFLFA	GVEATT.TVG	RAAGRSAYLF	
Type_3a_CB	GAHWGILAGL	AYYSMQGNWA	KVAIIMVMFS	GVDAVTYTTG	GSAAHATRGL	
TypeV_D	GAHWGILAGL	AYYSMQGNWA	KVAVIMVMFS	GVDAETYITG	GSAAHGVSTL	
	VN004	GAHWGVLAGL	LYFSMVANWA	KVIAVLFLFA	GADATT.YTG	SAVSSTTGAF
	VN235	GGHWGILAGI	LYYSMVANWA	KVLCILFLFA	GVDATTTRTG	AQAARATLGF
	VN405	EGHWGVIGAL	LYYSMVANWA	KVFAVLLLLFA	GVDATT.HIG	SSASATTNRL

	401				450
BEBE1	TSMFSLGSQQ	RVQLIHTNGS	WHINRTALNC	NDSLETGFGLA	ALFYTSSFNS
D89815	TSLFRPGASQ	KIQLVNTNGS	WHINRTALNC	NDSLKTGFGLA	ALFYTHKFNA
ED43type_4	ANLFSSGSKQ	NLQLINSNGS	WHINRTALNC	NDSLNTGFGLA	SLFYTHKFNS
HC_C2	TSLFSRGPSP	KIQLVNTNGS	WHINRTALNC	NDSFNTGFGLA	ALFYAHRFNS
HC_G9	ASFLAPGAKQ	KIQLINTNGS	WHINRTALNC	NESLDTGWFLA	GLLYYHKFNS
HCU16326	TSLFSPGPVQ	HLQLINTNGS	WHINRTALSC	NDSLNTGFVFA	ALFYKYRFNA
HCV h CMR	VGLLTPGAKQ	NIQLINTNGS	WHINSTALNC	NDSLTTGWFLA	GLFYRHKFNS

HCV_J1	VSLFTPGAKQ	NIQLINTNGS	WHINSTALNC	NESLNTGWLA	GLIYQHKFNS
HCV_J483	ASLFSPGASQ	RIQLVNTNGS	WHINRTALNC	NDSLHTGFIA	ALFYTHRFNS
HCV_J8	AGLFTTGAKQ	NLYLINTNGS	WHINRTALNC	NDSLQTGFIA	SLFYTHKFNS
HCV_JK1	ASFFSPGSAQ	KIQLVNTNGS	WHINRTALNC	NESINTGFFA	ALFYVKKFNS
HCV_JS	ASLFNVGPHQ	KIQLVNTNGS	WHINRTALNC	NDTLQTGFIA	ALFYKHRFNA
HCV_K1_R1	TSIFTPGASQ	NIQLINTNGS	WHINRTALNC	NDSLQTGFIA	ALFYARRFNS
HCV_K1_R2	VSLFAPGAQQ	KIQLVNTNGS	WHINRTALNC	NDSLNTGFIA	ALFYTHRFNS
HCV_K1_R3	TSLFSSGAQQ	KIQLVNTNGS	WHINRTALNC	NDTLQTGFIA	ALFYTHRFND
HCV_K1_S1	ASLFTSGASQ	NIQLINTNGS	WHINRTALNC	NDSLQTGFIA	ALFYAHRFNS
HCV_K1_S2	ASLFTFGAQQ	RIQLVNTNGS	WHINRTALNC	NDSLNTGFIA	ALFYTHRFNS
HCV_K1_S3	TSLFSSGAQQ	KIQLVNTNGS	WHINRTALNC	NDTLQTGFIA	ALFYTHRFND
HCV_L2	TGLFRPGASQ	KIQLINTNGS	WHINRTALNC	NDSLNTGFIA	ALFYTHRFNA
HCV_N	AGLFTPGPSQ	RIQLINTNGS	WHINRTALNC	NDSLQTGFIA	ALSYTYRFNS
HCV12083	ASLLTPGAKQ	NIQLINTNGS	WHINRTALNC	NDSLQTGFIA	SLFYTHKFNS
HCV1480	TSFFNPGPQR	QLQFVNTNGS	WHINSTALNC	NDSLQTGFIA	GLMYAHKFNS
HCVPOLYP	TGFFSLGPKQ	KIQLVNTNGS	WHINRTALNC	NDSLNTGWLA	ALFYTHSFNA
HD_1	TSLYTRGPSQ	RIQLVNTNGS	WHINRTALNC	NDSLQTGFIA	ALFYTRSFNS
HPCCGAA	VGLLTPGAKQ	NIQLINTNGS	WHINSTALNC	NESLNTGWLA	GLFYQHKFNS
HPCFG	TSFFTTRGPSQ	NLQLVNSNGS	WHINSTALNC	NDSLNTGFIA	GLFYHKKFNS
HPCGENANTI	ASLFTQGASQ	KIQLINTNGS	WHINRTALNC	NDSLQTGFIA	SLFYAHRFNA
HPCGENOM	TSLFTPGASQ	KIQLINTNGS	WHINRTALNC	NDSLNTGFIA	ALFYTHRFNA
HPCHUMR	VSMFASGPSQ	KIQLINTNGS	WHINRTALNC	NDSLQTGFIA	ALFYTHSFNS
HPCJ	ASLFSAGSQE	NIQLINTNGS	WHINRTALNC	NDSLNTGFIA	ALFYTHKFNS
HPCJCG	VSWLSQGPSQ	KIQLVNTNGS	WHINRTALNC	NDSLQTGFIA	ALFYAHRFNA
HPCJK046	VSLFSAGARQ	NLQLINTNGS	WHINRTALNC	NDSLQTGFIA	SLFYRNKFNA
HPCJK049	TSLFSTGAKQ	PLHLVNTNGS	WHINRTALNC	NDSLNTGFIA	GLLYYHKFNS
HPCJTA	TSFFTQGPAQ	RIQLINTNGS	WHINRTALNC	NESLNTGFFA	ALFYAHKFNS
HPCJTB	ASFFTTPGPAQ	KIQLINTNGS	WHINRTALNC	NESLNTGFFA	ALFYAHKFNS
HPCK3A	TSLFSVGAKQ	NLQLINTNGS	WHINRTALNC	NESINTGFIA	GLFYHKKFNS
HPCPLYPRE	VSLLPAGAKQ	NVQLINTNGS	WHINSTALNC	NDSLNTGWLA	GLFYHKKFNS
HPCPOLP	TGMFSLGARQ	KIQLINTNGS	WHINRTALNC	NDSLHTGFIA	SLFYTHSFNS
HPCPP	TSFFSRGPSQ	KIQLVNTNGS	WHINRTALNC	NDSLNTGFIA	ALFYTHSFNA
HPCUNKCD	TSLFSPPGVQ	HLQLINTNGS	WHINRTALNC	NDSLNTGFVA	ALFYKYRFNA
MKC1A	TSFFSRGPSQ	KIQLVNTNGS	WHINRTALNC	NDSLNTGFIA	ALFYTHSFNA
NDM59	AGLFTSGAKQ	NIQLINTNGS	WHINRTALNC	NDSLNTGFIA	SLFYTYRFNS
NZLI	AGLFDIGPQQ	KLQLVNTNGS	WHINSTALNC	NESINTGFIA	GLFYHKKFNS
SA13	ASLFTPGPQQ	NLQLINTNGS	WHINRTALNC	NDSLQTGFVA	GLLYYHKFNS
Th580	TSIFSSGPNQ	KIQLINTNGS	WHINRTALNC	IDSLQTGFIA	ALFYRSNFNS
Type_3a_CB	TSLFSVGAQQ	KLQLVNTNGS	WHINSTALNC	NESINTGFIA	GLFYHHRFNS
TypeV_D	TSLFSSGPQQ	KLQLVKTNGS	WHINSTALNC	NESINTGFIA	GLFYHKKFNS
VN004	VSLFSPGPTQ	NLQLVNSNGS	WHINRTALNC	NDSLQTGFIA	GLFARYKFNS
VN235	TGLFQTGAKQ	NIHLINTNGS	WHINRTALNC	NDSLNTGFMA	ALFYLHKFNS
VN405	TSFFSPGSKQ	NVQLIKTNGS	WHINRTALNC	NDSLHTGFIA	GLLYAHRFNS

	451			500	
BEBE1	SGCPERLAAC	RSIESFRIGW	GSLEYEESVT	NDADMRPYCW	HYPPRPGCIV
D89815	SGCPERMASC	RSIDKFDQGW	GPITYAQP.	.NSDQRPYCW	HYAPRQCGIV
ED43type_4	SGCSERLACC	KSLDSYGQGW	GPLGVANISG	.SSDDRPHYCW	HYAPRPGCIV
HC_C2	SGCPERMASC	RSIDKFDQGW	GPITYYQGD.	.SPDQRPYCW	HYPPRPGCIV
HC_G9	SGCPERMASC	QPLTAFDQGW	GPITHEGNA.	.SDDQRPYCW	HYALRPGCIV
HCU16326	SGCPERLATC	RPIDTFAQGW	GPITYTEPH.	.DLDQRPYCW	HYAPQPCGIV
HCV_H_CMV	SGCPERLASC	RRLTDFAGQW	GPISYANGS.	.GLDERPHYCW	HYPPRPGCIV
HCV_J1	SGCPERLASC	RRLTDFDQGW	GPISHANGS.	.GPDQRPYCW	HYPPKPCGIV
HCV_J483	SGCPERMASC	RPIDWFAQGW	GPITYTEPD.	.SPDQRPYCW	HYAPRPGCIV
HCV_J8	SGCPERLSSC	RGLDDFRIGW	GTLEYETNVT	NDGDMRPYCW	HYPPRPGCIV
HCV_JK1	SGCSERMASC	RPIDRFAQGW	GPITHAESR.	.SSDQRPYCW	HYAPQPCGIV
HCV_JS	SGCPERMASC	RPIDKFAQGW	GPITYAEPD.	.RLDQRPYCW	HYPPRPGCIV
HCV_K1_R1	SGCPQRLASC	RSIDKFAQGW	GPITYAEGH.	.DSDQRPYCW	HYAPRPGCIV
HCV_K1_R2	SGCPERIASC	RSIDAFAGQW	GPITYAEPG.	.SSDQRPYCW	HYAPRPGCIV
HCV_K1_R3	SGCPERMASC	RPIDKFAQGW	GPITYVKPD.	.ILDQRPYCW	HYAPRPGCIV

HCV_K1_S1	SGCPQRLASC	RSIDKFAQGW	GPITYTEGH.	.NSDQRPYCW	HYAPRPGCIV
HCV_K1_S2	SGCPERIASC	RSIDAFQAGW	GPITYAEPG.	.SSDQRPYCW	HYAPRPGCIV
HCV_K1_S3	SGCPERMASC	RPIDKFAQGW	GPITYAKPD.	.ILDQRPYCW	HYAPRPGCIV
HCV_L2	SGCPERMASC	QSIDKFDQGW	GPITYAENG.	.SSDQRPYCW	HYAPRRCGIV
HCV_N	SGCPRGMASC	RSIDKFDQGW	GPITYADPK.	.DPDQRPYCW	HYAPQOCGII
HCV12083	SGCPERMAAC	KPLAEFRQGW	GQITHKN.VS	GPSDDRPYCW	HYAPRPPCEVV
HCV1480	SGCPERMSSC	RPLAAFDQGW	GTISYATISG	.PSDDKPYCW	HYPPrPCGVV
HCVPOLYP	SGCPERMASC	HPIDEFAQGW	GPITYAEHS.	.SSDQRPYCW	HYAPQPCGIV
HD_1	SGCPERMASC	RSIDQFDQGW	GPITYAEPR.	.DLDQRPYCW	HYAPRPGCIV
HPCCGAA	SGCPERLASC	RRLTDFAQGW	GPISYANGS.	.GLDERPYCW	HYPPrPCGIV
HPCFG	SGCPERMSSC	KPITYFNQGW	GPLTDANING	.PSEDRPYCW	HYPPrPCNIT
HPCGENANTI	SGCPERMASC	RSIDKFDQGW	GPITYTEAD.	.IQDQRPYCW	HYAPRPGCIV
HPCGENOM	SGCAERMASC	RPIDTFDQGW	GPITYTEPD.	.SSDQRPYCW	HYAPRKCGIV
HPCHUMR	SGCPERMAQC	RTIDKFDQGW	GPITYAESS.	.RSDQRPYCW	HYPPrPQCTIV
HPCJ	SRAESVLASC	RFIDEFDQGW	GPITYTERN.	.SSDQRPYCW	HYPPrPQCII
HPCJCG	SGCPERMASC	RPIDEFAQGW	GPITHDMPE.	.SSDQRPYCW	HYAPRPGCIV
HPCJK046	TGCPERLSAC	KTLDSDQGW	GPITYAN.IS	GPAVEKPYCW	HYPPrPCEVV
HPCJK049	SGCVERMSAC	SPLDRFAQGW	GPLGPANISG	.PSSEKPYCW	HYAPRPCDTV
HPCJTA	SGCPERMASC	SSIDKFAQGW	GPITYTEPR.	.DLDQRPYCW	HYAPRQCIV
HPCJTB	SGCPERMASC	SSIDKFAQGW	GPITYTEPG.	.DLDQRPYCW	HYAPRQCIV
HPCK3A	TGCPQRLSSC	KPITFFKQGW	GPLTDANITG	.PSDDKPYCW	HYAPRPGCIV
HPCPLYPRE	SGCPERLASC	RPLTDFDQGW	GPISYANGS.	.GPDQRPYCW	HYPPrKPCGIV
HPCPOLP	SGCPERMSAC	RSIEAFRVGW	GALQYEDNVT	NPEDMRPYCW	HYPPrQCGVV
HPCPP	SGCPERMAGC	RPIDEFAQGW	GPITHVVPN.	.ISDQRPYCW	HYAPRPGCIV
HPCUNKCD	SGCPERLATC	RPIDTFAQGW	GPITYTEPH.	.DLDQRPYCW	HYAPQPCGIV
MKC1A	SGCPERMAGC	RPIDEFAQGW	GPITHVVPN.	.ISDQRPYCW	HYAPRPGCIV
NDM59	SGCPERLSAC	RGIQAFRIGW	GTLRYEDNVT	NPEDMRPYCW	HYPPrKQCIV
NZLI	TGCPQRLSSC	KPITFFRQGW	GPLTDANITG	.PSDDRPYCW	HYAPRPCDIV
SA13	TGCPQRMASC	RPLAAFDQGW	GTISYAAVSG	.PSDDKPYCW	HYPPrPCGIV
Th580	TGCSERLGAC	KPLEHFQQGW	GPITHKSNIT	GPSEDRPYCW	HYAPRECSVV
Type_3a_CB	TGCPQRLSSC	KPITFFKQGW	GPLTDANISG	.PSDDKPYCW	HYAPRPPCKVV
TypeV_D	TGCPQRLSSC	KPITFFRQGW	GSLTDANVTG	.ASADKPYCW	HYAPRPPCDVV
VN004	TGCPERMASKC	RPLHSFEQGW	GPISYVN.IS	GSSSEDKPYCW	HYAPRPGCIV
VN235	TGCPERLSAC	KSITQFAQGW	GPVTYAN.VS	GSSSEDRPYCW	HYAPRPPCGVV
VN405	SGCPERLSSC	RPLHAFEQGW	GPLTYAN.IS	GPSNDKPYCW	HYPPrPCDIV

	501			550	
BEBE1	PARTVCGPVY	CFTSPVVVG	TTDRAGAPTY	NWGENETDVF	LLNSTRPPKG
D89815	PASQVCGPVY	CFTSPVVVG	TTDRFGAPTY	NWGDNETDVL	LLNNTRPPHG
ED43type_4	PASSVCGPVY	CFTSPVVVG	TTDHVGVPTY	TWGENETDVF	LLNSTRPPHG
HC_C2	PASEVCGPVY	CFTSPVVVG	TTDRLGVPTY	NWGENETDVL	LLNNTRPPQG
HC_G9	PAKKVCGPVY	CFTSPVVVG	TTDRAGVPTY	RWGANETDVL	LLNNSRPPMG
HCU16326	PTLQVCGPVY	CFTSPVAVG	TTDRFGAPTY	RWGANETDVL	LLNNAGPPQG
HCV_H_CMV	PAKSVCVPY	CFTSPVVVG	TTDRSGAPTY	SWGANDTDVF	VLNNTTRPPLG
HCV_J1	PAKSVCVPY	CFTSPVVVG	TTDRSGAPTY	NWGANDTDVF	VLNNTTRPPLG
HCV_J483	PASQVCGPVY	CFTSPVVVG	TTDRSGVPTY	SWGNETDVM	LLNNTRPPQG
HCV_J8	PARTVCGPVY	CFTSPVVVG	TTDKQGVPTY	TWGENETDVF	LLNSTRPPRG
HCV_JK1	PALQVCGPVY	CFTSPVVVG	TTDRFGVPTY	NWGDNETDVL	LLNNTRPPQG
HCV_JS	PALEVCGPVY	CFTSPVVVG	TTDRFGVPTY	SWGNETDVL	LLNNTRPPQG
HCV_K1_R1	PAQVCGPVY	CFTSPVVVG	TTDRFGAPTY	NWGANETDVL	LLNNTRPPQG
HCV_K1_R2	PASEVCGPVY	CFTSPVVVG	TTDRSGAPTY	SWGNETDVL	LLNNTRAPQG
HCV_K1_R3	PASEVCGPVY	CFTSPVVVG	TTDRSGAPTY	NWGGNETDVL	LLNNTRPPQG
HCV_K1_S1	PASQVCGPVY	CFTSPVVVG	TTDRFGAPTY	NWGANETDVL	LLNNTRPPQG
HCV_K1_S2	PASEVCGPVY	CFTSPVVVG	TTDRSGAPTY	SWGNETDVL	LLNNTRAPQG
HCV_K1_S3	PASEVCGPVY	CFTSPVVVG	TTDRSGAPTY	NWGGNETDVL	LLNNTRPPQG
HCV_L2	PASQVCGPVY	CFTSPVVVG	TTDRSGAPTY	SWGNETDVL	LLNNTRPPQG
HCV_N	PRSEACGPVY	CSTSPVVVG	TTDRFGAPTY	NWGDNETDVL	LLNNTRPPQG
HCV12083	PARSVCVPY	CFTSPVVVG	TTDKRGNPTY	TWGENETDVF	MLESLRPPTG
HCV1480	PARDVCGPVY	CFTSPVVVG	TTDRRGCPY	NWGSNETDIL	LLNNIRPPAG
HCVPOLYP	PASEVCGPVY	CFTSPVVVG	TTDRHGVPTY	SWGNETDVL	LLNNTRPPQG



HD_1	PASQVCGPVY	CFTSPVTVVG	TTDRSGVPTY	SWGENETDVL	LLNNTRPPQG
HPCCGAA	PAKSVC GPVY	CFTSPVTVVG	TTDRSGAPTY	SWGANDTDVF	VLNNT RPPLG
HPCFG	KPLNVC GPVY	CFTSPVTVVG	TTDIKGLPTY	RFGVNESDVF	LLTSLRPPQG
HPCGENANTI	PASQVCGPVY	CFTSPVTVVG	TTDRFGAPTY	SWGENETDVL	ILNNTRPPQG
HPCGENOM	PASEVCGPVY	CFTSPVTVVG	TTDRFGVPTY	SWGENETDVL	LLNNTRPPQG
HPCHUMR	PASEVCGPVY	CFTSPVTVVG	TTDRFGVPTY	RWGENETDVL	LLNNTRPPQG
HPCJ	PASEVCGPVY	CFTSPVTVVG	TTDRFGVPTY	SWGENETDVL	VLNNT RPPLG
HPCJCG	PASQVCGPVY	CFTSPVTVVG	TTDRFGAPTY	SWGENETDVL	LLSNTRPPQG
HPCJK046	SALNVC GPVY	CFTSPVTVVG	TTDRGNPTY	TWGANETDVF	MMSSLRPPAG
HPCJK049	PAQSVCGPVY	CFTSPVTVVG	ATDKRGAPTY	TWGENESDVF	LLESARPPTE
HPCJTA	PASQVCGPVY	CFTSPVTVVG	TTDRSGAPTY	NWGANETDVL	LLNNTRPPQG
HPCJTB	PASQVCGPVY	CFTSPVTVVG	TTDRSGAPTY	NWGANETDVL	LLNNTRPPQG
HPCK3A	PALNVC GPVY	CFTSPVTVVG	TTDAKGAPTY	TWGANKTDVF	LLESLRPPSG
HPCPLYPRE	PAKSVC GPVY	CFTSPVTVVG	TTDRSGAPTY	SWGENETDVF	VLNNT RPPLG
HPCPOLP	SASSVC GPVY	CFTSPVTVVG	TTDRLGAPTY	TWGENETDVF	LLNSTRPPQG
HPCPP	PASQVCGPVY	CFTSPVTVVG	TTDRFGAPTY	NWGNNETDVL	LLNNTRPPQG
HPCUNKCD	PTLQVC GPVY	CFTSPVAVG	TTDRFGAPTY	RWGANETDVL	LLNNAGPPQG
MKC1A	PASQVCGPVY	CFTSPVTVVG	TTDRFGAPTY	NWGNNETDVL	LLNNTRPPQG
NDM59	SARSVC GPVY	CFTSPVTVVG	TTDRLGVPTY	TWGENETDVF	ILNSTRPPGG
NZLI	PASSVC GPVY	CFTSPVTVVG	TTDARGVPTY	TWGENEKDVF	LLKSQRPPSG
SA13	PARGVC GPVY	CFTSPVTVVG	TTDRKGNPTY	SWGENETDIF	LLNNTRPPTG
Th580	PASSVC GPVY	CFTSPVTVVG	TTDRLGNPTY	NWGENETDVF	MLESLRPPQG
Type_3a_CB	PASGVC GPVY	CFTSPVTVVG	TTDAKGVPTY	TWGANDTDVF	LLESLRPPGG
TypeV_D	PALNVC GPVY	CFTSPVTVVG	TTDRKGVPTY	NWGENESDVF	LLESLRPPSG
VN004	PARNVC GPVY	CFTSPVTVVG	TTDQRGIPTY	TWGENVSDVF	LLHSARPPLG
VN235	SARSVC GPVY	CFTSPVTVVG	TTDRRGVPTY	TWGENESDVF	LLESLRPPAG
VN405	PARSVC GPVY	CFTSPVTVVG	TTDRKGLPTY	TWGANESDVF	LLRSTRPPRG

	551		600
BEBE1	AWFGCTWMNG	TGFTKTCGAP	PCRIRKDFN. .A..SEDLLC PTDCFRKHPG
D89815	NWFGCTWMNS	TGFTKTCGGP	PCNIRG.... VG..NNTLTC PTDCFRKHPD
ED43type_4	AWFGCVWMNS	TGFTKTCGAP	PCEVN..... TN..NGTWHC PTDCFRKHPE
HC_C2	NWFGCTWMNT	TGFTKTCGGP	PCNIGG.... AG..NNTLTC PTDCFRKHPE
HC_G9	NWFGCTWMNS	SGFTKTCGAP	ACNIGG.... SG..NNTLLC PTDCFRKHPD
HCU16326	NWFGCTWMNG	TGFTKTCGGP	PCNIGG.... VG..NNTLTC PTDCFRKHPG
HCV_H_CMV	NWFGCTWMNS	TGFTKVC GAP	PCVIGG.... VG..NNTLLC PTDCFRKHPE
HCV_J1	NWFGCTWMNS	TGFTKVC GAP	PCVIGG.... GG..NNTLHC PTDCFRKHPE
HCV_J483	NWFGCTWMNS	TGFTKTCGGP	PCNIGG.... VG..NHTLTC PTDCFRKHPE
HCV_J8	AWFGCTWMNG	TGFTKTCGAP	PCRIRKDYN. .S..TIDLLC PTDCFRKHPD
HCV_JK1	NWFGCTWMNS	TGFTKTCGGP	PCNIGG.... AG..NNTLTC PTDCFRKHPE
HCV_JS	NWFGCTWMNS	TGYTKTCGGP	PCNIGG.... VG..NNTLTC PTDCFRKHPE
HCV_K1_R1	NWFGCTWMNG	TGFTKTCGGP	PCNIGG.... AG..NNTLTC PTDCFRKHPE
HCV_K1_R2	NWFGCTWMNG	TGFTKTCGGP	PCNIGG.... VG..NNTLTC PTDCFRKHPE
HCV_K1_R3	NWFGCTWMNS	TGFTKTCGGP	PCNIGG.... AG..NNTFTC PTDCFRKHPE
HCV_K1_S1	NWFGCTWMNG	TGFTKTCGGP	PCNIGG.... AG..NDTLTC PTDCFRKHPE
HCV_K1_S2	NWFGCTWMNG	TGFTKTCGGP	PCNIGG.... VG..NNTLTC PTDCFRKHPE
HCV_K1_S3	NWFGCTWMNS	TGFTKTCGGP	PCNIGG.... AG..NNTLTC PTDCFRKHPE
HCV_L2	NWFGCTWMSS	TGFTKTCGGP	PCNIGG.... AG..NNTLTC PTDCFRKHPE
HCV_N	NWFGCTWMNS	TGFTKTCGAP	PCNIGG.... VG..NNTLTC PTDCFRKHPE
HCV12083	GWFGCTWMNS	TGFTKTCGAP	PCQIVPGNYN SS..ANELLC PTDCFRKHPE
HCV1480	NWFGCTWMNS	TGFVKNC GAP	PCNLGP.... TG..NNSLKC PTDCFRKHPD
HCVPOLYP	NWFGCTWMNG	TGFTKTCGGP	PCNIGG.... VG..NNTLTC PTDCFRKHPE
HD_1	NWFGCTWMNS	TGFTKTCGGP	PCGIGG.... VG..NNTLIC PTDCFRKHPE
HPCCGAA	NWFGCTWMNS	TGFTKVC GAP	PCVIGG.... VG..NNTLLC PTDCFRKYPE
HPCFG	RWFGCVWMNS	TGFVKTCGAP	PCNIYGGMKD IEANQTHLKC PTDCFRKHHD
HPCGENANTI	NWFGCTWMNS	TGFTKTCGGP	PCNIGG.... GG..NNTLVC PTDCFRKHPE
HPCGENOM	NWFGCTWMNG	TGFTKTCGGP	PCNIGG.... VG..NNTLTC PTDCFRKHPE
HPCHUMR	NWFGCTWMNS	TGFTKTCGGP	PCNIGG.... VG..NNTLTC PTDCFRKHPE
HPCJ	NWFGCTWMNG	TGFTKTCGGP	PCHIGG.... RG..NNTLTC PTDCFRKHPE
HPCJCG	NWFGCTWMNS	TGFTKTCGGP	PCNIGG.... VG..NNTLVC PTDCFRKHPE

HPCJK046	GWYGCTWMNT	SGFVKTCGAP	PCNIRPNPEE	NR..TETLRC	PTDCFRKHPPG
HPCJK049	PWFGCTWMNG	SGYVKTCGAP	PCHIYGGREG	KS..NNSLVC	PTDCFRKHDP
HPCJTA	NWFGCTWMNS	TGFTKTCGGP	PCNIGG....	VG..NLTLTC	PTDCFRKHPE
HPCJTB	NWFGCTWMNS	TGFTKTCGGP	PCNIGG....	VG..NLTLTC	PTDCFRKHPE
HPCK3A	RWFGCTWMNS	TGFVKTCGAP	PCNIYGDGRD	AQ.NESDLFC	PTDCFRKHPE
HPCPLYPRE	NWFGCTWMNS	TGFTKTCGAP	PCVIGG....	AG..NNTLHC	PTDCFRKHDP
HPCPOLP	SWFGCTWMNS	TGYTKTCGAP	PCRIRADFN.	.A..SMDLLC	PTDCFRKHDP
HPCPP	NWFGCTWMNG	TGFTKTCGGP	PCNIGG....	VG..NNTLTC	PTDCFRKHPE
HPCUNKCD	NWFGCTWMNG	TGFTKTCGGP	PCNIGG....	VG..NNTLTC	PTDCFRKHPPG
MKC1A	NWFGCTWMNG	TGFTKTCGGP	PCNIGG....	VG..NNTLTC	PTDCFRKHPE
NDM59	SWFGCTWMNS	TGFTKTCGAP	PCRIRADFN.	.A..SMDLLC	PTDCFRKHDP
NZLI	RWFGCSWMNS	TGFLKTCGAP	PCNIYGGEGN	PH.NESDLFC	PTDCFRKHPE
SA13	NWFGCTWMNS	TGFVKTCGAP	PCNLGP....	TG..NNSLKC	PTDCFRKHDP
Th580	GWFGCTWMNS	TGFTKTCGAP	PCQLIPGDYN	SS..SNQLLC	PTDCFRKHPE
Type_3a_CB	RWFGCTWMNS	TGFVKTCGAS	PCDIYGGGGN	SG.NESDLFC	PTDCFRKHPE
TypeV_D	RWFGCAWMNS	TGFLKTCGAP	PCNIYGGGGN	PN.NESHLFC	PTDCFRKHDP
VN004	AWFGCTWMNS	SGFVKTCGAP	PCRIKPTIN.	....ETDLVC	PTDCFRKHDP
VN235	AWYGCTWMNS	TGYTKTCGAP	PCHIGP.PDQ	.....FC	PTDCFRKHPE
VN405	SWFGCTWMNS	TGFVKTCGAP	PCNTRPVGSG	....NDTLVC	PTDCFRKHPE

	601				650
BEBE1	ATYIKCGAGP	WLTPRCLVDY	PYRLWHYPCT	VNYTIYKVRM	FVGGIEHRLQ
D89815	ATYTKCGSGP	WLTPRCLVDY	PYRLWHYPCT	VNFTIFKVRM	YVGGVEHRLD
ED43type_4	TTYAKCGSGP	WITPRCLIDY	PYRLWHFPCT	ANFSVFNIRT	FVGGIEHRMQ
HC_C2	ATYTKCGSGP	WLTPRCLVDY	PYRLWHYPCT	VNFTIFKVRM	YVGGVEHRLD
HC_G9	ATYSRCGSGP	WLTPRCLVDY	PYRLWHYPCT	VNYTIFKIRM	FVGGVEHRLD
HCU16326	ATYTKCGSGP	WLTPRCLVDY	PYRLWHYPCT	VNFTIFKVRM	YVGGAEHRLD
HCV_H_CMR	ATYSRCGSGP	WITPRCMVDY	PYRLWHYPCT	INYTIFKVRM	YVGGVEHRLD
HCV_J1	ATYSRCGSGP	WITPRCLVDY	PYRLWHYPCT	INYTIFKVRM	YVGGVEHRLD
HCV_J483	ATYTKCGSGP	WLTPRCLVDY	PYRLWHYPCT	FNFSIFKVRM	YVGGVEHRLN
HCV_J8	ATYKCGAGP	WLTPRCLVDY	PYRLWHYPCT	VNFTIFKARM	YVGGVEHRFS
HCV_JK1	ATYTKCGSGP	WLTPRCMVDY	PYRLWHYPCT	FNFTIFKIRM	YVGGVEHRLN
HCV_JS	ATYTKCGSGP	WLTPRCLVHY	PYRLWHYPCT	VNFTIFKVRM	YVGGIEHRLD
HCV_K1_R1	ATYAKCGSGP	WLTPRCIVDY	PYRLWHYPCT	VNFSIFKVRM	YVGGVEHRLT
HCV_K1_R2	ATYTKCGSGP	WLTPRCMVDY	PYRLWHYPCT	VNFTIFKVRM	YVGGVEHRLN
HCV_K1_R3	ATYTKCGSGP	WLTPRCIVDY	PYRLWYYPCT	VNFTIFTIRM	YVGGVEHRLK
HCV_K1_S1	ATYAKCGSGP	WLTPRCIVDY	PYRLWHYPCT	VNFSIFKVRM	YVGGVEHRLT
HCV_K1_S2	ATYTKCGSGP	WLTPRCMVDY	PYRLWHYPCT	VNFTIFKVRM	YVGGVEHRLN
HCV_K1_S3	ATYTKCGSGP	WLTPRCIVDY	PYRLWYYPCT	VNFTIFTIRM	YVGGVEHRLK
HCV_L2	ATYTKCGSGP	WLTPRCLVDY	PYRLWHYPCT	VNFTTFKVRM	YVGGVEHRLI
HCV_N	ATYSKCGSGP	WLTPRCMVDY	PYRLWHYPCT	VNFSIFKVRM	YVGGVEHRLN
HCV12083	ATYQRCGSGP	WVTPRCLVDY	AYRLWHYPCT	VNFTLHKVRM	FVGGTEHRFD
HCV1480	ATYTRCGSGP	WLTPRCLVHY	PYRLWHYPCT	VNYTIFKVRM	FIGGLEHRLD
HCVPOLYP	ATYTKCGSGP	WLTPRCMVDY	PYRLWHYPCT	VNFTIFKVRM	YVGGVEHRLS
HD_1	ATYTRCGSGP	WLTPRCMVDY	PYRLWHYPCT	VNFTIFKVRM	YVGGVEHRLN
HPCCGAA	ATYSRCGSGP	RITPRCMVDY	PYRLWHYPCT	INYTIFKVRM	YVGGVEHRLD
HPCFG	ATFTRCGSGP	WLTPRCLVDY	PYRLWHYPCT	VNFSIFKVRM	FVGGHEHRFS
HPCGENANTI	ATYTKCGSGP	WLTPRCMVDY	PYRLWHYPCT	VNFTIFKVRM	YVGGVEHRLN
HPCGENOM	ATYTRCGSGP	WLTPRCLVDY	PYRLWHYPCT	VNFAIFKVRM	YVGGVEHRLD
HPCHUMR	ATYTKCGSGP	WLTPRCMVDY	PYRLWHYPCT	VNFTIFKVRM	YVGGVEHRLN
HPCJ	ATYTKCGSGP	WLTPRCMVDY	PYRLWHYPCT	VNFTTFKVRM	YVGGVEHRLI
HPCJCG	ATYKCGSGP	WLTPRCMVDY	PYRLWHYPCT	VNFTVFKVRM	YVGGVEHRLN
HPCJK046	ATYAKCGSGP	WLTPRCLVDY	PYRLWHYPCT	VNYTLHKVRM	YIAGSEHRT
HPCJK049	ATYNRCGAGP	WLTPRCLVDY	PYRLWHYPCT	VNYTIFKVRM	FVGGLEHRFN
HPCJTA	ATYTKCGSGP	WLTPRCIVDY	PYRLWHYPCT	VNFTIFKVRM	YVGGVEHRLS
HPCJTB	ATYTKCGSGP	WLTPRCIVDY	PYRLWHYPCT	VNFTIFKVRM	YVGGVEHRLS
HPCK3A	ATYSRCGAGP	WLTPRCLVDY	PYRLWHYPCT	VNFTLHKVRM	FVGGFEHRT
HPCPLYPRE	ATYSRCGSGP	WITPRCLVDY	PYRLWHYPCT	INYTIFKIRM	YVGGVEHRLD
HPCPOLP	TTYIKCGSGP	WLTPRCLIDY	PYRLWHYPCT	VNYTIFKIRM	YVGGVEHRLT
HPCPP	ATYTKCGSGP	WLTPRCLVHY	PYRLWHYPCT	VNFTIFKVRM	YVGGVEHRLD

HPCUNKCD	ATYTKCGSGP	WLTPRCLVDY	PYRLWHYPCT	VNFTIFKVRM	YVGGAEHRLD
MKC1A	ATYTKCGSGP	WLTPRCLVHY	PYRLWHYPCT	VNFTIFKVRM	YVGGVEHRLE
NDM59	ATYIKCGSGP	WLTPRCLVDY	PYRLWHYPCT	INYTIFKIRM	YVGGVEHRLT
NZLI	TTYSRCGAGP	WLTPRCMVDY	PYRLWHYPCT	VDFRLFVKVRM	FVGGFEHRFT
SA13	ATYTKCGSGP	WLTPRCLVHY	PYRLWHYPCT	LNFTIFKVRM	YIGGLEHRLE
Th580	ATYQKCGSGP	WLTPRCLVDY	PYRLWHYPCT	VNYTIHKVRM	FIGGVEHRFD
Type_3a_CB	ATYSRCGAGP	WLTPRCMVDY	PYRLWHYPCT	VNFTLFKVRM	FVGGFEHRFT
TypeV_D	ATYSRCGAGP	WLTPRCMVDY	PYRLWHYPCT	VNFTLFKVRM	FVGGFEHRFT
VN004	ASFVKCGSGP	WLTPRCMVDY	PYRLWHYPCT	VNFTIHKVRV	FVGGVEHRFN
VN235	ATYRKCGSGP	WLTPRCLVDY	PYRLWHYPCT	VNYTIHKVRL	FINGLEHRFD
VN405	ATYARCGSGP	WLTPRCLVNY	PYRLWHYPCT	VNYTIHKVRM	FVGGIEHRFE

	651			700	
BEBE1	AACNFTRGDR	CNLEDNRDRSQ	LSPLLHSTTE	WAILPCSYTD	LPALSTGLLH
D89815	AACNWTRGER	CDLEDNRDRAE	LSPLLLSTTE	WQILPCSYTT	LPALSTGLIH
ED43type_4	AACNWTRGEV	CGLEHRDRVE	LSPLLLTTTA	WQILPCSFTT	LPALSTGLIH
HC_C2	AACNWTRGER	CALEDNRDRSE	LSPLLLSTTE	WQILPCSFTT	LPALSTGLIH
HC_G9	AACNWTRGER	CDLDDRDRAE	LSPLLLSTTQ	WQVLPCSFTT	LPALSTGLIH
HCU16326	AACNWTRGER	CDLEDNRDRSE	LSPLLLSTTE	WQVLPCSFTT	LPALSTGLIH
HCV_H_CMV	AACNWTRGER	CDLEDNRDRSE	LSPLLLSTTQ	WQVLPCSFTT	LPALSTGLIH
HCV_J1	AACNWTRGER	CDLEDNRDRSE	LSPLLLSTTQ	WQVLPCSFTT	LPALSTGLIH
HCV_J483	AACNWTRGER	CNLEDNRDRSE	LSPLLLSTTE	WQILPCAFTT	LPALSTGLIH
HCV_J8	AACNFTRGDR	CRLEDNRDRGQ	QSPLLHSTTE	WAVLPCSFSF	LPALSTGLLH
HCV_JK1	AACNWTRGER	CNIEDNRDRSE	LSPLLLSTTE	WQILPCSFTT	LPALSTGLIH
HCV_JS	AACNWTRGER	CDLEDNRDRSE	LSPLLLSTTE	WQILPCSFTT	LPALSTGLIH
HCV_K1_R1	AACNWTRGER	CDLEDNRDRSE	LSPLLLSTTE	WQILPCSFTT	LPALSTGLIH
HCV_K1_R2	AACNWTRGER	CDLEDNRDRSE	LSPLLLSTTE	WQILPCSFTT	LPVLSTGLIH
HCV_K1_R3	AACNWTRGER	CNLEDNRDRAE	LSPLLLSTTE	WQILPCSFTT	LPALSTGLIH
HCV_K1_S1	AACNWTRGER	CDLEDNRDRSE	LSPLLLSTTE	WQILPCSFTT	LPALSTGLIH
HCV_K1_S2	AACNWTRGER	CDLEDNRDRSE	LSPLLLSTTE	WQILPCSFTT	LPVLSTGLIH
HCV_K1_S3	AACNWTRGER	CNLEDNRDRAE	LSPLLLSTTE	WQILPCSFTT	LPALSTGLIH
HCV_L2	AACNWTRGER	CNLEDNRDRSE	LSPLLLSTTE	WQILPCSFTT	LPALSTGLIH
HCV_N	AACNWTRGER	CDLDDRDRSE	LSPLLLSTTE	WQVLPCSFTT	LPALSTGLIH
HCV12083	VACNWTRGER	CELHNRNRRIE	MSPLLFSTTQ	LSILPCSFSF	MPALSTGLIH
HCV1480	AACNWTYGER	CDLEDNRDRAE	LSPLLLHSTTQ	WAILPCSFTP	TPALSTGLIH
HCVPOLYP	AACNWTRGER	CDLEDNRDRSE	LSPLLLSTTE	WQVLPCSFTT	LPALSTGLIH
HD_1	AACNWTRGER	CDLEDNRDRSE	LSPLLLSTTE	WQVLPCSFTT	LPALSTGLIH
HPCCGAA	AACNWTRGER	CDLEDNRDRSE	LSPLLLSTTQ	WQVLPCSFTT	LPALSTGLIH
HPCFG	AACNWTRGER	CDLEDNRDRSE	QSPLLHSTTD	SLILPCSFTP	MRRLLSTGLIH
HPCGENANTI	AACNWTRGER	CDLEDNRDRSE	LSPLLLSTTE	WQILPCSFTG	LPALSTGLIH
HPCGENOM	AACNWTRGER	CNLEDNRDRSE	LSPLLLSTTE	WQILPCAFTT	LPALSTGLIH
HPCHUMR	AACNWTRGER	CDLEDNRDRPE	LSPLLLSTTE	WQVLPCSFTT	LPALSTGLIH
HPCJ	AACNWTRGDR	CNLEDNRDRSE	LSPLLLSTTE	WQILPCSFTT	LPALSTGLIH
HPCJCG	AACNWTRGER	CDLEDNRDRSE	LSPLLLSTTE	WQILPCSFTT	LPALSTGLIH
HPCJK046	AACNWTRGER	CDLADRDRIE	MSPLLFSTTE	LAILPCSFTT	MPALSTGLIH
HPCJK049	AACNWTRGER	CNLEDNRDRSE	MYPLHSTTE	QAILPCSFPV	IPALSTGLIH
HPCJTA	AACNWTRGER	CDLEDNRDRSE	LSPLLLSTTE	WQTLPCSFTT	LPALSTGLIH
HPCJTB	AACNWTRGER	CDLEDNRDRSE	LSPLLLSTTE	WQTLPCSFTT	LPALSTGLIH
HPCK3A	AACNWTRGER	CDIEDNRDRSE	QHPLHSTTE	LAILPCSFTP	MPALSTGLIH
HPCPLYPRE	AACNWTRGER	CDLEDNRDRSE	LSPLLLTTTQ	WQVLPCSFTT	LPALSTGLIH
HPCPOLP	AACNFTRGDR	CNLEDNRDRSQ	LSPLLHSTTE	WAILPCTYSD	LPALSTGLLH
HPCPP	AACNWTRGER	CDLEDNRDRSE	LSPLLLSTTE	WQVLPCSFTT	LPALSTGLIH
HPCUNKCD	AACNWTRGER	CDLEDNRDRSE	LSPLLLSTTE	WQVLPCSFTT	LPALSTGLIH
MKC1A	AACNWTRGER	CDLEDNRDRSE	LSPLLLSTTE	WQVLPCSFTT	LPALSTGLIH
NDM59	AACNFTRGDP	CNLEDNRDRSQ	LSPLLHSTTE	WAILPCSYSF	LPALSTGLLH
NZLI	AACNWTRGER	CDIEDNRDRSE	QHPLHSTTE	LAILPCSFTP	MPALSTGLIH
SA13	VACNWTRGER	CDLEDNRDRAE	LSPLLLHSTTQ	WAILPCSFTP	TPALSTGLIH
Th580	AACNWTRGDR	CDLYDRDRIE	MSPLLFSTTQ	LAILPCSFTT	MPALSTGLIH
Type_3a_CB	AACNWTRGER	CDIEDNRDRSE	QHPLHSTTE	LAILPCSFTP	MPALSTGLIH
TypeV_D	AACNWTRGER	CNIEDNRDRSE	QHPLHSTTE	LAILPCSFTP	MPALSTGLIH

VN004	AACNWTRGDR	CELDDRRDRFE	MSPLLFSTTQ	LAILPCSFTT	MPALSTGLIH
VN235	AACNWTRGER	CELEDRDRIE	MSPLLFSTTE	LAILPCSFTT	MPALSTGLVH
VN405	AACNWTRGER	CELDDRRDRVE	MSPLLFSTTQ	LSILPCSFTT	MPALSTGLIH
	701				750
BEBE1	LHQNIVDVQY	LYGLSPAITK	YVVKWEWVVL	LFLLLADARV	CACLWMLLLL
D89815	LHQNIVDIQY	LYGIGSAVVS	IAIKWEYVVL	LFLLLADARV	CACLWMMLLI
ED43type_4	LHQNIVDVQY	LYGVGSVAVS	WALKWEYVVL	AFLLLADARV	SAYLWMMFMV
HC_C2	LHRNIVDVQY	LYGIGSAVVS	FAIKWEYVLL	LFLLLADARV	CACLWMMLLI
HC_G9	LHQNIVDVQY	LYGLSSAVTS	WVIKWEYVVL	LFLLLADARI	CACLWMMLLI
HCU16326	LHQNIVDIQY	LYGIGSAVVS	FAIKWEYIVL	LFLLLADARV	CACLWMMLLV
HCV_H_CMV	LHQNIVDVQY	LYGVGSSIAS	WAIKWEYVVL	LFLLLADARV	CSCLWMMLLI
HCV_J1	LHQNIVDVQY	LYGVGSSIAS	WAIKWEYVVL	LFLLLADARV	CSCLWMMLLI
HCV_J483	LHQNIVDVQY	LYGVGSFVVS	FAIKWEYILL	LFLLLADARV	CACLWMMLLI
HCV_J8	LHQNIVDVQY	LYGLSPALTR	YIVKWEWVIL	LFLLLADARI	CACLWMLIIL
HCV_JK1	LHQNIVDVQY	LYGVGSVAVS	IVIKWEYVLL	LFLLLADARV	CACLWMMLLI
HCV_JS	LHRNIVDVQY	LYGIGSAVVS	FAIKWEYVLL	LFLLLADARV	CACLWMMLLI
HCV_K1_R1	LHQNIVDVQY	LYGVGSVAVS	FAIKWEYVLL	LFLLLADARV	CACLWMMLLV
HCV_K1_R2	LHQNIVDVQY	LYGVGSVAVS	FVIKWEYILL	LFLLLADARV	CACLWMMLLI
HCV_K1_R3	LHQNIVDVQY	LYGVGSVAVS	VVIRWEYVLL	LFLLLADARV	CACLWMMLLI
HCV_K1_S1	LHQNIVDVQY	LYGVGSVAVS	FAIKWEYVLL	LFLLLADARV	CACLWMMLLV
HCV_K1_S2	LHQNIVDVQY	LYGVGSVAVS	FVIKWEYILL	LFLLLADARV	CACLWMMLLI
HCV_K1_S3	LHQNIVDVQY	LYGVGSVAVS	VVIRWEYVLL	LFLLLADARV	CACLWMMLLI
HCV_L2	LHQNIVDVQY	LYGIGSAVVS	FVIKWEYVLL	LFLLLADARV	CACLWMMLLI
HCV_N	LHQNIVDVQY	LYGIGSAVVS	FAIKWEYVVL	LFLLLADARV	CACLWMMLLI
HCV12083	LHQNIVDVQY	LYGVSTNVTS	WVVKWEYIVL	MFLVLADARI	CTCLWLMLLI
HCV1480	LHQNIVDTQY	LYGLSSSIIVS	WAVKWEYIML	VFLLLADARI	CTCLLILLLI
HCVPOLYP	LHQNIVDVQY	LYGIGSVVVS	FAIKWEYVVL	LFLLLADARV	CACLWMMLLI
HD_1	LHQNVVDVQY	LYGIGSVVVS	FAIKWEYILL	LFLLLADARV	CACLWMMLLI
HPCCGAA	LHQNIVDVQY	LYGVGSSIAS	WAIKWEYVVL	LFLLLADARV	CSCLWMMLLI
HPCFG	LHQNIVDVQY	LYGVGSVAVS	WALKWEFVVL	VFLLLADARV	CVALWMMLLI
HPCGENANT1	LHQNVVDVQY	LYGIGSAVVS	FAIKWEYILL	LFLLLADARV	CACLWMMLLI
HPCGENOM	LHQNIVDVQY	LYGIGSAVAS	FAIKWEYVLL	LFLLLADARV	CACLWMMLLI
HPCHUMR	LHQNIVDVQY	LYGIGSAVVS	FAIKWEYVLL	LFLLLADARV	CACLWMMLLI
HPCJ	LHQNIVDVQY	LYGIGSAVVS	IAIRWEYVLL	LFLLLADARV	CACLWMMLLI
HPCJCG	LHRNIVDVQY	LYGIGSAVVS	FAIKWEYILL	LFLLLADARV	CACLWMMLLI
HPCJK046	LHQNVVDVQY	LYGLSTSIVN	WAIKWEYVVL	LFLVLADSRI	CLALWLMLLI
HPCJK049	LHQNIVDVQY	LYGISSGLVG	WAIKWEFVIL	IFLLLLADARV	CVVLWMMLLI
HPCJTA	LHQNIVDVQY	LYGIGSAVVS	FVIKWEYIVL	LFLLLADARV	CACLWMMLLI
HPCJTB	LHQNIVDVQY	LYGIGSAVVS	FVIKWEYIVL	LFLLLADARV	CACLWMMLLI
HPCK3A	LHQNIVDVQY	LYGIGSGMVG	WALKWEFVIL	IFLLLLADARV	CVALWLILTI
HPCPLYPRE	LHQNIVDVQY	LYGVGSSIAS	WAIKWEYVVL	LFLLLADARV	CSCLWMMLLI
HPCPOLP	LHQNIVDVQF	MYGLSPALTK	YIVRWEWVVL	LFLLLADARV	CACLWMLLIL
HPCPP	LHQNIVDVQY	LYGIGSAVVS	FAIKWEYILL	LFLPLADARV	CAWLWMMLLI
HPCUNKCD	LHQNIVDIQY	LYGIGSAVVS	FAIKWEYIVL	LFLLLADARV	CACLWMMLLV
MKC1A	LHQNIVDVQY	LYGIGSAVVS	FAIKWEYILL	LFLPLADARV	CAWLWMMLLI
NDM59	LHQNIVDVQY	MYGLSPALTK	YIVRWEWVVL	LFLLLADARV	CACLWMLLIL
NZLI	LHQNIVDVQY	LYGVGSGMVG	WALKWEFVIL	VFLLLADARV	CVALWLMLMI
SA13	LHQNIVDTQY	LYGLSSSIIVS	WAVKWEYIVL	AFLLLADARI	CTCLWIMLLV
Th580	LHQNIVDVQY	LYGVSSSIIVS	WAVKWEYVVL	MFLVLADARI	CTCLWLMLLV
Type_3a_CB	LHQNIVDVQY	LYGVGSGMVG	WALKWEFVIL	IFLLLLADRRV	CVALWLMLMI
TypeV_D	LHQNIVDVQY	LYGVGSGMVG	WALKWEFVIL	IFLLLLADARV	CVALWLMLMI
VN004	LHQNIVDIQY	LYGVSTAVVS	WAMKWEYVVL	AFLVLADARV	CACLWLMFLV
VN235	LHQNIVDIQY	LYGLAPALVS	WAVRWEYVVL	AFLLLADARI	CACLWMVLLI
VN405	LHQNIVDVQY	LYGVSSAVVS	WAVKWEYIVL	AFLVLAVARV	CACLWLMFLV
	751				800
BEBE1	GQAEAALEKL	VILHAASAAS	SNGLLYFILF	FVAAWCIKGR	AVPMVITYTLL
D89815	AQAEAALENL	VVLNAASVVG	AHGMLPFFMF	FCAAWYMKGR	LVPGAAYAFY
ED43type_4	SQVEAALSNL	ININAASAAG	AQGFWYAILF	ICIVWHVKGR	FPAAAAAYAC

HC_C2	AQAEAALENL	VVLNAASVAG	VHGILSFLVF	FCAAWYIKGR	LVPGAAYAFY
HC_G9	SQVEAALENL	IVLNAASLVG	THGIVPFFIF	FCAAWYLKGR	WAPGLAYSVY
HCU16326	AQAEAALENL	VVLNAASVAG	AHGILSFIVF	FCAAWYIKGR	LVPGAAYALY
HCV_H_CMV	SQAEAALENL	VILNAASLAG	THGLVSFLVF	FCFAWYLKGR	WVPGAVYAFY
HCV_J1	SQAEAALENL	VILNAASLAG	TRGLVSFLVF	FCFAWYLKGR	WVPGAAAYALY
HCV_J483	AQAEAALENL	VVLNAASVAG	AHGILSFLVF	FCAAWYIKGR	LAPGAAYAFY
HCV_J8	GQAEAALEKL	IILHSASAAS	ANGPLWFFIF	FTAAWYLKGR	VVPVATYSVL
HCV_JK1	AQAEAALENL	VVLNAASVAG	AHGILSFLVF	FCAAWYIKGR	LVPGAAYAFY
HCV_JS	AQAEAALENL	VVLNAASVAG	AHGILSFLVF	FCAAWCIKGR	LVPGAAYAFY
HCV_K1_R1	AQAEAALENL	VVLNAASLAG	VHGILSFLVF	FCAAWYIKGR	LVPGAAYALY
HCV_K1_R2	AQAEAALENL	VVLNAASVAG	AHGFLSFLVF	FCAAWYIKGR	LVPGAAYAFY
HCV_K1_R3	AQAEAALENL	VILNAASVAG	AHGILSFLVF	FCAAWYIKGR	LVPGAAYAFY
HCV_K1_S1	AQAEAALENL	VVLNAASLAG	VHGILSFLVF	FCAAWYIKGR	LVPGAAYALY
HCV_K1_S2	AQAEAALENL	VVLNAASVAG	AHGFLSFLVF	FCAAWYIKGR	LVPGAAYAFY
HCV_K1_S3	AQAEAALENL	VILNAASVAG	AHGILSFLVF	FCAAWYIKGR	LVPGAAYAFY
HCV_L2	AQAEAALENL	VVLNAASVAG	AHGILSFLVF	FCAAWYIKGR	LVPGAAYASY
HCV_N	ARAEAALENL	VALNAASVAG	AHGILSFLVF	FCAAWYIKGR	LVPGAAYAFY
HCV12083	STVEAAVERL	VVLNAASAAG	TAGWWWAVLF	LCCVWYVKGR	LVPACTYMAL
HCV1480	CQAEATCKNV	IVLNAAAAAG	NHGFFWGLLV	VCLAWHVKGR	LVPGATYLCL
HCVPOLYP	AQAEAALENL	VVLNAASVAG	AHGILSFLVF	FCAAWYIKGR	LVPGAAYAIY
HD_1	AQAEAALENL	VVLNAASLAG	THGILSFLVF	FCAAWYIKGR	LVPGAAYALY
HPCCGAA	SQAEAALENL	VILNAASLAG	THGLVSFLVF	FCFAWYLKGR	WVPGAVYALY
HPCFG	SQAEAALENL	VMLNALSAG	QQGYVWYLVA	FCAAWHIRGK	LVPLITYGLT
HPCGENANTI	AQAEAALENL	VVFNAASVAG	MHGTLISFLVF	FCAAWYIKGR	LVPGAAYALY
HPCGENOM	AQAEAALENL	VVLNAASVAD	AHGILSFLVF	FCAAWYIKGR	LVPGAAYAFY
HPCHUMR	AQAEAALENL	VVLNSASVAG	AHGILSFLVF	FCAAWYIKGR	LVPGATYALY
HPCJ	AQAEAALENL	VVLNAASVAG	AHGILSFLVF	FCAAWYIKGR	LVPGAAYALY
HPCJCG	AQAEATLENL	VVLNAASVAG	AHGILSFLVF	FCAAWYIKGR	LVPGAAYALY
HPCJK046	GQAEAALENL	IVLNAASAAA	TRGWECFLLF	MCWAWYVRGR	VVPAVITYGLL
HPCJK049	SQAEAALENL	IVLNAISAAG	THGIWWSLVA	FCVAWHVRGR	IFPIAVYSIV
HPCJTA	AQAEAALENL	VVLNAASLAG	ADGILSFLVF	FCAAWYIKGR	LVPGAAYALY
HPCJTB	AQAEAALENL	VVLNAASLAG	AHGILSFLVF	FCAAWYIKGR	LVPGAAYALY
HPCK3A	SQAEAALENL	VTLNAVAAAAG	THGIGWYLVA	FCAAWYVRGK	LVPLVITYSLT
HPCPLYPRE	SQAEAALENL	VILNAASLAG	THGLVSFLVF	FCFAWYLKGR	WVPGAVYTFY
HPCPOLP	GQAEAALEKL	VVLHAASAAS	CNGFLYFVIF	FVAAWYIKGR	VVPLATYSLT
HPCPP	AQAEAALENL	VVLNAASMAG	AHGILSFLVF	FCAAWYIKGR	LVPGAAYAFY
HPCUNKCD	AQAEAALENL	VVLNAASVAG	AHGILSFIVF	FCAAWYIKGR	LVPGAAYALY
MKC1A	AQAEAALENL	VVLNAASMAG	AHGILSFLVF	FCAAWYIKGR	LVPGAAYAFY
NDM59	GQAEAALEKL	VVLHAASAAS	CNGFLYFVIF	FVAAWYIKGR	AVPLAAYSALT
NZLI	SQTEAALENL	VTLNAVAAAAG	THGIGWYLVA	FCAAWYVRGK	LVPLVITYSLT
SA13	CQAEAALENV	IVLNAAAAAG	THGFFWGLLV	ICFAWHFKGR	LVPGATYLCL
Th580	GKVEAALERL	VVLNAASAAG	TAGWCWTLIF	LCCVWHVKGR	LVPACTYTAL
Type_3a_CB	TQAEAALENL	VTLNAVAAAAG	THGIGWYLVA	FCAAWYVRGK	LVPVITYSLT
TypeV_D	TQAEAALENL	VTLKAVAAAAG	THGIGWYLVA	FCAAWHVRGK	LVPLVITYSLT
VN004	GQAEAALENV	IVLNAASAAS	CQGLLWGLIF	ICCAWHVRGR	AVPVTTYALL
VN235	SQVEAALENL	IVLNAASAAS	SQGWYICLVF	ICCAWYIKGR	VVPGATYAIL
VN405	GQAEAALENL	IVLNATSAAAG	SQGWVWGVVF	ICAAWYIRGR	AAPITTYAIL

	801				850
BEBE1	GCWSFVLLLM	ALPHQAYALD	AAEQGQIGMA	LLIAITAFTI	TPAYKILLSR
D89815	GVWPLLLLLL	ALPPRAYAMD	REMVASCGGG	VFVGLALLTL	SPYCKVFLAR
ED43type_4	GLWPFCFLLLL	MLPERAYAYD	QEVAGSLGGA	IVVMLTILTL	SPHYKLWLAR
HC_C2	GVWPLLLLLL	ALPPRAYAMA	REMAASCGGA	VFVGLALLTL	SPYYKVFLAR
HC_G9	GMWPLLLLLL	ALPQRAYALD	QELAASCGAT	VFICLAVLTL	SPYYKQYMAR
HCU16326	GVWPLLLLLL	ALPPRAYAMD	REMAASCGGA	VFVGLVLLTL	SPHYKVFLAR
HCV_H_CMV	GMWPLLLLLL	ALPQRAYALD	TEVAASCGGV	VLVGLMALTL	SPYYKRYISW
HCV_J1	GMWPLLLLLL	ALPQRAYALD	TEVAASCGGV	VLVGLMALTL	SPYYKRCISW
HCV_J483	GVWPLLLLLL	ALPPRAYAMD	REMAASCGGA	VLVGLVFLTL	SPYYKVFLTR
HCV_J8	GLWSFLLLV	ALPQQAYALD	AAEQGELGLA	ILVIISIFTL	TPAYKILLSR
HCV_JK1	GVWPLLLLLL	ALPPRAYAMD	REMAASCGGA	VFVGLALLTL	SPHYKAFLAR

HCV_JS	GVWPLLLLLL	ALPPRAFAMD	REMAASCGBA	VFVGLALLTL	SPHYKVFLAR
HCV_K1_R1	GVWPLLLLLL	ALPPRAYAMD	REMAASCGBA	VFIGLALLTL	SPYYKVFLAK
HCV_K1_R2	GVWPLLLLLL	ALPPRAYAMD	REMAASCGBA	VFVGLALLTL	SPHYKVVLAR
HCV_K1_R3	GVWPLLLLLL	SLPPRAYAMD	REMAASCGBA	VFIGLMALLTL	SPHYKAFLAK
HCV_K1_S1	GVWPLLLLLL	ALPPRAYAMD	REMAASCGBV	VFVGLALLTL	SPYYKVFLAR
HCV_K1_S2	GVWPLLLLLL	ALPPRAYAMD	REMAASCGBA	VFVGLALLTL	SPHYKVVLAR
HCV_K1_S3	GVWPLLLLLL	SLPPRAYAMD	REMAASCGBA	VFIGLILLTL	SPHYKAFLAK
HCV_L2	GVWPLLLLLL	ALPPRAYAMD	QGMAASSGGT	VLVGLMALLTL	SPYYKVVLAR
HCV_N	GAWPLLLLLL	TLPPRAYAMD	REMAASCGBA	VFVGLALLTL	SPYYKVFLAR
HCV12083	GMWPLLLTIL	ALPPRAYAMD	NEQAASLGAV	GLLVITIFSI	TPMYKKLLNC
HCV1480	GVWPLLLVRL	LRPHRALALD	SSDGGTVGCL	VLIVLTIFTL	TPGYKKKVVL
HCVPOLYP	GVWPLLLLLL	ALPPRAYALD	REMAASCGBA	VFVGLVLLTL	SPHYKEFLAR
HD_1	GVWPLLLLLL	ALPPRAYALD	REMAASCGBA	VFVGLIILLTL	SPHYKAFLAR
HPCCGAA	GMWPLLLLLL	ALPQRAYALD	TEVAASCGBV	VLVGLMALLTL	SPYYKRYISW
HPCFG	GLWPLALLDL	LLPQRAYAWT	GEDDATIGAG	VLLLGLGFFTL	SPWYKHWIGR
HPCGENANTI	GVWPLLLLLL	ALPPRAYAMD	REMAASCGBA	VFVGLVLLTL	SPHYKMFLAR
HPCGENOM	GVWPLLLLLL	TLPPRAYAMD	REMAASCGBA	VFVGLVFLTL	SPYYKVFLAR
HPCHUMR	GVWPLLLLLL	ALPPRAYAMD	REMAASCGBA	VFVGLVLLTL	SPYYKVFLAR
HPCJ	GVWPLLLLLL	ALPPRAYAMD	REMAASCGBA	VFMGLAFLTL	SPHYKVFLAR
HPCJCG	GVWPLLLLLL	ALPPRAYAMD	REMAASCGBA	VFVGLVLLTL	SPYYKVFLAR
HPCJK046	NLWPLLLLVL	LLPHRAYAYD	GVQAGSIGAA	VIAALTIFSL	TPAYKTLLAH
HPCJK049	GLWPLLLLVL	MLPYRAYAWT	GTDTSTLGAG	VLSLFALFTL	SPWYKHWIAR
HPCJTA	GVWPLLLLLL	ALPPRAYAMD	REMAASCGBV	VFVGLIILLTL	SPHYKVFLAR
HPCJTB	GVWPLLLLLL	ALPPRAYAMD	REMAASCGBV	VFLGLILLTL	SPHYKVFLAR
HPCK3A	GLWSLALLVL	LLPQRAYAWS	GEDSATLGAG	ILVLFGLFTL	SPWYKHWIAR
HPCPLYPRE	GMWPLLLLLL	ALPQRAYALD	TEVAASCGBV	VLVGLMALLTL	SPYYKRYISW
HPCPOLP	GLWSFGLLLL	ALPQQAYAYD	ASVHGQIGAA	LLVLITLFTL	TPGYKTLLSR
HPCPP	GVWPLLLLLM	ALPARAYAMD	REMAASCGBA	VFVGLVLLTL	SPYYKVFLAK
HPCUNKCD	GVWPLLLLLL	ALPPRAYAMD	REMAASCGBA	VFVGLVLLTL	SPHYKVFLAR
MKC1A	GVWPLLLLLM	ALPARAYAMD	REMAASCGBA	VFVGLVLLTL	SPYYKVFLAK
NDM59	GLWPFCLLLL	ALPQQAYAYD	ASVHGQTGVA	LLILITLFTL	TPGYKILLSR
NZLI	GLWSLALLVL	LLPQRAYAWS	GEDSATLGAG	VLVLFGLFTL	SPWYKHWIGR
SA13	GIWPLLLLLF	LLPQRALALD	SSDGGTVGCL	VLITLIFTL	TPGYKKMVVL
Th580	GMWPILLVIL	ALPQRAYAWD	NSQAASLGVV	ALLVLTIFTL	SPMYKQLLTH
Type_3a_CB	GLWPLALLVL	MLPQRAYAWS	GEDSATLGAG	VLALFGFFTL	SPWYKHWIGR
TypeV_D	GLWSLALLVL	LLPQRAYAWS	GEDSATLGAG	VLVLFGLFTL	SPWYKHWIGR
VN004	QLWPLLLLIL	ALPRRAYAFD	SEQAASAGLL	VLGLITIFTL	TPAYKQLLIS
VN235	HLWPLLLLVL	ALPQRAYAQD	REQGASIGVV	VIAAITIFTL	TPAYKTMLVH
VN405	QLWPLLLLVL	ALPRRAYAYN	GEEAASLGML	AIVIITIFTL	TPAYKTLLIS

	851			900	
BEBE1	CLWWTCYMLV	LAEALIQDWI	PPLQARGGRD	GVIWAMTMFY	PGVVFEDITKW
D89815	LIWWLQYFIT	KAE AHLQVSL	PPLNVRGGRD	AIILLMCAVH	PELIFDITKL
ED43type_4	GLWWIQYFIA	RTEAVLHVYI	PSFNVRGPRD	SVIVLAVLVC	PDLVFDITKY
HC_C2	LIWWLQYFIT	RAE AHLQVWI	PPLNVRGGRD	AIILLTCAAH	PELIFDITKL
HC_G9	GIWWLQYMLT	RAE ALLQVWV	PPLNARGGRD	GVVLLTCVLH	PHLLFEITKI
HCU16326	FIWWLQYLIT	RTEAHLQVWV	PPLNVRGGRD	AIILLTCVVH	PELIFDITKY
HCV_H_CMV	CMWWLQYFLT	RVEAQLHVWV	PPLNVRGGRD	AVILLMCVVH	PTLVFDITKL
HCV_J1	CLWWLQYFLT	RVEAQLHVWV	PPLNVRGGRD	AVILLMCVVH	PTLVFDITKL
HCV_J483	LIWWLQYFIT	RAE AHMQVWV	PPLNVRGGRD	AIILLTCAVH	PELIFDITKL
HCV_J8	SVWWLSYMLV	LAE AQIQWV	PPLEVRGGRD	GIIWVAVILH	PRLVFEVTKW
HCV_JK1	LIWWLQYFIT	RVEACLQVWV	PPLNVRGGRD	AIILLTCAVH	SELIFDITKI
HCV_JS	LMWRLQYLIT	RAE AHLQIWV	PPLNIRGGRD	AIILLMCAVH	PELIFDITKL
HCV_K1_R1	LIWWLQYLIT	RAE AQLQVWI	PPLNVRGGRD	AIILLTCAVH	PELIFDITKI
HCV_K1_R2	LIWWLQYFIT	RAE ACLQVWI	PPLNVRGGRD	AIILLTCALH	PELIFSITKI
HCV_K1_R3	LIWWLQYFIT	RAE AHLQVWI	PPLNVRGGRD	AIILLTCAVH	SELVFEITKI
HCV_K1_S1	LIWWLQYLIT	RAE AQLQVWI	PPLNVRGGRG	AIILLTCVVH	PELIFDITKI
HCV_K1_S2	LIWWLQYFIT	RAE ACLQVWI	PPLNVRGGRD	AIILLTCALH	PELIFSITKI
HCV_K1_S3	LIWWLQYFIT	RAE AHLQVWI	PPLNVRGGRD	AIILLTCAVH	SELVFEITKI
HCV_L2	LIWWLQYFIT	RAE AHLQVWV	PPLNVRGGRD	AVILLTCAVY	PELVFDITKL

HCV_N	LIWWLQYLIA	RAEAHLHVWV	PPLNVRGGRD	AIILLTCAVH	PELIFDITKL
HCV12083	FIWWNQYFLA	RAEAMVHEWV	PDLRVRGGRD	SIILLTCLLH	PQLGFEVTKI
HCV1480	VMWWLQYFIA	RVEAIIHVWV	PPLQVKGGRD	AVIMLTCLFH	PALGFEITKI
HCVPOLYP	LIWWLQYYIT	RAEALLQVWI	PPLNVRGGRD	AIILLTCVVH	PELIFDITKL
HD_1	LIWWLQYFIT	RAEALLQVWI	PPLNVRGGRD	AIILLTCAVH	PGLIFDITRL
HPCCGAA	CMWWLQYFLT	RVEAQLHVWV	PPLNVRGGRD	AVILLTCVVH	PALVFDITKL
HPCFG	LIWWNQYAIC	RGEAALQVWV	PPLLVRGSRD	SVILLASLLY	PSLIFDITKL
HPCGENANTI	LIWWLQYFIT	RAEAHLQVWI	PPLNVRGGRD	AIILLTCAAY	PELIFDITKI
HPCGENOM	LIWWLQYFLT	IAEAHLQVWI	PPLNIRGGRD	AIILLTCAIH	PESIFDITKL
HPCHUMR	LIWWLQYFTT	RAEADLHVWI	PPLNARGGRD	AIILLMCAVH	PELIFDITKL
HPCJ	LIWWLQYLLT	RAEAHLHMI	PPLNVRGGRD	AIILLACAAH	PELIFDITKL
HPCJCG	LIWWLQYFIT	RAEAHLQVWV	PPLNVRGGRD	AIILLTCAVH	PELIFDITKL
HPCJK046	FLWWTQYFIA	HIEAKLHVWV	PFLRVRGGRD	AIILLTCVFH	PSLGFEVTKI
HPCJK049	LIWWNQYTIA	RCEAALQIWI	PPLLARGARD	GIILLAGLFY	PALVFDITKL
HPCJTA	LIWWLQYFIT	RAEAHLQVWV	PPLNVRGGRD	AIILLTCAAH	PELIFDITKL
HPCJTB	LIWWLQYFIT	RAEAHLQVWV	PPLNVRGGRD	AIILLTCAAH	PELIFDITKL
HPCK3A	LIWWNQYTIC	RCEAHLQVWV	PPLLARGGRD	GVILLTSLLY	PSLIFDITKL
HPCPLYPRE	CLWWLQYFLT	RVEAQLHVWI	PPLNVRGGRD	AVILLMCAVH	PTLVFDITKL
HPCPOLP	FLWWLCYLLT	LAEAMVQEWA	PPMQVRGGRD	GIIWAVAIFC	PGVVFDTKW
HPCPP	LIWWLQYLIT	RAEAHLQVWI	PPLNVRGGRD	AIILLTCAVH	PELIFDITKL
HPCUNKCD	FIWWLQYLIT	RTEAHLQVWV	PPLNVRGGRD	AIILLTCVVH	PELIFDITKY
MKC1A	LIWWLQYLIT	RAEAHLQVWI	PPLNVRGGRD	AIILLTCAVH	PELIFDITKL
NDM59	SLWWLCYLLT	LGEAMIQEWV	PPMQARGGRD	GIIWAATMFC	PGVVFDTKW
NZLI	LMWWNQYTIC	RCEAHLQVWV	PPLLARGSRD	GVILLTSLLY	PSLIFDITKL
SA13	VIWWLQYFIA	RVEAFIHVWV	PPLQVRGGRD	AIIMLTCLFH	PALGFEVTKI
Th580	AIWWNQYMLA	RAEAMIHDWV	PDLRVRGGRD	AIILLTCLLH	PHLGFEVTKI
Type_3a_CB	LIWWNQYTIC	RCEAHLQVWV	PPLLARGSRD	GVILLTSLLY	PSLIFDITKL
TypeV_D	LIWWNQYTIC	RCEAHLQVWV	PPLLARGSRD	GVILLTSLLY	PSLIFDITKL
VN004	MLWWIQYFIA	LTEAQLHQWV	PSLLVRGGRD	AVILLACLFLH	PQLGFEVTKI
VN235	FLWWNQYFIA	RSEALIQQWV	PSLRVRGGRD	AVILLTCLLH	PSLGFDITKM
VN405	TLWWIQYYIA	RAEAMLYVWV	PSLQVRGGRD	AVILLTCLLH	PQLGFEVTKA

	901			950	
BEBE1	LLAILGPGYL	FRAAVMRTPY	FVRANALLRM	CALVKQLAGG	KYVQVALITL
D89815	LLSILGPLMV	LQASLIRVPY	FVRAQGLIRA	CMLVRKAAGG	HYVQMAFVKL
ED43type_4	LLAILGPLHI	LQASLLRIPY	FVRAQALVKI	CSLLRGVVYV	KYFQMVVLKS
HC_C2	LLAIFGPIMV	LQAGITKMPY	FVRAQGLIRA	CMLVRKVAGG	HYVQMAFMKL
HC_G9	MLAILGPLWI	LQASLLKVPY	FVRAHGLIRL	CMLVRKTAGG	QYVQMAALLKL
HCU16326	LLAIFGPLMV	LQAGITRVPY	FVRAQGLIRA	CMLARKVVGG	HYVQMVFMKL
HCV_H_CMV	LLAIFGPLWI	LQASLLKVPY	FVRVQGLLRI	CALARKIAGG	HYVQMAI IKL
HCV_J1	LLAVLGPLWI	LQASLLKVPY	FVRVQGLLRI	CALARKMVGG	HYVQMAI IKL
HCV_J483	LLAILGPLMV	LQAGITRVPY	FVRAQGLIRA	CMLVRKVAGG	HYVQMAFMKL
HCV_J8	LLAILGPAYL	LKASLLRIPY	FVRAHALLRV	CTLVKHLAGA	RYIQMLLITI
HCV_JK1	LLAIFGPLMV	LQAGLTRVPY	FVRAQGLLRA	CMLVRKVAGG	HYVQMALMKL
HCV_JS	LLAILGPLMV	LQAGITRVPY	FVRAQGLIRA	CMLVRKVAGG	HYVQMAFVKL
HCV_K1_R1	VLAILGPLMV	LQAGIAKVPD	FVRAQGVIRE	CILVRKVGGG	QYVQMAFMKL
HCV_K1_R2	LVAILGPLMV	LQAGITKMPY	FVRAQGLIRA	CMLVRKVAGG	HYVQMAFMKL
HCV_K1_R3	LLAIFGPLMV	LQAGLTKVPY	FVRAQGLIRA	CMLVRKVAGG	HYVQMAFVKL
HCV_K1_S1	MLAILGPLMV	LQAGIAKVPD	FVRAQGVIRE	CILVRKVGGG	QYVQMAFMKL
HCV_K1_S2	LVAILGPLMV	LQAGITKMPY	FVRAQGLIRA	CMLVRKVAGG	HYVQMAFMKL
HCV_K1_S3	LLAIFGPLMV	LQAGLIRVPY	FVRAQGLIRV	CMLVRKVAGG	HYVQMAFVKL
HCV_L2	LLAIFGPLMV	LQAGIIMKPY	FVRAQGLIRA	CMLVRKVAGG	HYVQMAFMKL
HCV_N	LLAILGPLMV	LQAGITRVPY	FVRAQGLIRA	CMLVRKVAGG	HYVQMAFMRL
HCV12083	LLAVLAPLYI	LQYSLLKVPY	FVRAHILLRA	CLLVRRLAGG	KYVQACLLRL
HCV1480	LFGILGPLYL	LQHSLLKVPY	FLRARALLRL	CLLAKHLVYG	KYVQAALLHL
HCVPOLYP	LLAMLGPPMV	LQAVITKVPY	FVRAQGLIRA	CMLVRKVAGG	HYVQMALMKL
HD_1	LLAILGPLMV	LQAGITRVPY	FVRAHGLIRA	CMLVRKVAGG	HYVQMAFMKL
HPCCGAA	LLAIFGPLWI	LQASLLKVPY	FVRVQGLLRI	CALARKIAGG	HYVQMAI IKL
HPCFG	LI AVLGPLYL	IQAALTSTPY	FVRAHVLIRI	CMLVRSAMGG	KYVQMAVLTV
HPCGENANTI	LLAILGPLMV	LQAGLTRIPY	FVRAQGLIRA	CMLVRKAAGG	HYVQMALMKL

HPCGENOM	LLATLGPLL	LQAGITRVPY	FVRAHGLIRA	CMLLRKVAGG	HYVQMAFMKL
HPCHUMR	LIALLGPLMV	LQAGITRVPY	FVRAQGLIHA	CMLVRKVAGG	HYVQMAFMKL
HPCJ	LLAILGPLYM	LQAGITAVPY	FVRAQGLIRA	CMLVRKVAGG	HYVQMAFMKL
HPCJCG	LLAILGPLMV	LQAGITRVPY	FVRAQGLIRA	CMLVRKVAGG	HYVQMAFMKL
HPCJK046	LLALIGPLYL	LHASLLRVPY	YVRAHALIRI	CALVQNVAGG	KYVQAAILRA
HPCJK049	LLAILGPLYI	LQASLVRVPY	FVRAHAVVRL	CILVRNITGG	KYVQMVLLAL
HPCJTA	LLAILGPLMV	LQAAITAMPY	FVRAQGLIRA	CMLVRKVAGG	HYVQMAFMKL
HPCJTB	LLAILGPLMV	LQAAITAMPY	FVRAQGLIRA	CMLVRKVAGG	HYVQMAFMKL
HPCK3A	LIAALGPLYL	IQATITATPY	FVRAHVLVRL	CMLVRSVMGG	KYFQMIILSL
HPCPLYPRE	LLAVFGPLWI	LQASLLKVPY	FVRVQGLLRF	CALARKMIGG	HYVQMVIIKL
HPCPOLP	LLAVLGPAYL	LKGALTRVPY	FVRAHALLRM	CTMVRHLAGG	RYVQMVLLAL
HPCPP	LLAILGPLMV	LQAGLTQMPY	FVRAQGLIRM	CMLVRKAAGG	HYVQMALMKL
HPCUNKCD	LLAIFGPLMV	LQAGITRVPY	FVRAQGLIRA	CMLARKVVG	HYVQMVFMKL
MCK1A	LLAILGPLMV	LQAGITRVPY	FVRAQGLIRA	CMLVWKAAGG	HYVQMAFVKL
NDM59	LLAMLGPAYL	LRDALTRVPY	FVRAHALLRL	CTMVRHLAGG	RYVQMALLAL
NZLI	LMAVLGPLYL	IQATITTTTPY	FVRAHVLVRL	CMLVRSVIGG	KYFQMIILSI
SA13	LLGILGPLYL	LQYSLIKLPY	FIRARALLRA	CLLAKHLACG	RYVQAALLHL
Th580	LLAILAPLYI	LQHSLLKVPY	FVRAHILLRA	CMFFRKVAAG	KYVQACLLRL
Type_3a_CB	LIAVLGPLYL	IQAAVTTTPY	FVRAQVLVRL	CMLVRSVMGG	KYFQMIILSI
TypeV_D	LIAVLGPLYL	IQASITATPY	FVRAHVLVRL	CMLVRSMMGG	KYFQMIILSV
VN004	LLALLGPLYL	LQYSLLKTPY	FVRAHILLRA	CMFFRGMARG	RYAQAILLRI
VN235	LLALLGPLYL	LQVSLLRVPY	YVRAHALLRV	CILVRRVAGG	KYIQAALLKL
VN405	ILALLGPLYI	LQYSLLKTPY	FVRAHILLRV	CMFLRGVAGG	KYVQAALLRL

	951				1000
BEBE1	GKWTGTYYID	HLSPMSDWAA	DGLRDLAVAV	EPIVFSFPMER	KVIVWGAETT
D89815	AALTGTYYVD	HLTPLQDWAH	VGLRDLAVAV	EPVVFSAFMET	KVITWGADTA
ED43type_4	RGLTGTYYID	HLTPMSDWPP	YGLRDLAVAL	EPVVFTPMER	KVIVWGADTA
HC_C2	AALTGTYYVD	HLTPLRDWAH	TGLRDLAVAV	EPVVFSDMET	KIITWGADTA
HC_G9	GAFAGTYIYN	HLSPQLDWAH	SGLRDLAVAT	EPVIFSRMEI	KTITWGADTA
HCU16326	AALAGTYVYD	HLTPLRDWAH	TGLRDLAVAV	EPVVFSDMET	KVITWGADTA
HCV_H_CM	GALTGTYYVN	HLTPLRDWAH	NGLRDLAVAV	EPVVFSDMET	KLITWGADTA
HCV_J1	GALTGTYYVN	HLTPLRDWAH	NGLRDLAVAV	EPVVFSDMET	KLITWGADTA
HCV_J483	GALTGTYYVN	HLTPLRDWAH	AGLRDLAVAV	EPVVFSDMET	KVITWGADTA
HCV_J8	GRWTGTYYID	HLSPPLSTWAA	QGLRDLAIAV	EPVVFSPMEK	KVIVWGAETV
HCV_JK1	AALTGTYYVD	HLTPLRDWAH	SGLRDLVAV	EPVVFSDMET	KIITWGADTA
HCV_JS	AALTGTYYVD	HLAPLQHWAH	TGLRDLAVAV	EPVVFSDMET	KIITWGADTA
HCV_K1_R1	AELKGTSVYD	HLTPLRDWAH	TGLRDLAVAV	EPVVFSDMET	KIITWGADTA
HCV_K1_R2	AALTGTYYVD	HLTPLQDWAH	TGLRDLAVAV	EPVVFSDMET	KIITWGADTA
HCV_K1_R3	AALTGTYYVN	HLTPLQDWAH	TGLRDLAVAV	EPVVFSDMET	KIITWGADTA
HCV_K1_S1	AELKGTSVYD	HLTPLQDWAH	TGLRDLAVAV	EPVVFSDMET	KIITWGADTA
HCV_K1_S2	AALTGTYYVD	HLTPLQDWAH	AGLRDLAVAV	EPVVFSDMET	KIITWGADTA
HCV_K1_S3	AALTGTYYVN	HLTPLQDWAH	TGLRDLAVAV	EPVVFSDMET	KIITWGADTA
HCV_L2	AALTGTYYVD	HLTPLRDWAH	TGLRDLAVAV	EPVVFSDMET	KIITWGADTA
HCV_N	GALTGTYYVN	HLTPLRDWAH	AGLRDLAVAV	EPVTFSDMET	KIITWGADTA
HCV12083	GAWTGTFFVD	HLAPLSDWAS	DGLRDLAVAV	EPVIFSPMEK	KIITWGADTA
HCV1480	GRLTGTYYID	HLAPMKDWAA	SGLRELTVAT	EPIVFSFAMET	KVITWGADTA
HCVPOLYP	AGLTSTYYVD	HLTPLQDWAH	GGLRDLAVAV	EPVVFSDMET	KIITWGADTA
HD_1	AALTGTYYVD	HLTPLRDWRH	AGLRDLAVAV	EPVVFSAFMET	KIITWGADTA
HPCCGAA	GALTGTVCYN	HLAPLRDWAH	NGLRDLAVAV	EPVVFSDMET	KLITWGADTA
HPCFG	GRWFNTYLYD	HLSPQLDWAH	EGLKGLAVAT	EPVIFSPMEI	KVITWGADTA
HPCGENANTI	AALTGTYYVD	HLTPLQDWAH	TGLRDLAVAV	EPVVFSDMET	KIITWGADTA
HPCGENOM	GALTGTYYVN	HLTPLQYWRP	AGLRELAVAV	EPVIFSDMET	KIITWGADTA
HPCHUMR	GALTGTYYIYN	HLTPLRDWRP	AGLRDLAVAV	EPVVFSDMET	KIITWGADTA
HPCJ	AALTGTYYVD	HLTPLRDWAH	AGLRDLAVAV	EPVVFSDMET	KIITWGADTA
HPCJCG	AALTGTYYVD	HLTPLRDWAH	AGLRDLAVAV	EPVVFSDMET	KLITWGADTA
HPCJK046	GSWTGTYYID	HLVPLRTWAS	DGLRDLAVAV	EPVVFSPMEK	KVITWGADTA
HPCJK049	ARGFNTYLYD	HLSPMTDWAA	EGLKDLAVAV	EPVIFSPMEV	KVITWGADTT
HPCJTA	AALTGTYYVD	HLTPLQDWAH	AGLRDLAVAV	EPVVFSDMET	KIITWGADTA
HPCJTB	AALTGTYYVD	HLTPLQDWAH	AGLRDLAVAV	EPVVFSDMET	KIITWGADTA



HPCCK3A	ADGSNTYLYD	HLAPMQHWAA	AGLKDLAVAT	EPVIFSPMEI	KVITWGADTA
HPCPLYPRE	GALTGTYYVN	HLTPLRDWAH	NGLRDLAVAV	EPVVFSQMET	KLITWGADTA
HPCPOLP	GRWTGTYYID	HLTPMSDWAA	NGLRDLAVAV	EPIIFSPMEK	KVIVWGAETA
HPCPP	AALTGTYYVD	HLTPLQDWAH	AGLRDLAVAV	EPVVFSQMET	KIITWGAETA
HPCUNKCD	AALAGTYVYD	HLTPLRDWAH	TGLRDLAVAV	EPVVFSQMET	KVITWGADTA
MKC1A	AALTGTYYID	HLTPLRDWAH	AGLRDLAVAV	EPVVFSQMET	KIITWGADTA
NDM59	GRWTGTYYID	HLSPMSDWAA	SGLRDLAVAV	EPIIFSPMEK	KVIVWGAETA
NZLI	GRWFNTYLYD	HLAPMQHWAA	AGLKDLAVAT	EPVIFSPMEI	KVITWGADTA
SA13	GRLTGTYYID	HLAPMKDWAA	SGLRDLAVAT	EPIIFSPMET	KVITWGADTA
Th580	GAWTGTYYID	HLAPLSEWAS	DGLRDLAVAV	EPVIFSPMEK	KIITWGADTA
Type_3a_CB	GRWFNTYLYD	HLAPMQHWAA	AGLKDLAVAT	EPVIFSPMEI	KVITWGADTA
TypeV_D	GRWFNTYLYD	HLAPMQHWAA	AGLKDLAVAT	EPVIFSPMEI	KVITWGADTA
VN004	GAWTGTYYID	HLAPLSDWAC	DGLRDLAVAV	EPVVFSQMET	KVITWGADTA
VN235	GAWTGTYYID	HLAPLSTWAS	DGLRDLAVAV	EPVTFSPMEK	KIITWGADTA
VN405	GAWTGTYYID	HLTPLSDWAC	DGLRDLAVAV	EPVVFSQMET	KVITWGADTV

	1001				1050
BEBE1	ACGDIHGLP	VSARLGQEV	LGPADGYTSK	GWRLAPITA	YAQQRGLLS
D89815	ACGDIISGLP	VSARRGKEIL	LGPADSFEQ	GWRLAPITA	YSQQRGLLG
ED43type_4	ACGDIIRGLP	VSARLGNEIL	LGPADTETSK	GWRLAPITA	YAQQRGLFS
HC_C2	ACGDIILGLP	VSARRGKEIL	LGPADSLEGQ	GWRLAPITA	YSQQRGLLG
HC_G9	ACGDIINGLP	VSARRGREVL	LGPADALTDK	GWRLAPITA	YAQQRGLLG
HCU16326	ACGDIILACP	ASARRGKEIL	LGPADSLEGQ	GWRLAPITA	YSQQRGLLG
HCV_H_CMR	ACGDIINGLP	VSARRGQEIL	LGPADGMVSK	GWRLAPITA	YAQQRGLLG
HCV_J1	ACGDIINGLP	VSARRGREIL	LGPADGMVSK	GWRLAPITA	YAQQRGLLG
HCV_J483	ACGDIILGLP	VSARRGKEIF	LGPADSLEGQ	GWRLAPITA	YSQQRGLVG
HCV_J8	ACGDIHGLP	VSARRGREVL	LGPADGYTSK	GWRLAPITA	YTQQRGLLG
HCV_JK1	ACGDIILGLP	VSARRGREIL	LGPADGFREQ	GWRLAPITA	YSQQRGLFG
HCV_JS	ACGDIILGLP	VSARRGREIL	LGPADSLEGQ	GWRLAPITA	YSQQRGLLG
HCV_K1_R1	ACGDIIMGLP	VSARRGREIL	LGPADSLEGQ	GWRLAPITA	YSQQRGLFG
HCV_K1_R2	ACGDIILGLA	VSARRGKEIF	LGPADSLEGS	GWRLAPITA	YSQQRGLLG
HCV_K1_R3	ACGDIISGLA	VSARRGREIL	LGPADSFEQ	GWRLAPITA	YSQQRGLLG
HCV_K1_S1	ACGDIIMGLP	VSARRGREIL	LGPADSLEGQ	GWRLAPITA	YSQQRGLFG
HCV_K1_S2	ACGDIILGLA	VSARRGKEIF	LGPADSLEGS	GWRLAPITA	YSQQRGLLG
HCV_K1_S3	ACGDIISGLP	VSARRGREIL	LGPADSFEQ	GWRLAPITA	YSQQRGLLG
HCV_L2	ECGDIILGYR	SSARRGREIL	LGPADSLEGQ	GWRLAPITA	YAQQRGLLG
HCV_N	ACGDIILGLP	VSARRGREIL	LGPADSLVGQ	GWRLAPITA	YSRQRGLLG
HCV12083	ACGDILSGLP	VSARLGNLVL	LGPADDMQRG	GWRLAPITA	YAQQRGLVG
HCV1480	ACGNILAVLP	VSARRGREIF	LGPADDIKTS	GWRLAPITA	YAQQRGLVG
HCVPOLYP	ACGDIISGLP	VSARRGREIL	LGPADSLKEQ	GWRLAPITA	YSQQRGLLG
HD_1	ACGDIILGLP	VSARRGREIL	LGPADSLEGQ	GWRLAPITA	YAQQRGLLG
HPCCGAA	ACGDIINGLP	VSARRGQEIL	LGPADGMVSK	GWRLAPITA	YAQQRGLLG
HPCFG	ACGDILCGLP	VSARLGRELL	LGPADDYKKM	GWRLSPISA	YAQQRGLFG
HPCGENANTI	ACGDIILGLP	VSARRGREIL	LGPADSLEGR	GWRLAPITA	YAQQRGLFG
HPCGENOM	ACGDIILGLP	VSARRGKEIL	LGPADSLEGQ	GWRLAPITA	YSQQRGLLG
HPCUMR	ACGDIILGLP	VSARRGKEIL	LGPADSLEGR	GLRLAPITA	YSQQRGLLG
HPCJ	ACGDIILGLP	VSARRGREIL	LGPADSLEGQ	GWRLAPITA	YSQQRGLLG
HPCJCG	ACGDIISGLP	VSARRGKEIL	LGPADSFEQ	GWRLAPITA	YSQQRGLLG
HPCJK046	ACGDILAGLP	VSARRGNLIL	LGPADDVKDK	GWRLAPITA	YAQQRGLLG
HPCJK049	ACGDILCGLP	VSARLGKEVL	LGPADDYRSM	GWRLAPITA	HAQQRGLFG
HPCJTA	ACGDIILGLP	VSARRGREIL	LGPADSIQEQ	GWRLAPITA	YAQQRGLLG
HPCJTB	ACGDIILGLP	VSARREREIL	LGPADSIQEQ	GWRLAPITA	YXQQRGLLG
HPCCK3A	ACGDILCGLP	VSARLGREVL	LGPADDYREM	GWRLAPITA	YAQQRGLLG
HPCPLYPRE	ACGDIINGLP	VSARRGREIL	LGPADGMVSK	GWRLAPITA	YAQQRGLLG
HPCPOLP	ACGDIHGLP	VSARLGREVL	LGPADGYTSK	GWRLAPITA	YAQQRGLLG
HPCPP	ACGDIISLP	VSARRGRELL	LGPADSFQEQ	GWRLAPITA	YSQQRGLLG
HPCUNKCD	ACGDIILALP	ASARRGKEIL	LGPADSLEGQ	GWRLAPITA	YSQQRGLLG
MKC1A	ACGDIILGLP	VSARRGKEIL	LGPADSLEGQ	GWRLAPITA	YSQQRGLLG
NDM59	ACGDVLHGLP	VSARLGREIL	LGPADGYTSK	GWRLAPITA	YAQQRGLLG
NZLI	ACGDILCGLP	VSARLGREVL	LGPADDYREM	GWRLAPITA	YAQQRGLLG

SA13	ACGDILAGLP	VSARRGHEIF	LGPADDIREA	GWRLAPITA	YAQQTRGVLG
Th580	ACGDILRGLP	VSARLGDLVL	LGPADDMRHG	GWKLLAPITA	YAQQTRGLVG
Type_3a_CB	ACGDILCGLP	VSARLGREVL	LGPADDYREM	GWRLAPITA	YAQQTRGLLG
TypeV_D	ACGDILCGLP	VSARLGREVL	LGPADDYREM	GWRLAPITA	YAQQTRGLLG
VN004	ACGDIIAGLP	VAARRGNLLF	LGPADDVKGK	GWRLAPITA	YAQQTRGIVG
VN235	ACGDILAGLP	VSARLGHLIF	LGPADDMKSM	GWRLAPITA	YCQQTRGLLG
VN405	ACGDIISGLP	VSARRGNLIF	LGPADDIRDG	GWRLAPITA	YAQQTRGLVG

	1051		1100
BEBE1	AIVVSMTGRD	KTDQAGEIQV	LSTVTQSFLG
D89815	CIITSLTGRD	KNQVEGEVQV	VSTAKQSFLA
ED43type_4	TIVTSLTGRD	TNENCGEVQV	LSTATQSFLG
HC_C2	CIITSLTGRD	KNQVEGEVQV	VSTATQSFLA
HC_G9	CIITSLTGRD	KNQVEGEVQI	VSTATQTFLA
HCU16326	CIITSLTGRD	KNQVEGEVQV	VSTATQSFLA
HCV_H_CMV	CIITSLTGRD	KNQVEGEVQI	VSTATQTFLA
HCV_J1	CIITSLTGRD	KNQVEGEVQI	VSTAAQTFLA
HCV_J483	CIITSLTGRD	KNQVEGEVQV	VSTATQSFLA
HCV_J8	AIVVSLTGRD	KNEQAGQVQV	LSSVTQTFLG
HCV_JK1	CIITSLTGRD	KNQVEGEAQV	VSTATQSFLA
HCV_JS	CIITSLTGRD	KNQVEGEVQV	VSTATQSFLA
HCV_K1_R1	CIITSLTGRD	KNQVEGEVQV	VSTATQSFLA
HCV_K1_R2	CIITSLTGRD	KNQVEGEVQV	VSTATQSFLA
HCV_K1_R3	CIITSLTGRD	KNQVEGEVQV	VSTATQSFLA
HCV_K1_S1	CIITSLTGRD	KNQVEGEVQV	VSTATQSFLA
HCV_K1_S2	CIITSLTGRD	KNQVEGEVQV	VSTATQSFLA
HCV_K1_S3	CIITSLTGRD	KNQVEGEVQV	VSTATQSFLA
HCV_L2	CIITSLTGRD	KNQVEGEVQV	VSTATQSFLA
HCV_N	CIITSLTGRD	KNQVEGEVQV	VSTATQSFLA
HCV12083	TIVTSLTGRD	KNEVEGEVQV	VSTDTQSFLA
HCV1480	AIVLSLTGRD	KNEAEGEVQF	LSTATQTFLG
HCVPLYP	CIITSLTGRD	KNQVEGEVQV	VSTATQSFLA
HD_1	CIITSLTGRD	KNQVEGEVQV	VSTATQSFLA
HPCCGAA	CIITSLTGRD	KNQVEGEVQI	VSTATQTFLA
HPCFG	TIVTSLTGRD	KNVVTGEVQV	LSTATQTFLG
HPCGENANTI	CIITSLTGRD	KNQVEGEVQV	VSTATQSFLA
HPCGENOM	CIITSLTGRD	KNQVEGEVQV	VSTATQSFLA
HPCUMR	CIITSLTGRD	KNQVEGEVQV	VSTATQSFLA
HPCJ	CIITSLTGRD	KNQVEGEVQV	VSTATQSFLA
HPCJCG	CIITSLTGRD	KNQVDGEVQV	LSTATQSFLA
HPCJK046	TIVTSLTGRD	KNEAAGEIQI	LSTATQTFLA
HPCJK049	TIVTSLTGRD	KNIVTGEIQV	LSTSTQTFLG
HPCJTA	CIITSLTGRD	KNQVEGEVQV	VSTATQSFLA
HPCJTB	CIITSLTGRD	KNQVEGEVQV	VSTATQSFLA
HPCK3A	TIVTSLTGRD	KNVVAGEVQV	LSTATQTFLG
HPCPLYPRE	CIITSLTGRD	KNQVEGEVQI	VSTAAQTFLA
HPCPOLP	TIVVSMTGRD	KTEQAGEIQV	LSTVTQSFLG
HPCPP	CIITSLTGRD	KNQVEGEVQV	VSTATQSFLA
HPCUNKCD	CIITSLTGRD	KNQVEGEVQV	VSTATQSFLA
MKC1A	CIITSLTGRD	KNQVEGEVQV	VSTATQSFLA
NDM59	AIVVSMTGRD	KTEQAGEIQV	LSTVTQSFLG
NZLI	TIVTSLTGRD	KNVVTGEVQV	LSTATQTFLG
SA13	AIIVSLTGRD	KNEAEGEVQV	LSTATQTFLG
Th580	TIVTSLTGRD	KNEAEGEVQV	VSTATQSFLA
Type_3a_CB	TIVTSLTGRD	KNVVTGEVQV	LSTATQTFLG
TypeV_D	TIVTGLTGRD	KNVVTGEVQV	LSTATQTFLG
VN004	TIVTSLTGRD	KNEVEGEIQV	VSTATQSFLA
VN235	TIVTSLTGRD	RNVVEGEIQV	LSTATQSFLG
VN405	TIVTSLTGRD	KNEVEGEIQV	VSTATQSFLA

	1101		1150
BEBE1	GSRGPVTQMY	SSAEGDLVGW	PSPPGTRSLE PCTCGAVDLY LVTRNADVIP
D89815	AAKGPITQMY	TNVDQDLVGW	PAPPGARSLT PCTCGSSDLY LVTRHADVIP
ED43type_4	GPKGPVNQMY	TNVDQDLVGW	PAPPGVRSLS PCTCGSADLY LVTRYADVIP
HC_C2	GPKGPITQMY	TNVDQDLVGW	PAPSGARSLT PCTCGSSDLY LVTRYADVIP
HC_G9	SASGPVIQMY	TNVDQDLVGW	PAPQGARSLT PCTCGASDLY LVTRHADVIP
HCU16326	GPKGPITQMY	TNVDQDLVGW	PAPPGARSLT PCTCGSSDLY LVTRHADVIP
HCV_H_CMR	SPKGPVIQMY	TNVDQDLVGW	PAPQGSRSLS PCTCGSSDLY LVTRHADVIP
HCV_J1	SPKGPVIQMY	TNVDQDLVGW	PAPQGARSLT PCTCGSSDLY LVTRHADVIP
HCV_J483	GPKGPITQMY	TNVDLDLVGW	QAPPGARSMT PCTCGSSDLY LVTRHADVIP
HCV_J8	GPKGPVTQMY	TSAEGDLVGW	PSPPGTKSLD PCTCGAVDLY LVTRNADVIP
HCV_JK1	GPKGPINQMY	TNVDQDLVGW	QAPSGAASLT PCTYGSSDLY LVTRHADVIP
HCV_JS	GPKGPITQMY	TNVDQDLVGW	QAPPGARSMT PCTCGSSDLY LVTRHADVIP
HCV_K1_R1	GPKGPITQMY	TNVDQDLVGW	PAPPGARSLT PCTCGSSDLY LVTRHADVIP
HCV_K1_R2	GPKGPITQMY	TNVDQDLVGW	PAPSGARSLT PCTCGSSDLY LVTRHADVIP
HCV_K1_R3	GPKGPITQMY	TNVDQDLVGW	QAPPGARSLT PCTCGSSDLY LVTRHADVIP
HCV_K1_S1	GPKGPITQMY	TNVDQDLVGW	PAPPGARSLT PCTCGSSDLY LVTRHADVIP
HCV_K1_S2	GSKGPITQMY	TNVDQDLVGW	QAPSGARSLT PCTCGSSDLY LVTRHADVIP
HCV_K1_S3	GPKGPITQMY	TNVDQDLVGW	QAPPGARSLT PCTCGSSDLY LVTRHADVIP
HCV_L2	GPKGPITQMY	TNVDQDLVGW	QAAPGMRSLS PCTCGSSDLY LVTRHADVIP
HCV_N	GPKGPPIAQMY	TNVDQDLVGW	PAPPGARSLT PCTCGSSDLY LVTRHADVIP
HCV12083	GPKGPVCQMY	TNVDLDLVGW	PSPPGARSLT PCNCGSSDLY LVTRHADVIP
HCV1480	GPKGPVVQMY	TNVDKDLVGW	PSPPGKGSLS RCTCGSADLY LVTRHADVIP
HCVPOLYP	GPKGPVTQMY	TNVDQDLVGW	PAPPGARSLT PCTCGSSDLY LVTRHADVIP
HD_1	GPKGPVTQMY	TNVDQDLVGW	QAPPGARSLT PCTCGSSDLY LVTRHADVIP
HPCCGAA	SPKGPVIQTY	TNVDQDLVGW	PAPQGSRSLS PCTCGSSDLY LVTRHADVIP
HPCFG	GNKRPALQMY	TNVDQDLVGW	PAPAGTKSLD PCTCGSSDLY LVTRHADVIP
HPCGENANTI	GPKGPITQMY	TNVDQDLVGW	HAPQGARSLT PCTCGSSDLY LVTRHADVIP
HPCGENOM	GPKGPITQMY	TNVDQDLVGW	HRPPGARSLT PCTCGSSDLY LVTRHADVIP
HPCHUMR	APKGPITQMY	TNVDQDLVGW	PKPPGARSLT PCTCGSSDLY LVTRHADVIP
HPCJ	GPKGPITQMY	TNVDQDLVGW	QAPPGARSMT PCTCGSSDLY LVTRHADVIP
HPCJCG	GPKGPITQMY	TNVDQDLVGW	PAPPGARSMT PCTCGSSDLY LVTRHADVIP
HPCJK046	GRPGPVCQMY	TNVDQDMVGW	PAPAGTRSYP PCTCGASDLY LITRQADVIP
HPCJK049	GNKRPALQMY	TNVDQDLVGW	PSPPGAKSLV PCTCGSADLY LITRDADVLP
HPCJTA	GPKGPITQMY	TNVDQDLVGW	HAPPGARSLT PCTCGSSDLY LVTRHADVIP
HPCJTB	GPKGPITQMY	TNVDQDLVGW	HAPPGARSLT PCTCGSSDLY LVTRHADVIP
HPCK3A	GVKHPALQMY	TNVDQDLVGW	PAPPGAKSLE PCTCGSADLY LVTRDADVLP
HPCPLYPRE	SPKGPVIQMY	TNVDQDLVGW	PAPQGSRSLS PCTCGSSDLY LVTRHADVIP
HPCPOLP	GSRGPVTQMY	SSAEGDLVGW	PSPPGTKSLE PCTCGAVDLY LVTRNADVIP
HPCPP	GPKGPITQMY	TNVDQDLVGW	SAPPGARSLT PCTCGSSDLY LVTRHADVIP
HPCUNKCD	GPKGPITQMY	TNVDQDLVGW	PAPPGARSLT PCTCGSSDLY LVTRHADVIP
MKC1A	GPKGPITQMY	TNVDQDLVGW	PAPPGARSMT PCTCGSSDLY LVTRHADVIP
NDM59	GSRGPVTQMY	SSAEGDLVGW	PSPPGTKSLE PCTCGAVDLY LVTRNADVIP
NZLI	GAKHPALQMY	TNVDQDLVGW	PAPPGAKSLE PCACGSSDLY LVTRDADVLP
SA13	GPKGPVVQMY	TNVDKDLVGW	PTPPGTRSLS PCTCGSADLY LVTRHADVIP
Th580	GPKGPVCQMY	TNVDQDLVGW	PAPLGARSLA PCTCGSSDLY LVTRGADVIP
Type_3a_CB	GAKHPALQMY	TNVDQDLVGW	PAPPGAKSLE PCACGSADLY LVTRDADVLP
TypeV_D	GAKHPALQMY	TNVDQDLVGW	PAPPGAKSLE PCACGSADLY LVTRDADVLP
VN004	GPKGPVCQMY	TNVDQDLVGW	PAPAGARSLT PCSCGSSDLY LVTRNADVIP
VN235	GPKGPVCQMY	TNVDQDMVGW	PAPPGTRSLS PCTCGASDLY LVTRNADVIP
VN405	GPKGPICQMY	TNVDQDLVGW	PAPPGARSLT PCTCGSSDLY LVTRNADVIP
	1151		1200
BEBE1	ARRRGDRRGA	LLSPRPLSSL	KGSSGGPVLC PRGHAVGIFR AAVCSRGVAK
D89815	VRRRGDSRGS	LLSPRPISYL	KGSSGGPLLC PSGHVVGIFR AAVCTRGVAK
ED43type_4	VRRRGDTRGA	LLSPRPISIL	KGSSGGPLLC PMGHRAGIFR AAVCTRGVAK
HC_C2	VRRRGDSRGS	LLSPRPVSYL	KGSSGGPLLC PSGHAAGIFR AAVCTRGVAK
HC_G9	VRRRGDNRRGS	LLSPRPISYL	KGSSGGPLLC PMGHAVGIFR AAVCTRGVAK
HCU16326	VRRRGDGRGS	LLPPRPVSYL	KGSSGGPLLC PSGHAVGILP AAVCTRGVAM
HCV_H_CMR	VRRRGDSRGS	LLSPRPISYL	KGSSGGPLLC PAGHAVGLFR AAVCTRGVTK

HCV_J1	VRRRGDSRGS	LLSPRPISYL	KGSSGGP LLC	PAGHVVGIFR	AAVCTRGVAK
HCV_J483	VRRRGDSRGS	LLSPRPVSYL	KGSSGGP LLC	PSGHVVG VFR	AAVCTRGVAK
HCV_J8	VRRKDDRRGA	LLSPRP LSTL	KGSSGGP VLC	SRGHAVGLFR	AAVCARGVAK
HCV_JK1	VRRRGDSRGS	LLSPRPVSYL	KGSSGGP LLC	PSGHAVGIFR	AAVCTRGVAK
HCV_JS	VRRRGDSRGS	LLSPRPVSYL	KGSSGGP LPLC	PSGHAVGIFR	AAVCTRGVAK
HCV_K1_R1	VRRRGDSRGS	LLSPRPISYL	KGSSGGP LLC	PSGHVVGIFR	AAVCTRGVAK
HCV_K1_R2	VRRRGDGRGS	LLSPRPVSYL	KGSSGGP LLC	PSGHAVGIFR	AAVCTRGVAK
HCV_K1_R3	VRRRGDSRGS	LLSPRPVSYL	KGSSGGP LLC	PSGHAVGIFR	AAVCTRGVAK
HCV_K1_S1	VRRRGDSRGS	LLSPRPISYL	KGSSGGP LLC	PSGHVVGIFR	AAVCTRGVAK
HCV_K1_S2	VRRRGDGRGS	LLSPRPVSYL	KGSSGGP LLC	PSGHAVGIFR	AAVCTRGVAK
HCV_K1_S3	VRRRGDSRGS	LLSPRPVSYL	KGSSGGP LLC	PSGHAVGIFR	AAVCTRGVAK
HCV_L2	VRRRGDGRGS	LLSPRPVSYL	KGSSGGP LLW	PSGHAVGIFR	AAVCTRGVAK
HCV_N	VRRRGDN RGS	LLSPRPVSYL	KGSSGGP LLC	PSGHAVGVFR	AAVCTRGVAK
HCV12083	ARRRGDSRAA	LLSPRPISYL	KGSSGGP IMC	PSGHVVG LFR	AAVCTRGVAK
HCV1480	ARRRGDTRAS	LLSPRPISYL	KGSSGGP IMC	PSGHVVG VFR	AAVCTRGVAK
HCVPOLYP	VRRRGDSRGS	LLSPRPVSYL	KGSSGGP LLC	PSGHAVGIFR	AAVCTRGVAK
HD_1	VRRRGDSRGS	LLSPRPVSYL	KGSSGGP LLC	PSGHAVGIFR	AAVCTRGVAK
HPCCGAA	VRRRGDSRGS	LLSPRPISYL	KGSSGGP LLC	PTGHAVGLFR	AAVCTRGVAK
HPCFG	ARRRGDSTAS	LLSTRPLSCL	KGSSGGP VMC	PSGHVVGIFR	AAVCTRGVAK
HPCGENANTI	VRRRGDSRGS	LLSPRPISYL	KGSSGGP LLC	PSGHVVGIFR	AAVCTRGVAK
HPCGENOM	VRRRGDSRGS	LLSPRPVSYL	KGSSGGP LLC	PFGHVAGIFR	AAVCTRGVAK
HPCHUMR	VRRRGDSRGS	LLSPRPVSYL	KGSSGGP LLC	PFGHAVGIFR	AAVCTRGVAK
HPCJ	VRRRGDGRGS	LLSPRPVSYL	KGSSGGP LLC	PSGHAVGIFR	AAVCTRGVAK
HPCJCG	VRRRGDSRGS	LLSPRPISYL	KGSSGGP LLC	PSGHVVGIFR	AAVCTRGVAK
HPCJK046	ARRRGDN RAG	LLSPRPISYL	KGSSGGP LLC	PSGHVVG LFR	AAVCTRGVAK
HPCJK049	ARRRGDSTAS	LLSPRP LACL	KGSSGGP IMC	PSGHVAGIFR	AAVCTRGVAK
HPCJTA	VRRRGDGRGS	LLSPRPVSYL	KGSSGGP LLC	PSGHAVGIFR	AAVCTRGVAK
HPCJTB	VRRRGDGRGS	LLSPRPVSYL	KGSSGGP LLC	PSGHAVGIFR	AAVCTRGVAK
HPCK3A	ARRRGDSTAS	LLSPRP LARL	KGSSGGP VMC	PSGHVAGIFR	AAVCTRGVAK
HPCPLYPRE	VRRRGDSRGS	LLSPRPISYL	KGSSGGP LLC	PAGHAVGIFR	AAVCTRGVAK
HPCPOLP	ARRRGDKRGA	LLSPRP LSTL	KGSSGGP VLC	PRGHAVGVFR	AAVCSRGVAK
HPCPP	VHRRGDSRGS	LLSPGPISYL	KGSSGGP LPLC	PSGRVVGIFR	AAVCTRGVAK
HPCUNKCD	VRRRGDGRGS	LLPPRPVSYL	KGSSGGP LLC	PSGHAVGILP	AAVCTRGVAM
MKC1A	VRRRGDSRGS	LLSPRPISYL	KGSSGGP LLC	PSGHVVGIFR	AAVCTRGVAK
NDM59	ARRRGDKRGA	LLSPRP LSTL	KGSSGGP VLC	PRGHAVGIFR	AAVCSRGVAK
NZLI	ARRRGDSTAS	LLSPRP LACL	KGSSGGP VMC	PSGHVAGIFR	AAVCTRGVAK
SA13	ARRRGDTRAS	LLSPRPISYL	KGSSGGP VMC	PSGHVVG VFR	AAVCTRGVAK
Th580	ARRRGDTRAA	LLSPRPISYL	KGSSGGP LMC	PSGHVVG LFR	AAVCTRGVAK
Type_3a_CB	ARRRGDSTAS	LLSPRP LACL	KGSSGGP VMC	PSGHVAGIFR	AAVCTRGVAK
TypeV_D	ARRRGDSTAS	LLSPRP LACL	KGSSGGP VMC	PSGHVAGIFR	AAVCTRGVAK
VN004	ARRRGDNRAA	LLSPRPISYL	KGSSGGP MLC	PSGHVAGIFR	AAVCTRGVAK
VN235	ARRRGDTRAG	LLSPRP LSTL	KGSSGGP LMC	PSDHVVG LFR	AAVCTRGVAK
VN405	ARRRGDTRAA	LLSPRPISYL	KGSSGGP MLC	PSGHVAGIFR	AAVCTRGVAK

	1201			1250	
BEBE1	SIDFIPVESL	DVVT RSPNFT	DNSTPPAVPQ	TYQVGYLHAP	TGSGKSTKVP
D89815	AVDFIPVESM	ETTMRSPVFT	DNSTPPAVPQ	TFQVAHLHAP	TGSGKSTKVP
ED43type_4	AVDFVPVESL	ETTMRSPVFT	DNSTPPAVPQ	TYQVAHLHAP	TGSGKSTKVP
HC_C2	AVDFVPVESM	ETTMRSPVFT	DNSSPPAVPQ	TFQVAHLHAP	TGSGKSTKVP
HC_G9	AVDFVPVESL	ETTMRSPVFT	DNSSPPAVPQ	SYQVAHLHAP	TGSGKSTKVP
HCU16326	AVEFIPVESM	ETTMRSPVFT	DNPSPPAVPQ	TFQVAHLHAP	TGSGKSTRVP
HCV_H_CMV	AVDFIPVENL	ETTMRSPVFT	DNSSPPAVPQ	SFQVAHLHAP	TGSGKSTKVP
HCV_J1	AVDFIPVESL	ETTMRSPVFT	DNSSPPAVPQ	SFQVAHLHAP	TGSGKSTKVP
HCV_J483	AVDFIPVESM	ETTMRSPVFT	DNSSPPAVPQ	TFQVAHLHAP	TGSGKSTKVP
HCV_J8	SIDFIPVESL	DVATRTPSFS	DNSTPPAVPQ	SYQVGYLHAP	TGSGKSTKVP
HCV_JK1	AVDFIPVESM	ETTMRSPVFT	DNSSPPAVPQ	TFQVAHLHAP	TGSGKSTKVP
HCV_JS	AVDFIPVESM	ETTMRAPVFT	DNSSPPAVPQ	TFQVAHLHAP	TGSGKSTKVP
HCV_K1_R1	AVDFVPVESM	ETTMRSPVFT	DNSSPPAVPQ	TFQVAHLHAP	TGSGKSTKVP
HCV_K1_R2	AVDFIPVESM	ETTMRSPVFT	DNSSPPAVPQ	TFQVAHLHAP	TGSGKSNKVP
HCV_K1_R3	AVDFVPVESM	ETTMRSPVFT	DNSSPPAVPQ	TFQVAHLHAP	TGSGKSTKVP

HCV_K1_S1	AVDFVPVESM	ETTMRSPVFT	DNSSPPAVPQ	TFQVAHLHAP	TGSGKSTKVP
HCV_K1_S2	AVDFIPVESM	ETTMRSPVFT	DNSSPPAVPQ	TFQVAHLHAP	TGSGKSNKVP
HCV_K1_S3	AVDFVPVESM	ETTMRSPVFT	DNSSPPAVPQ	TFQVAHLHAP	TGSGKSTKVP
HCV_L2	AVDFVPVESM	ETTMRSPVFT	DNSSPPAVPQ	TFQVAHLHAP	TGSGKSTKVP
HCV_N	SLDFVPVESM	ETTMRSPVFT	DTSSPPAVPQ	TFQVAHLHAP	TGSGKSTRVP
HCV12083	SLDFIPVENM	ETTMRSPTSFT	DNSTPPAVPQ	TYQVGYLHAP	TGSGKSTRVP
HCV1480	ALEFVPVENL	ETTMRSPVFT	DNSTPPAVPH	EFQVGHLHAP	TGSGKSTKVP
HCVPOLYP	AVDFVPVESM	ETTMRSPVFT	DNSSPPAVPE	TFQVAHLHAP	TGSGKSTKVP
HD_1	AVDFVPVESM	ETTMRSPVFT	DNSSPPAVPQ	TFQVAHLHAP	TGSGKTTKVP
HPCCGAA	AVDFIPVENL	ETTMRSPVFT	DNSSPPAVPQ	SFQVAHLHAP	TGSGKSTKVP
HPCFG	ALQFIPVETL	STQVRSPTSFS	DNSTPPAVPE	SYQVGYLHAP	TGSGKSTKVP
HPCGENANTI	AVDFVPVESM	ETTMRSPVFT	DNSSPPAVPQ	AFQVAHLHAP	TGSGKSTKVP
HPCGENOM	AVDFIPVETM	ETTMRSPVFT	DNSSPPAVPQ	TFQVAHLHAP	TGSGKSTKVP
HPCHUMR	AVDFVPVESM	ETTMRSPVFT	DNSSPPAVPQ	SFQVAHLHAP	TGSGKSTKVP
HPCJ	AVDFIPVESM	ETTMRSPVFT	DNSSPPAVPQ	TFQVAHLHAP	TGSGKSTKVP
HPCJCG	AVDFIPVESM	ETTMRSPVFT	DNSSPPAVPQ	TFQVAHLHAP	TGSGKSTKVP
HPCJK046	ALDFVPCEAM	DATTRSPTFT	DNSTPPAVPQ	AYQVGYLHAP	TGSGKSTKVP
HPCJK049	ALQFIPVESL	SAQTRSPSFS	DNSTPPAVPQ	TFQVGYLHAP	TGSGESTKVP
HPCJTA	AVDFIPVESM	ETTMRSPVFT	DNSSPPAVPQ	TFQVAHLHAP	TGSGKSTKVP
HPCJTB	AVDFIPVESM	ETTMRSPVFT	DNSSPPAVPQ	TFQVAHLHAP	TGSGKSTKVP
HPCK3A	ALQFIPVETL	STQARSPSFS	DNSTPPAVPQ	SYQVGYLHAP	TGSGKSTKVP
HPCPLYPRE	AVDFIPVENL	ETTMRSPVFT	DNSSPPVVPQ	SFQVAHLHAP	TGSGKSTKVP
HPCPOLP	SIDFIPVETL	DIVTRSPTFS	DNSTPPAVPQ	TYQVGYLHAP	TGSGKSTKVP
HPCPP	AVDFVPVESM	ETTMRSPVFT	DNSTPPAVPQ	TFQVAHLHAP	TGSGKSTRVP
HPCUNKCD	AVEFIPVESM	ETTMRSPVFT	DNPSPPAVPQ	TFQVAHLHAP	TGSGKSTRVP
MKC1A	AVDFVPVESM	ETTMRSPVFT	DNSTPPAVPQ	SFQVAHLHAP	TGSGKSTKVP
NDM59	SIDFIPVEAL	DVVTRSPTFS	DNSTPPAVPQ	TYQVGYLHAP	TGSGKSTKVP
NZLI	SLQFIPVETL	STQARSPSFS	DNSTPPAVPQ	SYQVGYLHAP	TGSGKSTKVP
SA13	ALDFIPVENL	ETTMRSPVFT	DNSTPPAVPH	EFQVGHLHAP	TGSGKSTKVP
Th580	ALDFIPVENM	DTTMRSPVFT	DNSSPPAVPQ	TYQVGYLHAP	TGSGKSTRVP
Type_3a_CB	ALQFIPVETL	STQTRSPSFS	DNSTPPAVPQ	SYQVGYLHAP	TGSGKSTKVP
TypeV_D	ALQFIPVETL	STQARSPSFS	DNSTPPAVPQ	TYQVGYLHAP	TGSGKSTKVP
VN004	SLDFVPVESM	QSSQSRSPSFS	DNTSPPAVPQ	TYQVGYLHAP	TGSGKSTKVP
VN235	ALDFVPVENM	ETTMRSPVFT	DNSTPPAVPQ	TYQVGYLHAP	TGSGKSTKVP
VN405	SLDFVPVENM	QSTARSPSFS	DNTTPPAVPQ	TYQVGYLHAP	TGSGKSTKVP

	1251			1300	
BEBE1	AAYAAQGYKV	LVLNPSVAAT	LGFGAYMSKA	YGINPNIRTG	VRTVTTGDAI
D89815	AAYAAQGYMV	LVLNPSVAAT	LGFGAYMSKA	HGIDPNIRTG	VRTITTGAPI
ED43type_4	AAHAAQGYKV	LVLNPSVAAT	LGFGVYMSKA	YGIDPNIRSG	VRTITTGAPI
HC_C2	AAYAAQGYKV	LVLNPSVAAT	LGFGAYMSKA	HGIDPNTRTG	VRTITTGAPI
HC_G9	AAYAAQGYKV	LVLNPSVAAT	LGFGAYMSKA	HGIDPNVRTG	VRTITTGSPI
HCU16326	AAYAAQGYKV	LVLNPSVAAT	LGFGAYMSKA	HGIDPNLRTG	VRTITTGAPI
HCV_H_CMR	AAYAAQGYKV	LVLNPSVAAT	LGFGAYMSKA	HGVDPNIRTG	VRTITTGSPI
HCV_J1	AAYAAQGYKV	LVLNPSVAAT	LGFGAYMSKA	HGIDPNIRTG	VRTITTGSPI
HCV_J483	AAYAAQGYKV	LVLNPSVAAT	LGFGAYMPKA	HGIDPNIRTG	VRTITTGGPI
HCV_J8	AAYASQGYKV	LVLNPSVAAT	LGFGAYMSKA	HGINPNIRTG	VRTVTTGDSI
HCV_JK1	AAYAAQGYKV	LVLNPSVAAT	LGFGAYMSKA	HGVDPNISTG	VRTITTGAPI
HCV_JS	AAYAAQGYKV	LVLNPSVAAT	LGFGAYMSKA	YGTDPNIRTG	VRTITTGAPI
HCV_K1_R1	AAYAAQGYKV	LVLNPSVTAT	LGFGAYMSKA	HGVDPNIRTG	VRTITTGAPI
HCV_K1_R2	VEYAAQGYKV	LVLNPSVAAT	LGFGAYMSKA	HGVDPNIRTG	VRTITTGAPI
HCV_K1_R3	AAYAAQGYKV	LVLNPSVAAT	LGFGAYMSKA	HGVDPNIRTG	ARTITTGAPI
HCV_K1_S1	AAYAAQGYKV	LVLNPSVTAT	LGFGAYMSKA	HGVDPNIRTG	VRTITTGAPI
HCV_K1_S2	VEYAAQGYKV	LVLNPSVAAT	LGFGAYMSKA	HGVDPNIRTG	VRTITTGAPI
HCV_K1_S3	AAYAAQGYKV	LVLNPSVAAT	LGFGAYMSKA	HGVDPNIRTG	ARTITTGAPI
HCV_L2	AAYAAQGYKV	LVLNPSVAAT	LGFGAYMSKA	HGTDPNIRTG	ARTITTGAPI
HCV_N	AAYATQGYKV	LVLNPSVAAT	LGFGAYMSKA	HGTDPNIRTG	VRTITTGAPI
HCV12083	AAYASQGYKV	LVLNPSVAAT	LSFGSYMRQA	YGVEPNIRTG	VRTVTTGGAI
HCV1480	AAYAAQGYKV	LVLNPSVAAT	FGFGAYMSRA	YGVDPNIRTG	VRTVTTGAGI
HCVPOLYP	AAYAAQGYKV	LVLNPSVAAT	LGFGAYMSKA	HGTDPNIRTG	VRTITTGAPI

HD_1	AAAYAAQGYKV	LVLNPSVAAT	LGFGAYMSKA	HGIDPNIRTG	VRTITTGAPI
HPCCGAA	AAAYAAQGYKV	LVLNPSVAAT	LGFGAYMSKA	HGVDPNIRTG	VRTITTGSPI
HPCFG	AAAYAAQGYKV	LVLNPSVAAT	LGFGAYMSKA	HGIDPNIRTG	TRTITTGAKL
HPCGENANTI	AAAYAAQGYKV	LVLNPSVAAT	LGFGAYMSKA	HGVDPNIRTG	VRTITTGAPI
HPCGENOM	AAAYAAQGYKV	LVLNPSVAAT	LGFGAYMSKA	HGVDPNIRTG	VRTITTGAPI
HPCHUMR	AAAYAAQGYKV	LVLNPSVAAT	LGFGAYMSKA	HGIDPNIRTG	VRTITTGAPI
HPCJ	AAAYAAQGYKV	LVLNPSVAAT	LGFGAYMSKA	YGTDPNVRTG	VRTITTGSPI
HPCJCG	AAAYAAQGYKV	LVLNPSVAAT	LGFGAYMSKA	HGIEPNIRTG	VRTITTGGPI
HPCJK046	VAYASQGYKV	LVLNPSVAAT	LSFGSYLSRA	HGIDPNIRTG	VRTITTGAPI
HPCJK049	ASYVAQGYTV	LVLNPSVAAT	LGFGRFMSHA	YGIDPNVRTG	TRTITTGAKL
HPCJTA	AAAYAAQGYKV	LVLNPSVAAT	LGFGAYMSKA	HGTDPNIRTG	VRTITTGAPI
HPCJTB	AAAYAAQGYKV	LVLNPSVAAT	LGFGAYMSKA	HGTDPNIRTG	VRTITTGGPI
HPCK3A	AAAYAAQGYKV	LVLNPSVAAT	LGFGSFMSRA	YGIDPNIRTG	NRTVTTGAKL
HPCPLYPRE	AAAYAAQGYKV	LVLNPSVAAT	LGFGAYMSKA	HGIDPNIRTG	VRTITTGSPI
HPCPOLP	VAYAAQGYKV	LVLNPSVAAT	LGFGAYLSKA	HGINPNIRTG	VRTVTTGAPI
HPCPP	AAAYAAQGYKV	LVLNPSVAAT	LGFGAYMSKA	HGVDPNIRTG	VRTITTGAPI
HPCUNKCD	AAAYAAQGYKV	LVLNPSVAAT	LGFGAYMSKA	HGIDPNLRTG	VRTITTGAPI
MKC1A	AAAYAAQGYKV	LVLNPSVAAT	LGFGAYMSKA	HGVDPNIRTG	VRTITTGAPI
NDM59	VAYAAQGYKV	LVLNPSVAAT	LGFGAYLSKA	HGINPNIRTG	VRTVTTGESI
NZLI	AAAYAAQGYKV	LVLNPSVAAT	LGFGSFMSRA	YGIDPNIRTG	NRTVTTGAKL
SA13	AAAYAAQGYKV	LVLNPSVAAT	LGFGAYMSRA	YGVDPNIRTG	VRTVTTGAAI
Th580	AAAYATQGYKV	LVLNPSVAAT	LSFGAYMSKA	HGIDPNIRTG	VRTITTGGPV
Type_3a_CB	AAAYVAQGYTV	LVLNPSVAAT	LGFGSFMSRA	YGIDPNIRTG	NRTVTTGAKL
TypeV_D	AAAYVAQGYTV	LVLNPSVAAT	LGFGSFMSRA	YGTDPNIRTG	NRTVTTGAKL
VN004	AAAYAAQGYKV	LVLNPSVAAT	LGFGSYMSTS	HGIDPNIRTG	VRTITTGGAI
VN235	AAAYASQGYKV	LVLNPSVAAT	LGFGSYMSTA	HGIDPNIRTG	VRTITTGGPI
VN405	AAAYAAQGYKV	LVLNPSVAAT	LGFGSYMSTA	HGIDPNIRTG	VRTITTGGAI

	1301		1350		
BEBE1	TYSTYKFLA	DGGCSGGAYD	VIICDECHSV	DSTTILGIGT	VLDQAETAGV
D89815	TYSTYKFLA	DGGCSGGAYD	IIICDECHST	DSTSILGIGT	VLDQAETVGA
ED43type_4	TYSTYKFLA	DGGCSGGAYD	IIICDECYST	DSTTILGIGT	VLDQAETAGV
HC_C2	TYSTYKFLA	DGGCSGGAYD	IIICDECHST	DSTTILGIGT	VLDQAETAGA
HC_G9	THSTYKFLA	DGGCSGGAYD	IIICDECHSV	DATSILGIGT	VLDQAETAGV
HCU16326	TYSTYKFLA	DGGCSGGAYD	IIMCDECHST	DSTTIYGIGT	VLDQAETAGA
HCV_H_CM	TYSTYKFLA	DGGCSGGAYD	IIICDECHST	DATSILGIGT	VLDQAETAGA
HCV_J1	TYSTYKFLA	DGGCSGGAYD	IIICDECHST	DATSVLGIGT	VLDQAETAGA
HCV_J483	TYSTYKFLA	DGGCSGGAYD	IIICDECHST	DSTTILGIGT	VLDQAETAGA
HCV_J8	TYSTYKFLA	DGGCAAGAYD	IIICDECHSV	DATTILGIGT	VLDQAETAGV
HCV_JK1	TYSTYKFLA	DGGCSGGAYD	IIICDECHST	DSTSILGIGT	VLDQAETAGA
HCV_JS	TYSTYKFLA	DGGCSGGAYD	IIMCDECHST	DSTTILGIGT	ALDQAETAGA
HCV_K1_R1	TYSTYKFLA	DGGCSGGAYD	IIMCDECHSI	DSTSILGIGT	VLDQAETAGA
HCV_K1_R2	TYSTYKFLA	DGGCSGGAYD	IIICDECHST	DSTSILGIGT	VLDQAETAGA
HCV_K1_R3	TYSTYKFLA	DGGCSGGAYD	IIICDECHST	DSTSILGIGT	VLDQAETAGA
HCV_K1_S1	TYSTYKFLA	DGGCSGGAYD	IIMCDECHSI	DSTSILGIGT	VLDQAETAGA
HCV_K1_S2	TYSTYKFLA	DGGCSGGAYD	IIICDECHST	DSTSILGIGT	VLDQAETAGA
HCV_K1_S3	TYSTYKFLA	DGGCSGGAYD	IIICDECHST	DSTSILGIGT	VLDQAETAGA
HCV_L2	TYSTYKFFA	DGGCSGGAYD	IIICDECHST	DSTTILGIGT	VLDQAETAGA
HCV_N	TYSTYKFLA	DGGCSGGAYD	IIMCDECHST	DSTTILGIGT	VLDQAETAGA
HCV12083	TYSTYGEFLA	DGGCSGGAYD	IIICDECHST	DPTTVLGVT	VLDQAETAGV
HCV1480	TYSTYKFFA	DGGCSGGAYD	VIICDECHSQ	DATTILGIGT	VLDQAETAGA
HCVPOLYP	TYSTYKFLA	DGGCSGGAYD	IIICDECHST	DSTTILGIGT	VLDQAETAGA
HD_1	TYSTYKFLA	DGGCSGGAYD	IIICDECHST	DSTSILGIGT	VLDQAETAGA
HPCCGAA	TYSTYKFLA	DAGCSGGAYD	IIICDECHST	DATSIIGIGT	VLDQAETAGA
HPCFG	TYSTYKFLA	DGGCSGGAYD	VIICDECHAQ	DATSILGIGT	VLDQAETAGV
HPCGENANTI	TYSTYKFLA	DGGCSGGAYD	IIMCDECHST	DSTTILGIGT	VLDQAETAGA
HPCGENOM	TYSTYKFLA	DGGCSGGAYD	IIICDECHST	DSTTILGIGT	VLDQAETAGA
HPCHUMR	TYSTYKFLA	DGGCSGGAYD	IIICDECHST	DSTTILGIGT	VLDQAETAGA
HPCJ	TYSTYKFLA	DGGCSGGAYD	IIICDECHST	DSTTILGIGT	VLDQAETAGA
HPCJCG	TYSTYCKFLA	DGGCSGGAYD	IIICDECHST	DSTTILGIGT	VLDQAETAGA

HPCJK046	TYSTYKFLA	DGGCSGGAYD	VIICDECHST	DPTTVLGIGT	VLDQAETAGC
HPCJK049	TYSTYKFLA	DGGCSGGAYD	VIICDECHAQ	DATSILGIGT	VLDQAETAGA
HPCJTA	TYSTYKFLA	DGGCSGGAYD	IIICDECHST	DSTTILGIGT	VLDQAETAGA
HPCJTB	TYSTYKFLA	DGGCSGGAYD	IIICDECHST	DSTTILGIGT	VLDQAETAGA
HPCK3A	TYSTYKFLA	DGGCSGGAYD	VIICDDCHAQ	DATSILGIGT	VLDQAETAGV
HPCPLYPRE	TYSTYKFLA	DGGCSGGAYD	IIICDECHST	DATSILGIGT	VLDQAETAGA
HPCPOLP	TYSTYKFLA	DGGCAGGAYD	IIICDECHAV	DSTTILGIGT	VLDQAETAGV
HPCPP	TYSTYKFLA	DGGCSGGAYD	IIICDECHST	DSTSILGIGT	VLDQAETAGA
HPCUNKCD	TYSTYKFLA	DGGSGGGAYD	IIMCDECHST	DSTTIYGIGT	VLDQAETAGA
MKC1A	TYSTYKFLA	DGGCSGGAYD	IIICDECHST	DSTSILGIGT	VLDQAETAGA
NDM59	TYSTYKFLA	DGGCAGGAYD	IIICDECHAV	DATTILGVGT	VLDQAETAGV
NZLI	TYSTYKFLA	DGGCSGGAYD	VIICDECHAQ	DATSILGIGT	VLDQAETAGV
SA13	TYSTYKFLA	DGGCSGGAYD	VIICDECHSQ	DATTILGIGT	VLDQAETAGA
Th580	TYSTYKFLA	DGGCSGGAYD	IIICDECHST	DPTTVLGIGT	VLDQAETAGV
Type_3a_CB	TYSTYKFLA	DGGCSGGAYD	VIICDECHAQ	DATSILGIGT	VLDQAETAGV
TypeV_D	TYSTYKFLA	DGGCSGGAYD	VIICDECHAQ	DATSILGIGT	VLDQAETAGV
VN004	TYSTYKFLA	DGGCSGGAYD	VIICDECHST	DPTTVSGIGT	VLDQAETSGV
VN235	TYSTYKFLA	DGGCSGGAYD	IIICDECHST	DPTTVLGIGT	VLDQAETAGV
VN405	TYSTYKFLA	DGGCSGGAYD	IIICDECHST	DPTTVLGIGT	VLDQAETAGV

	1351				1400
BEBE1	RLTVLATATP	PGSVTTPHPN	IEEVALGHEG	EIPFYGKAIP	LSAIKGRHL
D89815	RFVVLATATP	PGSITFPHPN	IEEVPLANTG	EIPFYAKTIP	IEVIRGGRHL
ED43type_4	RLTVLATATP	PGSVTTPHSN	IEEVALPTTG	EIPFYGKAIP	LELIKGRHL
HC_C2	RLVVLATATP	PGSVTVPHSN	IEEVALSTTG	EIPFYGKAIP	IETIKGRHL
HC_G9	RLTILATATP	PGSVTVPHSN	IEEVALSTEG	EIPFYGKAIP	LNYIKGRHL
HCU16326	RLVVLSTATP	PGSVTVPHLN	IEEVALSNTG	EIPFYGKAIP	IEAIKGRHL
HCV_H_CMV	RLVVLATATP	PGSVTVSHPN	IEEVALSTTG	EIPFYGKAIP	LEVIKGRHL
HCV_J1	RLVVLATATP	PGSITVPHAN	IEEVALSTTG	EIPFYGKAIP	LEAIKGRHL
HCV_J483	RLVVLATATP	PGSVTVPHPN	IEEIGLSNNG	EIPFYGKAIP	IEAIKGRHL
HCV_J8	RLVVLATATP	PGTVTTPHSN	IEEVALGHEG	EIPFYGKAIP	LAFIKGRHL
HCV_JK1	RLVVLAAATP	PGSVTVPHPN	IEEVALPNTG	EIPFYGKAIP	LETIKGRHL
HCV_JS	RLVVLATATP	PGSVTVPHPN	IEEVALSNTG	EIPFYGKAIP	LEVIKGRHL
HCV_K1_R1	RLVVLATATP	PGSVTVPHPN	IEEIALSNTG	EIPFYGKAIP	IETIKGRHL
HCV_K1_R2	RLVVLATATP	PGSVTVPHPN	IEEVALSNTG	EIPFYGKAIP	IETIKGRHL
HCV_K1_R3	RLVVLATATP	PGSVTVPHPN	IEEVALSNTG	EIPFYGKAIP	LDTIKGRHL
HCV_K1_S1	RLVVLATATP	PGSVTVPHPN	IEEIALSNTG	EIPFYGKAIP	IETIKGRHL
HCV_K1_S2	RLVVLATATP	PGSVTVPHPN	IEEVALSNIG	EIPFYGKAIP	IETIKGRHL
HCV_K1_S3	RLVVLATATP	PGSVTVPHPN	IEEVALSNTG	EIPFYGKAIP	LDTIKGRHL
HCV_L2	RLVVLATATP	PGSTTVPHPN	IEEVALPNTG	EIPFYGRAIP	IEFIKGRHL
HCV_N	RLVVLATATP	PGSVTVPHPN	IEEVALSNTG	EIPFYGKAIP	IEAIMGRHL
HCV12083	RLTVLPATP	PGSVTVPHPN	ITETALPTTG	EIPFYGKAIP	LEYIKGRHL
HCV1480	RLVVLATAIP	PGSVTTPHPN	IEEVALPSEG	EIPFYGRAIP	LVLIKGRHL
HCVPOLYP	RLVVLATATP	PGSVTVPHPN	IEEVALSNIG	EIPFYGKAIP	IETIKGRHL
HD_1	RLVVLATATP	PGSVTVPHSN	IEEVALSNIG	EIPFYGKAIP	LENIKGRHL
HPCCGAA	RLVVLATATP	PGSVTVSHPN	IEEVALSTTG	EIPFYGKAIP	LEVIKGRHL
HPCFG	RLTVLATATP	PGSITVPHPN	IEEVGLTSDG	EIPFYGKALP	LAMIKGRHL
HPCGENANTI	RLVVLATATP	PGSVTVPHPN	IEEIALSNTG	EIPFYGKAIP	IETIKGRHL
HPCGENOM	RLVVLATATP	PGSVTVPHPN	IEEVALSNTG	EIPFYGKAIP	IEAIRGRHL
HPCHUMR	RLVVLATATP	PGSVTVPHPN	IEEVALSNTG	EIPFYGKAIP	IEAIRGRHL
HPCJ	RLVVLATATP	PGSVTVPHPN	IEEVGLSNTG	EIPFYGKAIP	IEVIKGRHL
HPCJCG	RLVVLATATP	PGSITVPHPN	IEEVALSNTG	EIPFYGKAIP	IEAIKGRHL
HPCJK046	RLTVLATATP	PGSVTVPHPN	IQETALPLTG	EVPFYGKAIP	LEYIKGRHL
HPCJK049	RLVVLATATP	PGSITVPHSN	IEEVALTGE	EIPFYGRAIP	LGVIKGRHL
HPCJTA	RLVVLATATP	PGSVTVPHPN	IEEVALSNTG	EIPFYGKAIP	LEAIKGRHL
HPCJTB	RLVVLATATP	PGSVTVPHPN	IEEVALSNTG	EIPFYGKAIP	IEVIKGRHL
HPCK3A	RLTVLATATP	PGSITVPHSN	IEEVALGSEG	EIPFYGKAIP	IACIKGRHL
HPCPLYPRE	RLVVLATATP	PGSVTVPHPN	IEEVALSTTG	EIPFYGKAIP	LEVIKGRHL
HPCPOLP	RLTVLATATP	PGSVTTPHPN	IEEVALGQEG	EIPFYGRAIP	LSYIKGRHL
HPCPP	RLVVLATATP	PGSVTVPHPN	IEEVALSNTG	EIPFYGKAIP	LEAIKGRHL

HPCUNKCD	RLVVLSTATP	PGSVTVPHLN	IEEVALSNTG	EIPFYGKAIP	IEAIKGGRHL
MKC1A	RLVVLATATP	PGSVTVPHPN	IEEVALSNTG	EIPFYGKAIP	LEAIKGGRHL
NDM59	RLTVLATATP	PGSVTTPHPN	IEEVALGQEG	EIPFYGRAIP	LSYIKGGRHL
NZLI	RLTVLATATP	PGSITVPHSN	IEEVALGSEG	EIPFYGKAIP	IALLKGRHL
SA13	RLVVLATATP	PGSVTTPHPN	IEEVALPSEG	EIPFYGRAIP	LALIKGGRHL
Th580	RLTVLATATP	PGSVTVPHPN	ITETALPTTG	EIPFYGKCIP	LEFIKGGRHL
Type_3a_CB	RLTVLATRTP	PGSITVPHSN	IEEVALGSEG	EIPFYGKAIP	IALLKGRHL
TypeV_D	RLTVLATATP	PGSITVPHSN	IEEVALGSEG	EIPFYGKAIP	IALLKGRHL
VN004	RLTVLATATP	PGSVTVPHPN	ITESALPTTG	EIPFYGKAVP	LEYIKGGRHL
VN235	RLTVLATATP	PGSVTVPHPN	ITETALPSTG	EVPFYGKAIP	LECIKGGRHL
VN405	RLTVLATATP	PGSVTVPHPN	ITEVALSSTG	EVPFYGKAIP	LEYIKGGRHL

	1401				1450
BEBE1	IFCHSKKKCD	ELAVALLRGMG	LNAVAYYRGL	DVSIIPTQGD	VVVVATDALM
D89815	IFCHSKKKCD	ELPAKLSALG	LNAVAYYRGL	DVSVIPASGD	VVVVATDALM
ED43type_4	IFCHSKKKCD	ELARQLTSLG	LNAVAYYRGL	DVSVIPTSGD	VVVCATDALM
HC_C2	IFCHSKKKCD	ELAAKLSALG	LNAVAYYRGL	DVSVIPTSGD	VVVVATDALM
HC_G9	IFCHSKKKCD	ELAAKLVLGL	VNAVAFYRGL	DVSVIPTTGD	VVVVATDALM
HCU16326	IFCHSKKKCD	ELAAKLSGLG	LNAVAYYRGL	DVSVIPTSGD	VVVVATDALM
HCV_H_CMUR	IFCHSKKKCD	ELAAKLVALG	INAVAYYRGL	DVSVIPTNGD	VVVVSTDALM
HCV_J1	IFCHSKKKCD	ELAAKLVALG	VNAVAYYRGL	DVSVIPTSGD	VVVVATDALM
HCV_J483	IFCHSKKKCD	ELAAKLTLGL	LNAVAYYRGL	DVSVIPIGD	VAVVATDALM
HCV_J8	IFCHSKKKCD	ELAAALRGMG	VNAVAYYRGL	DVSVIPTQGD	VVVVATDALM
HCV_JK1	IFCHSKKKCD	ELAAKLSALG	VNAVAYYRGL	DVSVIPTSGD	VVVVATDALM
HCV_JS	IFCHSKKKCD	ELAAKLSTLG	LNAVAYYRGL	DVSVIPTSGD	VVVVATDALM
HCV_K1_R1	IFCHSKKKCD	ELAAKLSGLG	LNAVAYYRGL	DVSVIPASGD	VVVVATDALM
HCV_K1_R2	IFCHSKKKCD	ELAAKLSGLG	INAVAYYRGL	DVSVIPASGD	VVVVATDALM
HCV_K1_R3	IFCHSKKKCD	ELATKLSALG	VNAVAYYRGL	DVSVIPTSGN	VVVVATDALM
HCV_K1_S1	IFCHSKKKCD	ELAAKLSGLG	LNAVAYYRGL	DVSVIPASGD	VVVVATDALM
HCV_K1_S2	IFCHSKKKCD	ELAAKLSGLG	INAVAYYRGL	DVSVIPASGD	VVVVATDALM
HCV_K1_S3	IFCHSKKKCD	ELATKLSALG	VNAVAYYRGL	DVSVIPTSGN	VVVVATDALM
HCV_L2	IFCHSKKKCD	ELAAKLSALG	INAVAYYRGL	DVSVIPTSGD	VVVVATDALM
HCV_N	IFCHSKKKCD	ELAAKLSGLG	INAVAYYRGL	DVSVIPTSGD	VVVVATDALM
HCV12083	IFCHSKKKCD	ELAGKLKSLG	LNAVAFYRGV	DVSVIPTSGD	VVVCATDALM
HCV1480	IFCHSKKKCD	ELAKQLTSLG	VNAVAYYRGL	DVAVIPATGD	VVVCSTDALM
HCVPOLYP	IFCHSKKKCD	ELAAKLSGLG	LNAVAYYRGL	DVSVIPTSGD	VVVVATDALM
HD_1	IFCHSRKKCD	ELAAKLSGLG	INAVAYYRGL	DVSVIPTSGD	VVVVATDALM
HPCCGAA	IFCHSKKKCD	ELAAKLVALG	INAVAYYRGL	DVSVIPTSGD	VVVVSTDALM
HPCFG	VFCHSKEKCD	ELASKLRGMG	VNAVAFYRGL	DVSVIPVSGD	VVVCATDALM
HPCGENANTI	IFCHSKKKCD	ELAAKLSALG	INAVAYYRGL	DVSVIPASGN	VVVVATDALM
HPCGENOM	IFCHSKKKCD	ELAAKLSSLG	LNAVAYYRGL	DVSVIPSSGD	VVVVATDALM
HPCHUMR	IFCHSKKKCD	ELAAKLSGLG	INAVAYYRGL	DVSVIPTIGD	VVVVATDALM
HPCJ	IFCHSKKKCD	ELAAKLSALG	INAVAYYRGL	DVSVIPASGD	VVVVATDALM
HPCJCG	IFCHSKKKCD	ELAAKLTLGL	LNAVAYYRGL	DVSVIPTSGD	VVVVATDALM
HPCJK046	IFCHSKKKCD	ELAAQLRTLGL	LNAVAFYRGV	DVSVIPTSGD	VVVCATDALM
HPCJK049	IFCHSKKKCD	ELAKQLTSLG	VNAVAFYRGL	DVSVIPTQGD	VVVCATDALI
HPCJTA	IFCHSKKKCD	ELAAKLSGLG	INAVAYYRGL	DVSVIPTSGD	VVIVATDALM
HPCJTB	IFCHSKKKCD	ELAAKLSGLG	INAVAYYRGL	DVSVIPTSGD	VVVVATDALM
HPCK3A	IFCHSKKKCD	KMASKLRGMG	LNAVAYYRGL	DVSVIPTTGD	VVVCATDALM
HPCPLYPRE	IFCHSKKKCD	ELAAKLVALG	INAVAYYRGL	DVSVIPTSGD	VVVVATDALM
HPCPOLP	IFCHSKKKCD	ELAAALRGMG	LNAVAYYRGL	DVSVIPTQGD	VVVVATDALM
HPCPP	IFCHSKKKCD	ELAAKLSALG	VNAVAYYRGL	DVSIIPTSGD	VVVVATDALM
HPCUNKCD	IFCHSKKKCD	ELAAKLSGLG	LNAVAYYRGL	DVSVIPTSGD	VVVVATDALM
MKC1A	IFCHSKKKCD	ELAAKLSALG	VNAVAYYRGL	DVSIIPTSGD	VVVVATDALM
NDM59	IFCHSKKKCD	ELSAALRSMG	LNAVAYYRGL	DVSVIPTQGD	VVVVATDALM
NZLI	IFCHSKKKCD	EIASKLRGMG	LNAVAYYRGL	DVSVIPTTGD	VVVCATDALM
SA13	IFCHSKKKCD	ELAKQLTSQG	VNAVAYYRGL	DVAVIPATGD	VVVCSTDALM
Th580	IFCHSKKKCD	ELSKQLTSLG	LNAVAFYRGV	DVAVIPTSGD	VVVCATDALM
Type_3a_CB	IFCHSKKKCD	EIASKLRGMG	LNAVAYYRGL	DVSVIPTTGD	VVVCATDALM
TypeV_D	IFCHSKKKCD	EIASKLRGMG	LNAVAYYRGL	DVSVIPTTGD	VVVCATDALM



VN004	IFCHPKKKCD	ELAKQLVSLG	LNAVAFYRGV	DVSVIPTSGD	VVVCATDALM
VN235	IFCHSKKKCD	ELAKQLRTL	LNAVAFYRGV	DVSVIPTAGD	VVVCATDALM
VN405	IFCHSKKKCD	ELAKQLTSLG	LNAVAFYRGV	DVSVIPTSGD	VVVCATDALM
1451			1500		
BEBE1	TGYTGDFDSV	IDCNVAVTQV	VDFS LDPTFT	ITTQTV PQDS	VSR SQRRGRT
D89815	TGFTGDFDSV	IDCNTCVTQT	VDFS LDPTFT	IETTTVPQDA	VSRTQRRGRT
ED43type_4	TGFTGDFDSV	IDCNTSVIQT	VDFS LDPTFS	IEITTV PQDA	VSR SQRRGRT
HC_C2	TGFTGDFDSV	IDCNTCVTQT	VDFS LDPTFT	IETTTVPQDA	VSR SQRRGRT
HC_G9	TGYTGDFDSV	IDCNTCVVQT	VDFS LDPTFS	IETSTVPQDA	VSR SQRRGRT
HCU16326	TGFTGDFDSV	IDCNTCVTQT	VDFS LDPTFT	IETTTVPQDA	VSR SQRRGRT
HCV_H_CM	TGFTGDFDSV	IDCNTCVTQT	VDFS LDPTFT	IETTTLPQDA	VSRTQRRGRT
HCV_J1	TGYTGDFDSV	IDCNTCVTQT	VDFS LDPTFT	IETTTLPQDA	VSRTQRRGRT
HCV_J483	TGFTGDFDSV	IDCNTCVTQT	VDFS LDPTFT	IETTTVPQDA	VSR SQRRGRT
HCV_J8	TGYTGDFDSV	IDCNVAVSQI	VDFS LDPTFT	ITTQTV PQDS	VSR SQRRGRT
HCV_JK1	TGYTGDFDSV	IDCNTCVTQT	VDFS LDPTFT	IETTTLPQDA	VSR SQRRGRT
HCV_JS	TGFTGDFDSV	IDCNTCVTQT	VDFS LDPTFT	IETTTVPQDA	VSR SQRRGRT
HCV_K1_R1	TGFTGDFDSV	IDCNTCVTQT	VDFS LDPTFT	IETTTVPQDA	VSR SQRRGRT
HCV_K1_R2	TGFTGDFDSV	IDCNTCVTQT	VDFS LDPTFT	IETTTVPQDA	VSR SQRRGRT
HCV_K1_R3	TGYTGDFDSV	IDCNTCVIQT	VDFS LDPTFT	IETTTVPQDA	VSR SQRRGRT
HCV_K1_S1	TGYTGDFDSV	IDCNTCVTQT	VDFS LDPTFT	IETTTVPQDA	VSR SQRRGRT
HCV_K1_S2	TGFTGDFDSV	IDCNTCVTQT	VDFS LDPTFT	IETTTVPQDA	VSR SQRRGRT
HCV_K1_S3	TGYTGDFDSV	IDCNTCVIQT	DDFS LDPTFT	IETRTVPQDA	VSR SQRRGRT
HCV_L2	TGYTGDFDSV	IDCNTCVTQT	VDFS LDPTFT	IETTTVPQDA	VSRTQRRGRT
HCV_N	TGYTGDFDSV	IDCNTCVTQT	VDFS LDPTFT	IETTTVPQDA	VSR SQRRGRT
HCV12083	TGYTGDFDSV	IDCNVAVTQV	VDFS LDPTFS	IETTTVPQDA	VSR SQRRGRT
HCV1480	TGFTGDFDSV	IDCN SAVTQT	VDFS LDPTFT	IETTTVPQDA	VSR SQRRGRT
HCVPOLYP	TGFTGDFDSV	IDCNTCVTQT	VDFS LDPTFT	IETTTVPQDA	VSR SQRRGRT
HD_1	TGYTGDFDSV	IDCNVCVTQT	VDFS LDPTFT	IETTTVPQDA	VSR SQRRGRT
HPCCGAA	TGFTGDFDSV	IDCNTCVTQT	VDFS LDPTFT	IETTTLPQDA	VSRTQRRGRT
HPCFG	TGYTGDFDTV	IDCNVAVEQY	VDFS LDPTFS	IETRTVPQDA	VSR SQRRGRT
HPCGENANTI	TGFTGDFDSV	IDCNTCVTQT	VDFS LDPTFT	IETTTMPQDA	VSR SQRRGRT
HPCGENOM	TGFTGDFDSV	IDCNTCVTQT	VDFS LDPTFT	IETTTVPQDA	VSR SQRRGRT
HPCHUMR	TGYTGDFDSV	IDCNTCVTQT	VDFS LDPTFT	IETTTVPQDA	VSR SQRRGRT
HPCJ	TGFTGDFDSV	IDCNTCVTQT	VDFS LDPTFT	IETTTVPQDA	VSR SQRRGRT
HPCJCG	TGFTGDFDSV	IDCNTCVTQT	VDFS LDPTFT	IETTTLPQDA	VSRAQRRGRT
HPCJK046	TGYTGDFDSV	IDCNVAVTQI	VDFS LDPTFS	IETTTVPQDA	VARSQRRGRT
HPCJK049	TGYTGDFDSV	IDCNVAVEQY	VDFS LDPTFS	IETHTV PQDA	VSR SQRRGRT
HPCJTA	TGYTGDFDSV	IDCNTCVTQT	VDFS LDPTFT	IETTTVPQDA	VSR SQRRGRT
HPCJTB	TGYTGDFDSV	IDCNTCVTQT	VDFS LDPTFT	IETTTVPQDA	VSR SQRRGRT
HPCK3A	TGFTGDFDSV	IDCNVAVEQY	VDFS LDPTFS	IETCTAPQDA	VSR SQRRGRT
HPCPLYPRE	TGYTGDFDSV	IDCNTCVTQT	VDFS LDPTFT	IETITLPQDA	VSRTQRRGRT
HPCPOLP	TGFTGDFDSV	IDCNVAVTQV	VDFS LDPTFT	ITTQTV PQDS	VSR SQRRGRT
HPCPP	TGYTGDFDSV	IDCNTCVTQT	VDFS LDPTFT	IETTTVPQDA	VSR SQRRGRT
HPCUNKCD	TGFTGDFDSV	IDCNTCVTQT	VDFS LDPTFT	IETTTVPQDA	VSR SQRRGRT
MKC1A	TGYTGDFDSV	IDCNTCVTQT	VDFS LDPTFT	IETTTVPQDA	VSR SQRRGRT
NDM59	TGYTGDFDSV	IDCNVAVTQV	VDFS LDPTFT	ITTQTV PQDS	VSR SQRRGRT
NZLI	TGFTGDFDSV	IDCNVAVEQY	VDFS LDPTFS	IETRTAPQDA	VSR SQRRGRT
SA13	TGFTGDFDSV	IDCNTTVTQT	VDFS LDPTFT	IETTTVPQDA	VSR SQRRGRT
Th580	TGYTGDFDSV	IDCNVAVTQV	VDFS LDPTFS	IETTTVPQDA	VSR SQRRGRT
Type_3a_CB	TGYTGDFDSV	IDCNVAVEQY	VDFS LDPTFS	IETRTAPQDA	VSR SQRRGRT
TypeV_D	TGFTGDFDSV	IDCNVAVEQY	VDFS LDPTFS	IETRTAPQDA	VSR SQRRGRT
VN004	TGYTGDFDSV	IDCNVTVTQV	VDFS LDPTFT	IETTTVPQDA	VSR SQRRGRT
VN235	TGYTGDFDSV	IDCNVAVTQI	VDFS LDPTFS	IETTTVPQDA	VARSQRRGRT
VN405	TGYTGDFDSV	IDCNVSVTQV	VDFS LDPTFT	IETTTMPQDA	VSR SQRRGRT
1501			1550		
BEBE1	GRGRLGIYRY	VSSGERASGM	FDTVVLCECY	DAGAAWYELT	PAETTVRLRA
D89815	GRGRRGIYRF	VTPGERPSAM	FDSSVLCECY	DAGCAWYELT	PAETSVRLRA
ED43type_4	GRGRLGTIYR	VTPGERPSGM	FDTAELCECY	DAGCAWYELT	PAETTRLKA

HC_C2	GRGRRGIYRF	VTPGERPSGM	FDSSVLCECY	DAGCAWYELT	PAETSVRLRA
HC_G9	GRGKHGIYRY	VSPGERPSGM	FDSVVLCECY	DAGCAWYELT	PAETTVRLRA
HCU16326	GRGRAGIYRF	VTPGERPSGM	FDSSVLCECY	DAGCAWYELT	PAETSVRLRA
HCV_H_CMV	GRGKPGIYRF	VAPGERPSGM	FDSSVLCECY	DAGCAWYELM	PAETTVRLRA
HCV_J1	GRGKPGIYRF	VAPGERPSGM	FDSSILCECY	DTGCAWYELT	PAETTVRLRA
HCV_J483	GRGRSGIYRF	VTPGERPSGM	FDSSVLCECY	DAGCAWYELT	PAETSVRLRA
HCV_J8	GRGRLGVYRY	VSSGERPSGM	FDSVVLCECY	DAGAAWYELT	PAETTVRLRA
HCV_JK1	GRGRGGIYRF	VTPGERPSGM	FDSSVLCECY	DAGCAWYELT	PAVTSVRLRA
HCV_JS	GRGRGGIYRF	VTPGERPSGM	FDSSVLCECY	DAGCAWYELT	PAETSVRLRA
HCV_K1_R1	GRGRRGIYRF	VTPGERPSGM	FDSSVLCECY	DAGCAWYELT	PAETSVRLRA
HCV_K1_R2	GRGRAGIYRF	VTPGERPSGM	FDSSVLCECY	DAGCAWYELT	PAETSVRLRA
HCV_K1_R3	GRGRRGIYRF	VTPGERTSGM	FDSSVLCECY	DAGCAWYELT	PAETSVRLRA
HCV_K1_S1	GRGRRGIYRF	VTPGERPSGM	FDSSVLCECY	DAGCAWYELT	PAETSVRLRA
HCV_K1_S2	GRGRAGIYRF	VTPGERPSGM	FDSSVLCECY	DAGCAWYELT	PAETSVRLRA
HCV_K1_S3	GRGRRGIYRF	VTPGERTSGM	FDSSVLCECY	DAGCAWYELT	PAETSVRLRA
HCV_L2	GRGRGGIYRF	VTPGERPSGM	FDSSVLCECY	DAGCAWYELT	PAETTVRLRA
HCV_N	GRGRGGIYRF	VTPGERPSGM	FDSVVLCECY	DAGCAWYELT	PAETSVRLRA
HCV12083	GRGKPGVYRF	VSQGERPSGM	FDTVVLCEAY	DTGCAWYELT	PSETTVRLRA
HCV1480	GRGRHGIYRY	VSSGERPSGI	FDSVVLCECY	DAGCAWYDLT	PAETTVRLRA
HCVPOLYP	GRGRRGIYRF	VTPGERPSGM	FDSSVLCECY	DAGCAWYELT	PAETSVRLRA
HD_1	GRGRMGIYRF	VTPGERPSGM	FDSSVLCESY	DAGCAWYELT	PAEASVRLRA
HPCCGAA	GRGKPGIYRF	VAPGERPSGM	FDSSVLCECY	DAGCAWYELT	PAETTVRLRA
HPCFG	GRGRPGIYRF	VTPGERPSGM	FDSVVLCECY	DAGCSWYDLQ	PAETTVRLRA
HPCGENANTI	SRGRRGIYRF	VTPGERPSGM	FDSSVLCECY	DAGCAWYELT	PAETSVRLRA
HPCGENOM	GRGREGIYRF	VTPGERPSGM	FDSSVLCECY	DAGCAWYELT	PAETTVRLRA
HPCHUMR	GRGRRGIYRF	VTPGERPSGM	FDSSVLCECY	DAGCAWYELT	PAETSVRLRA
HPCJ	GRGRAGIYRF	VTPGERPSGM	FDSSVLCECY	DSGCAWYELT	PAETSVRLRA
HPCJCG	GRGRSGIYRF	VTPGERPSGM	FDSSVLCECY	DAGCAWYELT	PAETSVRLRA
HPCJK046	GRGKPGVYRY	VSQGERPSGM	FDTVVLCEAY	DTGAAWYELT	PAETTVRLRA
HPCJK049	GRGKSGTYRY	VSPGERPSGM	FDSVVLCECY	DAGCAWYELT	PSETTVRLRA
HPCJTA	GRGRGGIYRF	VTPGERPSGM	FDSSVLCECY	DAGCAWYELT	PAETTVRLRA
HPCJTB	GRGRGGIYRF	VTPGERPSGM	FDSSVLCECY	DAGCAWYELT	PAETTVRLRA
HPCK3A	GRGRLGTYYRY	VTPGERPSGM	FDSVVLCECY	DAGCSWYDLQ	PAETTVRLRA
HPCPLYPRE	GRGKPGIYRF	VAPGERPSGM	FDSSVLCECY	DAGCAWYELT	PAETTVRLRA
HPCPOLP	GRGRLGIYRY	VSTGERASGM	FDSVVLCECY	DAGAAWYELT	PAETTVRLRA
HPCPP	GRGRGGIYRF	VTPGERPSGM	FDSSVLCECY	DAGCAWYELT	PAETSVRLRA
HPCUNKCD	GRGRAGIYRF	VTPGERPSGM	FDSSVLCECY	DAGCAWYELT	PAETSVRLRA
MKC1A	GRGRGGIYRF	VTPGERPSGM	FDSSVLCECY	DAGCAWYELT	PAETSVRLRA
NDM59	GRGRLGIYRY	VSTGERASGM	FDSVVLCECY	DAGAAWYELT	PSETTVRLRA
NZLI	GRGRLGTYYRY	VASGERPSGM	FDSVVLCECY	DAGCSWYDLQ	PAETTVRLRA
SA13	GRGRHGIYRY	VSSGERPSGI	FDSVVLCECY	DAGCAWYDLT	PAETTVRLRA
Th580	GRGKPGVYRF	VSQGERPSGM	FDSVVLCEAY	DTGCAWYELT	PAETTVRLRA
Type_3a_CB	GRGRLGTYYRY	VAPGERPSGM	FDSVVLCECY	DAGCSWYDLQ	PAETTVRLRA
TypeV_D	GRGRLGTYYRY	VAPGERPSGM	FDSVVLCECY	DAGCSWYDLQ	PAETTVRLRA
VN004	GRGKHGVYRY	VSQGERPSGM	FDSVILCEAY	DTGCAWYELT	PAETTVRLRA
VN235	GRGKPGVYRY	VSQGERPSGM	FDTVVLCEAY	DVGCAWYELT	PSETTVRLRA
VN405	GRGKHGVYRY	VSQGERPSGI	FDTVVLCEAY	DTGCAWYELT	PSETTVRLRA

	1551			1600	
BEBE1	YFNTPLPVC	QDHLEFWEAV	FTGLTHIDAH	FLSQTQAGE	GFPYLVAYQA
D89815	YLNTPGLPVC	QDHLEFWESV	FTGLTHIDAH	FLSQTQAGD	NFPYLVAYQA
ED43type_4	YFDTPLPVC	QDHLEFWESV	FTGLTHIDGH	FLSQTQSGE	NFPYLVAYQA
HC_C2	YLNTPGLPVC	QDHLEFWESV	FTGLTHIDAH	FLSQTQAGD	NFPYLVAYQA
HC_G9	YLNTPGLPVC	QDHLEFWESV	FTGLTHIDAH	FLSQTQSGE	NFPYLVAYQA
HCU16326	YLNTPGLPVC	QDHLEFSEGV	FTGLTHIDAH	FLSQTQAGE	NFPYLVAYQA
HCV_H_CMV	YMNTPGLPVC	QDHLEFWEGV	FTGLTHIDAH	FLSQTQSGE	NFPYLVAYQA
HCV_J1	YMNTPGLPVC	QDHLEFWEGV	FTGLTHIDAH	FLSQTQSGE	NFPYLVAYQA
HCV_J483	YLNTPGLPVC	QDHLEFWESV	FTGLSHIDAH	FLSQTQAGD	NFPYLVAYQA
HCV_J8	YFNTPLPVC	QDHLEFWEAV	FTGLTHIDAH	FLSQTQSGE	NFAYLTAYQA
HCV_JK1	YLNTPGLPVC	QVHLEFWESV	FTGLTHIDAH	FLSQTQAGE	NFPYLVAYQA

HCV_JS	YLNTPLPVC	QDHLEFWESV	FTGLTHIDAH	FLSQTQAGD	NFPYLVAYQA
HCV_K1_R1	YLNTPLPFC	QDHLEFWEGV	FTGLTHIDAH	FLSQTQAGE	NLPYLVAYQA
HCV_K1_R2	YLNTPLPVW	QDHLEFWESV	FTGLTHIDAH	FLSQTQAGD	NFPYLVAYQA
HCV_K1_R3	YLNTPLPVC	QDHLEFWESV	FTGLTHIDAH	FLSQTQAGD	NFPYLVAYQA
HCV_K1_S1	YLNTPLPFC	QDHLEFWEGV	FTGLTHIDAH	FLSQTQAGE	NLPYLVAYQA
HCV_K1_S2	YLNTPLPVW	QDHLEFWESV	FTGLTHIDAH	FLSQTQAGD	NFPYLVAYQA
HCV_K1_S3	YLNTPLPVC	QDHLEFWESV	FTGLTHIDAH	FLSQTQAGD	NFPYLVAYQA
HCV_L2	YLNTPLPVC	QDHLEFWESV	FTGLNHIDAH	FLSQTQAGD	NFPYLVAYQA
HCV_N	YLNTPLPVC	QDHLEFWESV	FTGLTHIDAH	FLSQTQAGD	NFPYLVAYQA
HCV12083	YMNTPLPVC	QDHLEFWEGV	FTGLTHIDAH	FLSHTKQAGE	NFAYLVAYQA
HCV1480	YLNTPLPVC	QEHLEFWEGV	FTGLTNIDAH	MLSQAKQGGG	NFPYLVAYQA
HCVPOLYP	YLNTPLPVC	QDHLEFWESV	FTGLTHIDAH	FLSQTQAGE	NFPYLTAYQA
HD_1	YLNTPLPVC	QDHLEFWESV	FTGLTHIDAH	FLSQTQAGD	NFPYLVAYQA
HPCCGAA	YMNTPLPVC	QDHLEFWEGV	FTGLTHIDAH	FLSQTQSGE	NFPYLVAYQA
HPCFG	YLSTPLPVC	QDHLDWFERV	FTGLTHIDAH	FLSQAKQQGL	NFAYLVAYQA
HPCGENANTI	YLNTPLPVC	QDHLEFWESV	FTGLTHIDAH	FLSQTQAGD	NFPYLVAYQA
HPCGENOM	YLNTPLPVC	QDHLEFWEGV	FTGLTHIDAH	FLSQTQAGD	NFPYLVAYQA
HPCHUMR	YLNTPLPVC	QDHLEFWESV	FTGLTHIDAH	FLSQTQAGD	NFPYLVAYQA
HPCJ	YLNTPLPVC	QDHLEFWESV	FTGLTHIDAH	FLSQTQAGD	NFPYLVAYQA
HPCJCG	YLNTPLPVC	QDHLEFWESV	FTGLTHIDAH	FLSQTQAGD	NLPYLVAYQA
HPCJK046	YLNTPLPVC	QDHLEFWEAV	FTGLTHIDAH	FLSQTQGGG	NFAYLVAYQA
HPCJK049	YLSTPLPVC	QDHLEFWEGV	FTGLTHIDAH	FLSQTQQGL	NFPYLTAYQA
HPCJTA	YLNTPLPVC	QDHLEFWESV	FTGLTHIDAH	FLSQTQAGD	NFPYLVAYQA
HPCJTB	YLNTPLPVC	QDHLEFWESV	FTGLTHIDAH	FLSQTQAGD	NFPYLVVYQA
HPCK3A	YLSTPLPVC	QDHLDLWESV	FTGLTHIDAH	FLSQTQAGL	NFSYLTAYQA
HPCPLYPRE	YMNTPLPVC	QDHLEFWEGV	FTGLTHIDAH	FLSQTQSGE	NLPYLVAYQA
HPCPOLP	YFNTPLPVC	QDHLEFWEAV	FTGLTHIDAH	FLSQTQSGE	NFAYLTAYQA
HPCPP	YLNTPLPVC	QDHLEFWESV	FTGLTHIDAH	FLSQTQAGD	NFPYLVAYQA
HPCUNKCD	YLNTPLPVC	QDHLEFSEGV	FTGLTHIDAH	FLSQTQAGE	NFPYLVAYQA
MKC1A	YLNTPLPVC	QDHLEFWESV	FTGLTHIDAH	FLSQTQAGD	NFPYLVAYQA
NDM59	YFNTPLPVC	QDHLEFWEAV	FTGLTHIDAH	FLSQTQSGE	NFAYLVAYQA
NZLI	YLSTPLPVC	QDHLDWFESV	FTGLTHIDAH	FLSQTQQGL	NFSYLTAYQA
SA13	YLNTPLPVC	QDHLEFWEGV	FTGLTNIDAH	MLSQTQGGG	NFPYLVAYQA
Th580	YLNTPLPVC	QDHLEFWEGV	FTGLTHIDAH	FLSQTQGGG	NFAYLVAYQA
Type_3a_CB	YLSTPLPVC	QDHLDWFESV	FTGLTHIDAH	FLSQTQQGL	NFSYLTAYQA
TypeV_D	YLSTPLPVC	QDHLDWFESV	FTGLTHIDAH	FLSQTQQGL	NFSYLTAYQA
VN004	YLNTPLPVC	QDHLEFWEGV	FTGLTHIDAH	FLSQTQAGE	NFAYLVAYQA
VN235	YLNTPLPVC	QDHLEFWEGV	FTGMTHIDAH	FLSQTQGGG	NFAYLVAYQA
VN405	YLNTPLPVC	QDHLEFWEGV	FTGLTHIDAH	LLSQTQGGG	NFAYLVAYQA

	1601			1650	
BEBE1	TVCARAKAPP	PSWDVMWKCL	IRLKPTLVGP	TPLLYRLGSV	TNEVTLTHPV
D89815	TVCARAKAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEVTLTHPI
ED43type_4	TVSAKVLAP	PSWDTMWKCL	IRLKPTLHGP	TPLLYRLGSV	QNEVVLTHPI
HC_C2	TVCARAKAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEVTLTHPI
HC_G9	TVCARAKAPP	PSWDQMWKCL	IRLKPTLTGA	TPLLYRLGGV	QNEITLTHPI
HCU16326	TVCARAKAPP	PSWDEMWRCL	IRLKPTLHGP	TPLLYRLGAV	QNEVTLTHPI
HCV_H_CMR	TVCARAKAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEVTLTHPI
HCV_J1	TVCARAKAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QGEVTLTHPV
HCV_J483	TVCARAKAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEVTLTHPI
HCV_J8	TVCARAKAPP	PSWDVMWKCL	IRLKPTLTGP	TPLLYRLGAV	TNEVTLTHPV
HCV_JK1	TVCARAKAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEVTLTHPI
HCV_JS	TVCARAKAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEVTLTHPI
HCV_K1_R1	TVCARAKAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNDVTLTHPI
HCV_K1_R2	TVCARAKAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEVILTHPI
HCV_K1_R3	TVCARAKAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEVTLTHPI
HCV_K1_S1	TVCARAKAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNDVTLTHPI
HCV_K1_S2	TVCARAKAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEVILTHPI
HCV_K1_S3	TVCARAKAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEVILTHPI
HCV_L2	TVCARAKAPP	PSWDQMWKCL	IWLKPVHGP	TPLLYRLGAV	QNEITLTHPI

HCV_N	TVCARAQAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEVTLTTHPI
HCV12083	TVCARAKAPP	PSWDMMWKCL	IRLKPTLTGP	TPLLYRLGAV	QNGVITTHPI
HCV1480	TVCVRAKAPP	PSWDTMWKCM	ICLKPTLTGP	TPLLYRLGAV	QNEITLTTHPI
HCVPOLYP	TVCARAQAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEVVLTHPI
HD_1	TVCARAQAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEVTLTTHPI
HPCCGAA	TVCARAQAPP	PSWDQMRKCL	IRLKPTLHGP	TPLLYRLGAV	QNEVTLTTHPI
HPCFG	TVCARAKASP	PCWDEMWKCL	IRLKPTLQGP	TPLLYRLGAI	QNDICMTHPI
HPCGENANTI	TVCARAQAPP	PSWDQMWKCL	TRLKPTLHGP	TPLLYRLGAV	QNEVTLTTHPI
HPCGENOM	TVCARAKAPP	PSWDQMWKCL	TRLKPTLQGP	TPLLYRLGAV	QNEVTLTTHPI
HPCHUMR	TVCARAQAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEVTLTTHPI
HPCJ	TVCARSQAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEVTLTTHPI
HPCJCG	TVCARAQAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEVTLTTHPI
HPCJK046	TVCARAKAPP	PSWDTMWKCL	LRLKPTLTGP	TPLLYRLGAV	QNEVTPTHPV
HPCJK049	TVCARAAALP	PSWDETWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEICLTTHPV
HPCJTA	TVCARAQAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEITLTTHPI
HPCJTB	TVCARAQAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEITLTTHPI
HPCK3A	TVCARAQAPP	PSWDETWKCL	VRKPTLHGP	TPLLYRLGPV	QNEICLTTHPI
HPCPLYPRE	TVCARAQAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEITLTTHPV
HPCPOLP	TVCARAKAPP	PSWDVMWKCL	TRLKPTLVGP	TPLLYRLGSV	TNEVTLTTHPV
HPCPP	TVCARAKAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEVTLTTHPI
HPCUNKCD	TVCARAQAPP	PSWDEMWRCL	IRLKPTLHGP	TPLLYRLGAV	QNEVTLTTHPI
MKC1A	TVCARAKAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEVTLTTHPI
NDM59	TVCARAKAPP	PSWDVMWKCL	TRLKPTLVGP	TPLLYRLGPV	TNEVTLTTHPV
NZLI	TVCARAQAPP	PSWDEMWKCL	VRKPTLHGP	TPLLYRLGPV	QNETCLTTHPI
SA13	TVCVRAKAPP	PSWDTMWKCM	LRLKPTLTGP	TPLLYRLGAV	QNEITLTTHPI
Th580	TVCARAKAPP	PSWDVMWKCL	TRLKPTLTGP	TPLLYRLGAV	QNEIVTTHPI
Type_3a_CB	TVCARAQAPP	PSWDETWKCL	VRKPTLHGP	TPLLYRLGPV	QNEICLSHPI
TypeV_D	TVCARAQAPP	PSWDEMWKCL	VRKPTLHGP	TPLLYRLGPV	QNETCLTTHPV
VN004	TVCARAKAPP	PSWDTMWKCL	IRLKPMLTGP	TPLLYRLGPV	QNEVVTTTHPI
VN235	TVCARAKAPP	PSWDTMWKCL	IRLKPMLTGP	TPLLYRLGAV	QNEIITTHPI
VN405	TVCARAKAPP	PSWDTMWKCL	IRLKPMLTGP	TPLLYRLGAV	QNEITTTTHPI

	1651				1700
BEBE1	TKYIATCMQA	DLEIMTSTWV	LAGGVLAAVA	AYCLATGCVS	IIGRIHVNQK
D89815	TKYIMACMSA	DLEVVTSTWV	LVGGVLAALA	AYCLTTGSVV	IVGRIILSGR
ED43type_4	TKYIMACMSA	DLEVVTSTWV	LVGGVLAALA	AYCLSVGSVV	IVGRVVLGSGQ
HC_C2	TKYIMACMSA	DLEVVTSTWV	LVGGVLAALA	AYCLTTGSVV	IVGRIVLSGR
HC_G9	TKYIMACMSA	DLEVVTSTWV	LVGGVLAALA	AYCLSTGSVV	IVGRIILSGK
HCU16326	TKFIMTCMSA	DLEVVTSTWV	LVGGVLAALA	AYCLTTGSVV	IVGRIILSGK
HCV_H_CMV	TKYIMTCMSA	DLEVVTSTWV	LVGGVLAALA	AYCLSTGCVV	IVGRIVLSGK
HCV_J1	TKYIMTCMSA	DLEVVTSTWV	LVGGVLAALA	AYCLSTGCVV	IVGRIVLSGR
HCV_J483	TKYIMACMSA	DLEVVTSTWV	LVGGVLAALA	AYCLTTGSVV	IVGRIILSGK
HCV_J8	TKYIATCMQA	DLEIMTSSWV	LAGGVLAAVA	AYCLATGCIS	IIGRLHLNDR
HCV_JK1	TKFIMACMSA	DLEVVTSTWV	LVGGVLAALA	AYCLTTGSVV	IVGRIILSGR
HCV_JS	TKYIMACMSA	DLEVVTSTWV	LVGGVLAALA	AYCLTTGSVV	IVGRIILSGK
HCV_K1_R1	TKYIMTCMSA	DLEVVTSTWV	LVGGVLAALT	AYCLTTGSVV	IVGRIILSGK
HCV_K1_R2	TKYIMACMSA	DLEVVTSTWV	LVGGVLAALA	AYCLTTGSVV	IVGRIILSGK
HCV_K1_R3	TKFIMACMSA	DLEVVTSTWV	LVGGVLAALA	AYCLTTGSVV	IVGRIILSGK
HCV_K1_S1	TKYIMTCMSA	DLEVVTSTWV	LVGGVLAALT	AYCLTTGSVV	IVGRIILSGK
HCV_K1_S2	TKYIMACMSA	DLEVVTSTWV	LVGGVLAALA	AYCLTTGSVV	IVGRIILSGK
HCV_K1_S3	TKFIMACMSA	DLEVVTSTWV	LVGGVLAALA	AYCLTTGSVV	IVGRIILSGK
HCV_L2	TKLIMASMSA	DLEVVTSTWV	LVGGVLAALA	AYCLTTGSVV	IVGRIILSGR
HCV_N	TKYIMACMSA	DLEVVTSTWV	LVGGVLAALA	AYCLTTGSVV	IVGRIILSGR
HCV12083	TKYIMTCMSA	DLEVITSTWV	LVGGVLAALA	AYCLSVGCVV	ICGRITLTGK
HCV1480	TKYIMACMSA	DLEVITSTWV	LVGGVVAALA	AYCLTVGSVA	IVGRIILSGR
HCVPOLYP	TKYIMACMSA	DLEVVTSTWV	LVGGVLAALA	AYCLTTGSVV	IVGRIILSGR
HD_1	TKFIMACMSA	DLEVVTSTWV	LVGGVLAALA	AYCLTTGCVV	IVGRIILSGR
HPCCGAA	TKYIMTCMSA	DLEVVTSTWV	LVGGVLAALA	AYCLSTGCVV	IVGRIVLSGK
HPCFG	TKYIMACMSA	DLEVTTSAWV	LVGGVLAALA	AYCLSVGCVV	IVGHIELGGK
HPCGENANTI	TKYIMACMSA	DLEVVTSTWV	LVGGVLAALA	AYCLTTGSVV	IVGRIILSGK

HPCGENOM	TKYIMTCMSA	DLEVVTSTWV	LVGGVLAALA	AYCLTTGSVV	IVGRIVLSGS
HPCHUMR	TKYIMACMSA	DLEVVTSTWV	LVGGVLAALA	AYCLTTGSVV	IVGRIILSGR
HPCJ	TKFIMACMSA	DLEVVTSTWV	LVGGVLAALA	AYCLTTGSVV	IVGRIILSGR
HPCJCG	TKYIMACMSA	DLEVVTSTWV	LVGGVLAALA	AYCLTTGSVV	IVGRIILSGR
HPCJK046	TKYIMACMSA	DLEVITSTWV	VAGGILAAIA	AYCLTVGSVV	ICGRITSSR
HPCJK049	TKYIATCMAA	DLEVATSAWV	LLGGVMAALT	AYCLSVGSVV	IVGHLVLGGK
HPCJTA	TKFIMACMSA	DLEVVTSTWV	LVGGVLAALA	AYCLTTGSVV	IVGRIILSGR
HPCJTB	TKFIMACMSA	DLEVVTSTWV	LVGGVLAALA	AYCLTTGSVV	IVGRIILSGR
HPCK3A	TKYVMACMSA	DLEVTTSTWV	LLGGVLAAVA	AYCLSVGCVV	IVGHIELGGK
HPCPLYPRE	TKYIMTCMSA	DLEVVTSTWV	LVGGVLAALA	AYCLSTGCVV	IVGRVVLSGK
HPCPOLP	TKYIATCMQA	DLEVMTSTWV	LAGGVLAAVA	AYCLATGCVV	IIGRLHVNQR
HPCPP	TKFIMACMSA	DLEVVTSTWV	LVGGVLAALA	AYCLTTGSVV	IVGRIILSGR
HPCUNKCD	TKFIMTCMSA	DLEVVTSTWV	LVGGVLAALA	AYCLTTGSVV	IVGRIILSGK
MKC1A	TKFIMACMSA	DLEVVTSTWV	LVGGVLAALA	AYCLTTGSVV	IVGRIILSGR
NDM59	TKYIATCMQA	DLEVMTSTWV	LAGGVLAAVA	AYCLATGCVS	IIGRLHVNQR
NZLI	TKYLMACMSA	DLEVTTSTWV	LLGGVLAALA	AYCLSVGCVV	IVGHIELEGK
SA13	TKYIMACMSA	DLEVITSTWV	LVGGVVAALA	AYCLTVGSVA	IVGRIILSGR
Th580	TKYIMTCMSA	DLEVITSTWV	IVGGVLAALA	AYCLTVGCVV	ICGRIVTSGK
Type_3a_CB	TKYVMACMSA	DLEVTTSTWV	LLGGVLAALA	AYCLSVGCVV	IVGHIELGGK
TypeV_D	TKYIMACMSA	DLEVTTSTWV	LLGGVLAALA	AYCLSVGCVV	IVGHIELGGK
VN004	TKYIMTCMSA	DLEVITSTWV	LVGGVVAALA	AYCLSVGCVV	ICGRISTSGK
VN235	TKYIMTCMAA	DLEVITSTWV	LAGGIVAALA	AYCLTVGSVV	ICGRIVTSGK
VN405	TKYIMTCMSA	DLEVITSTWV	LVGGVLAALA	AYCLSVGCVV	VCGRISTTGK

	1701				1750
BEBE1	TIIAPDKEVL	YEAFFDEMEEC	ASRTALIEEG	HRIAEMLKSK	IQGLMQQASK
D89815	PAVIPDREVL	YQEFDEMEEC	ASHLPYIEQG	MQLAEQFKQK	ALGLLQTATK
ED43type_4	PAVIPDREVL	YQQFDEMEEC	SKHLPLVEHG	LQLAEQFKQK	ALGLLNFAGK
HC_C2	PAVIPDREVL	YQEFDEMEEC	GSHLPYIEQG	MQLAEQFKQK	ALGLLQIATK
HC_G9	PAVIPDREVL	YREFDEMEEC	AAHIPYLEQG	MHLAEQFKQK	ALGLLQTASK
HCU16326	PAIIPDREVL	YQEFDEMEEC	ASHLPYFEQG	MQLAEQFKQK	ALGLLQTATK
HCV_H_CMR	PAIIPDREVL	YQEFDEMEEC	SQHLPYIEQG	MMLAEQFKQK	ALGLLQTASR
HCV_J1	PAIIPDREVL	YREFDEMEEC	SQHLPYIEQG	MMLAEQFKQK	ALGLLQTASR
HCV_J483	PAVVPDREVL	YQEFDEMEEC	ASQLPYIEQG	MQLAEQFKQK	ALGLLQTATK
HCV_J8	VVVPDKEIL	YEAFFDEMEEC	ASKAALIEEG	QRMAEMLKSK	IQGLLQQATR
HCV_JK1	PAIIPDREVL	YQEFDEMEEC	ASHLPYIEQG	MQLAEQFKQK	ALGLLQTASK
HCV_JS	PAVIPDREVL	YREFDEMEEC	ASHLPYIEQG	MQLAEQFKQK	ALGLLQTATK
HCV_K1_R1	PAVIPDREAL	YQEFDEMEEC	ASHLPYIEQG	MQLAEQFKQK	ALGLLQTATN
HCV_K1_R2	PAIIPDREVL	YREFDEMEEC	ASHLPYIEQG	MQLAEQFKQK	ALGLLQTATK
HCV_K1_R3	PAVIPDREVL	YREFDEMEEC	ASHLPYIEQG	MQLAEQFKQK	ALGLLQTATK
HCV_K1_S1	PAVIPDREAL	YQEFDEMEEC	ASHLPYIEQG	MQLAEQFKQK	ALGLLQTATN
HCV_K1_S2	PAIIPDREVL	YREFDEMEEC	ASHLPYIEQG	MQLAEQFKQK	ALGLLQTATK
HCV_K1_S3	PAVIPDREVL	YREFDEMEEC	ASHLPYIEQG	MQLAEQFKQK	ALGLLQTATK
HCV_L2	PAVIPDREVL	YREFDEMEEC	ASHLPYIEQG	VQLAEQFKQK	ALGLLQTATK
HCV_N	PAVVPDREVL	YREFDEMEEC	ASHLPYIEQG	MQLAEQFKQK	ALGLLQTATK
HCV12083	PAVVPDREIL	YQQFDEMEEC	SRHIPYLAEG	QQIAEQFRQK	VLGLLQASAK
HCV1480	PAITPDREVL	YQQFDEMEEC	SASLPYVDEA	RAIAGQFKEK	VLGLIGTAGQ
HCVPOLYP	PAIIPDREVL	YQEFDEMEEC	ASHLPYIEQG	MQLAEQFKQK	ALGLLQTATK
HD_1	PAIIPDREVL	YQEFDEMEEC	ASHLPYIEQG	MQLAEQFKQK	ALGLLQTATK
HPCCGAA	PAIIPDREVL	YQEFDEMEEC	SQHLPYIEQG	MMLAEQFKQK	ALGLLQTASR
HPCFG	PALVPDRQVL	YQQYDEMEEC	SQSAPYIEQA	QAIAQQFKDK	VLGLLQRASQ
HPCGENANT1	PAVVPDREVL	YQEFDEMEEC	ASHLPYIEQG	MQLAEQFKQK	ALGLLQTATK
HPCGENOM	PAIVPDREVL	YQDFDEMEEC	ASHLPYIEQG	MQLAEQFKQK	ALGLLQTATK
HPCHUMR	PAIVPDRELL	YQEFDEMEEC	ASHLPYIEQG	MQLAEQFKQK	ALGLLQTATK
HPCJ	PAVIPDREVL	YREFDEMEEC	ASHLPYIEQG	MLLAEQFKQK	ALGLLQMATK
HPCJCG	PAVIPDREVL	YQEFDEMEEC	ASHLPYIEQG	MQLAEQFKQK	ALGLLQTATK
HPCJK046	PAVIPDREVM	YQQYDEMEEC	SRHLPYLVEG	QQLAEQFKQN	VLGLIQVTTK
HPCJK049	PALVPDKEVL	YQQYDEMEEC	SRAAPYIEQA	QGIAQQFKEK	VIGLLQQADQ
HPCJTA	PAVVPDREVL	YREFDEMEEC	ASHLPYIEQG	MQLAEQFKQK	ALGLLQTATK
HPCJTB	PAVVPDREVL	YREFDEMEEC	ASHLPYIEQG	MQLAEQFKQK	ALGLLQTATK

HPCK3A	PALVPDKEVL	YQQYDEMEEC	SQARPYIEQA	QVIAHQFKEK	VLGLLQQRATQ
HPCPLYPRE	PAIIPDREVL	YREFDEMEEC	SQHLPLYEQG	MMLAEQFKQK	ALGLLQQTASR
HPCPOLP	AVVAPDKEVL	YEAFFDEMEEC	ASRAALIEEG	QRIAEMLKSK	IQGLLQQASK
HPCPP	PAVIPDREVL	YQEFDEMEEC	ASHLPYIEQG	MQLAEQFKQK	ALGLLQQTATK
HPCUNKCD	PAIIPDREVL	YQEFDEMEEC	ASHLPYFEQG	MQLAEQFKQK	ALGLLQQTATK
MKC1A	PAVIPDREVL	YQEFDEMEEC	ASHLPYIEQG	MQLAEQFKQK	ALGLLQQTATK
NDM59	AVVAPDKEVL	YEAFFDEMEEC	ASRAALIEEG	QRIAEMLKSK	IQGLLQQASK
NZLI	PALVPDKEVL	YQQYDEMEEC	SQAAPYIEQA	QVIAHQFKEK	ILGLLQQRATQ
SA13	PAIIPDREVL	YQQFDEMEEC	SASLPYMDEA	RAIAEQFKEK	VLGLLQGTAGQ
Th580	PAVVPDREVL	YQQFDEMEEC	SKHIPYLVEG	QQIAEQFKQK	VLGLLQAGTK
Type_3a_CB	PALVPDKEVL	YQQYDEMEEC	SQAAPYIEQA	QAIAHQFKEK	VLGLLQQRATQ
TypeV_D	PALVPDKEVL	YQQYDEMEEC	SQAAPYIEQA	QAIAHQFKEK	VLGLLQQRATQ
VN004	PVLIPDREVL	YQQFDEMEEC	SRHIPYLAEG	HLIAEQFKQK	VLGLLIQSTSK
VN235	PVPLPDREVL	YRQFDEMEEC	SRHIPYLAEG	QQIAEQFKQK	ILGLLQNTAK
VN405	PVLIPDREVL	YQQFDEMEEC	SRHIPYLVEG	QHLAEQFKQK	VLGLLIQTTTR

	1751			1800	
BEBE1	QAQGVQPAVQ	ATWPKLEQFW	AKHMWNFISG	IQYLAGLSTL	PGNPAVASMM
D89815	QAEAAAAPVVE	SKWRALETFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIASLM
ED43type_4	QAQEATPVIQ	SNFAKLEQFW	ANDMWNFISG	IQYLAGLSTL	PGNPAIASLM
HC_C2	QAEAAAAPVVE	SKWRALETFW	AKHMWNFISG	VQYLAGLSTL	PGNPAIASLM
HC_G9	QAETITPAVH	TNWQKLESFV	AKHMWNFVSG	IQYLAGLSTL	PGNPAIASLM
HCU16326	QAEAAAAPVVE	SKWRALETFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIRSPM
HCV_H_CMR	HAEVITPAVQ	TNWQKLEVFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIASLM
HCV_J1	QAEVIAPTQV	TNWQKLEAFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIASLM
HCV_J483	QAEAAAAPVVE	SKWRALETFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIASLM
HCV_J8	QAQDIQPAIQ	SSWPKLEQFW	AKHMWNFISG	IQYLAGLSTL	PGNPAVASMM
HCV_JK1	QAEAAAAPVVE	SKWQALEAFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIVSLM
HCV_JS	QAEAAAAPVME	SKWRALETFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIASLM
HCV_K1_R1	QAEAAAAPVVE	SKWRALEAFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIASLM
HCV_K1_R2	QAEAAAAPVVE	SKWQALETFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIASLM
HCV_K1_R3	QAEAAAAPVVE	SKWRTLEVFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIASLM
HCV_K1_S1	QAEAAAAPVVE	SKWRALEAFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIASLM
HCV_K1_S2	QAEAAAAPVVE	SKWQALETFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIASLM
HCV_K1_S3	QAEAAAAPVVE	SKWRTLEVFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIASLM
HCV_L2	QAEAAAAPVVE	SKWRALETFW	AKHMWNFISG	IQYLAALSTL	PGNPAIASLM
HCV_N	QAEAAAAPVVG	SKWRAFETFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIASLM
HCV12083	QAEELKPAVH	SAWPRVEDFW	RKHMWNFVSG	IQYLAGLSTL	PGNPAVASLM
HCV1480	KAETLKPAAT	SMWSKAEQFW	AKHMWNFVSG	IQYLAGLSTL	PGNPAVATLM
HCVPOLYP	QAEAAAPVVE	SKWQALEAFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIASLM
HD_1	QAEAAAAPVVE	SKWRALEAFW	AKHMRNFISG	IQYLAGLSTL	PGNPAIASLM
HPCCGAA	HAEVITPAVQ	TNWQKLEVFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIASLM
HPCFG	QEAIEIRPIVQ	SQWQKAEAFW	QKHMWNFVSG	IQYLAGLSTL	PGNPAVASLM
HPCGENANTI	QAEAAAAPVVE	SKWRTLEAFW	ANDMWNFISG	IQYLAGLSTL	PGNPAIASLM
HPCGENOM	QAEAAAAPVVE	SKWRALETFW	EKHMWNFISG	IQYLAGLSTL	PGNPAMASLM
HPCJUMR	QAEAAAAPVVE	SKWRALETFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIASLM
HPCJ	QAEAAAAPVVE	TKWQALEVFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIASLM
HPCJCG	QAEAAAAPVVE	SKWRALEVFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIASLM
HPCJK046	QAEELKPAVH	SAWPKLEQFW	YKHMWNFISG	IQYLAGLSTL	PGNPAVAALM
HPCJK049	KAADIKPIAT	PYWQKLETFW	SKHMWNFVSG	IQYLAGLSTL	PGNPAIASLM
HPCJTA	QAEAAAAPVVE	SRWRALEAFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIASLM
HPCJTB	QAEAAAAPVVE	SRWRALEAFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIASLM
HPCK3A	QQAVIEPIV	SNWQKLEVLW	HKHMWNFVSG	IQYLAGLSTL	PGNPAVASLM
HPCPLYPRE	QAEVIAPAVQ	TNWQKLETFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIASLM
HPCPOLP	QAQDIQPAVQ	ASWPKVEQFW	AKHMWNFISG	IQYLAGLSTL	PGNPAVASMM
HPCPP	QAEAAAAPVVE	SKWRALETFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIASLM
HPCUNKCD	QAEAAAAPVVE	SKWRALETFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIRSPM
MKC1A	QAEAAAAPVVE	SKWRALETFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIASLM
NDM59	QAQDIQPAVQ	ASWPKVEQFW	AKHMWNFISG	IQYLAGLSTL	PGNPAVASMM
NZLI	QQAVIEPIVT	TNWQKLEAFW	HKHMWNFVSG	IQYLAGLSTL	PGNPAVASLM

SA13	KAETLKPAAT	SMWNRAEQFW	AKHMWNFVSG	IQYLAGLSTL	PGNPAVATLM
Th580	HAEELKPAIH	STWPRVEEFW	RKHMWNFVSG	IQYLAGLSTL	PGSPAVASLM
Type_3a_CB	QQAVIEPIVA	TNWQKLEAFW	HKHMWNFVSG	IQYLAGLSTL	PGNPAVASLM
TypeV_D	QQAVIEPIVA	TNWQKLEAFW	HKHMWNFVSG	IQYLAGLPTL	PGNPAVASLM
VN004	QAELKPAVH	AAWPKLEQFW	QKQLWNFVSG	IQYLAGLSTL	PGNPAIASLM
VN235	QAEDLKPAVQ	SAWPKLEQFW	QKHLWNFVSG	VQYLAGLSTL	PGNPAVASLM
VN405	QAEEIEPVVH	SAWPKLEQFW	QKHLWNFVSG	IQYLAGLSTL	PGNPAVASLM

	1801		1850
BEBE1	SFSAALTSPL	STSTTILLNI	MGGWLASQIA PPAGATGFVV SGLVGAAVGS
D89815	AFTASITSPL	ATQYTLLFNI	LGGWVAAQLA PPSAASAFVG AGIAGAAVGS
ED43type_4	SFTAAVTSP	TTQQTLLFNI	LGGWVASQIR DSDASTAFVV SGLAGAAVGS
HC_C2	AFTASVTSP	TTQSTLLFNI	LGGWVAAQLA PPSAASAFVG AGIAGAAVGS
HC_G9	SFTAAVTSP	TTQQTLLFNI	LGGWVAAQLA APAAATAFVG AGITGAVIGS
HCU16326	AFTASITSPL	TTQHTLLFNI	LGGWVAAQLA PPSAASAFVG AGIAGAAVGT
HCV_H_CM	AFTAAVTSP	TTQQTLLFNI	LGGWVAAQLA APGAATAFVG AGLAGAAIGS
HCV_J1	AFTAAVTSP	TTSQTLLFNI	LGGWVAAQLA APGAATAFVG SGLAGAAVGS
HCV_J483	AFTASITSPL	TTQNTLLFNI	LGGWVAAQLA PPSAASAFVG AGIAGAAVGS
HCV_J8	AFTASITSPL	PTSTTILLNI	MGGWLASQIA PPAGATGFVV SGLVGAAVGS
HCV_JK1	AFTASITSPL	TTQHTLLFNI	LGGWVAAQLA PPSAASAFVG AGIAGAAVGS
HCV_JS	AFTASITSPL	TTQSTLLFNI	LGGWVAAQLA PPSAASAFVG AGIVGAAVGS
HCV_K1_R1	AFTASITSPL	TTQSTLLFNI	LGGWVAAQLA PPRAVSFAVG AGIAGAAVGS
HCV_K1_R2	AFTASITSPL	TTQHTLLFNI	LGGWVAAQLA PPRAASAFVG AGIAGAAVGS
HCV_K1_R3	AFTASITSPL	TTQHTLLFNI	LGGWVAAQLA PPRAASAFVG AGIAGAAVGS
HCV_K1_S1	AFTASITSPL	TTQSTLLFNI	LGGWVAAQLA PPRAVSFAVG AGIAGAAVGS
HCV_K1_S2	AFTASITSPL	TTQHTLLFNI	LGGWVAAQLA PPRAASAFVG AGIAGAAVGS
HCV_K1_S3	AFTASITSPL	TTQHTLLFNI	LGGWVAAQLA PPRAASAFVG AGIAGAAVGS
HCV_L2	AFTASITSPL	TTQNTLLFNI	LGGWVAAQLA PASAASAFVG AGSAGAAIGT
HCV_N	AFTASITSPL	TTQNTLLFNI	LGGWVAAQLA PPSAASAFVG AGIAGAAVGS
HCV12083	SFTASLTSP	RTSQTLLLLNI	LGGWIAAQVA PPPASTAFVV SGLAGAAVGS
HCV1480	SFTAAVTSP	TTQHTLLFNI	LGGWVASQIA PPTAATAFVV SGMAGAAVGN
HCVPOLYP	AFTASITSPL	TTQHTLLFNI	LGGWVAAQLA PPSAASAFVG AGIAGAAVGS
HD_1	AFTASITSPL	TTQSTLLFDI	LGGWVAAQLA PPSAASAFVG AGIARAAGVS
HPCCGAA	AFTAAVTSP	TTGQTLLFNI	LGGWVAAQLA APGAATAFVG AGLAGAAIGS
HPCFG	AFTASVTSP	TTNQTMTFFNI	LGGWVATHLA GPAASSAFVV SGLAGAAVGG
HPCGENANTI	AFTASITSPL	TTQSTLLFNI	LGGWVAAQLA PPGAASAFVG AGIAGAAVGS
HPCGENOM	AFTASITSPL	TTQHTLLFNI	LGGWVAAQLA PPSAASAFVG AGIAGAAVGS
HPCCHUMR	AFTASITSPL	TTQSTLLFNI	LGGWVAAQLA PPSAASAFVG AGIAGAAVGS
HPCJ	AFTSSITSPL	TTQSTLLFNI	LGGWVAAQLA PPSAASAFVG AGIAGAAVGS
HPCJCG	AFTASITSPL	TTQNTLLFNI	LGGWVAAQLA PPSAASAFVG AGIAGAAVGS
HPCJK046	SFSASLTSP	TTAQTLLLLNV	LGGWVASQLA TPVPATAFVV SGLAGAAIGS
HPCJK049	AFTASVTSP	TTNQTLLFNI	MGGWVASNLA PPPASTAFVV SGLAGAAVGS
HPCJTA	AFTASITSPL	TTQNTLLFNI	LGGWVAAQLA PPSAASAFVG AGIAGAAIGS
HPCJTB	AFTASITSPL	TTQNTLLFNI	LGGWVAAQLA PPSAASAFVG AGIAGAAIGS
HPCK3A	AFTASVTSP	TTNQTMTFFNI	LGGWVATHLA GPQASSAFVV SGLAGAAIGG
HPCPLYPRE	AFTAAVTSP	TTSQTLLFNI	LGGWVAAQLA APGAATAFVG AGLAGAAIGS
HPCPOLP	AFTASLTSP	STSTTILLNI	LGGWLASQIA PPAGATGFVV SGLVGAAVGS
HPCPP	AFTASITSPL	TTQYTLLFNI	LGGWVAAQLA PPSAASAFVG AGIAGAAVGS
HPCUNKCD	AFTASITSPL	TTQHTLLFNI	LGGWVAAQLA PPSAASAFVG AGIAGAAVGT
MKC1A	AFTASITSPL	TTQYTLLFNI	LGGWVAAQLA PPSAASAFVG AGIAGAAVGS
NDM59	AFTASLTSP	STSTTILLNI	LGGWLASQIA PPAGATGFVV SGLVGAAVGS
NZLI	AFTASVTSP	TTNQTMTFFNI	LGGWVATHLA GPQSSSAFVV SGLAGAAIGG
SA13	SFTAAVTSP	TTQQTLLFNI	LGGWVASQIA PPTAATAFVV SGMAGAAVGS
Th580	SFTASLTSP	RTSQTLLLLNI	LGGWIASQVA PPSASTAFVV SGLAGATVAS
Type_3a_CB	AFTASVTSP	TTNQTMTFFNI	LGGWVATHLA GPQSSSAFVV SGLAGAAIGG
TypeV_D	AFTASVTSP	TTNQTMTFFNI	LGGWVATHLA GPQSSSAFVV SGLAGAAIGG
VN004	SFSASLTSP	STHTTLLLLNI	LGGWVASQLA NPTASTAFVV SGLAGAAVGS
VN235	SFSASLTSP	STSTTLLLLNI	LGGWVASQLA PPTASTAFVV SGLAGAAVGS
VN405	SFSASLTSP	STSTTLLLLNI	LGGWVASQLA NPTASTAFVV SGLAGATVGS

	1851				1900
BEBE1	IGLGKILVDV	LAGYGAGISG	ALVAFKIMSG	EKPSVEDVNV	LLPAILSPGA
D89815	IGLGKVLVDI	LAGYGAGVAG	ALVAFKIMSG	DMPSTEDLVN	LLPAILSPGA
ED43type_4	VGLGKILVDI	LPGYGAGVRG	AVVTFKIMSG	EMPSTEDLVN	LLPAILSPGA
HC_C2	IGLGKVLVDI	LAGYGAGVAG	ALVAFKIMSG	ETPSAEDLVN	LLPAILSPGA
HC_G9	VGLGKVLVDI	LAGYGAGVAG	ALVAFKIMSG	EAPTAEDLVN	LLPAILSPGA
HCU16326	IGLGKVLVDI	LAGYGAGVAG	ALVAFKIMSG	EMPSAEDMVN	LLPAILSPGA
HCV_H_CMV	VGLGKVLVDI	LAGYGAGVAG	ALVAFKIMSG	EVPSTEDLVN	LLPAILSPGA
HCV_J1	VGLGRVLVDI	LAGYGAGVAG	ALVAFKIMSG	ELPSTEDLVN	LLPAILSPGA
HCV_J483	IGLGKVLVDI	LAGYGAGVAG	ALVAFKIMSG	EVPSTEDLVN	LLPAILSPGA
HCV_J8	IGLGKILVDV	LAGYGAGISG	ALVAFKIMSG	EKPTVEDVNV	LLPAILSPGA
HCV_JK1	IGLGKVLVDI	LAGYGAGVAG	ALVAFKIMSG	EMPSTEDLVN	LLPAILSPGA
HCV_JS	IGLGKVLVDI	LAGYGAGVAG	ALVAFKIMSG	EMPATEDLVN	LLPAILSPGA
HCV_K1_R1	IGLGKVLVDI	LAGYGAGVAG	ALVAFKIMSG	EMPSTEDLVN	LLPAILSPGA
HCV_K1_R2	IGLGKVLVDI	LAGYGAGVAG	ALVAFKIMSG	DMPSTEDLVN	LLPAILSPGA
HCV_K1_R3	IGLGKVLVDI	LAGYGAGVAG	ALVDFKIMSG	EMPSAEDIVN	LLPAILSPGA
HCV_K1_S1	IGLGKVLVDI	LAGYGAGVAG	ALVAFKIMSG	EMPSTEDLVN	LLPAILSPGA
HCV_K1_S2	IGLGKVLVDI	LAGYGAGVAG	ALVAFKIMSG	DMPSTEDLVN	LLPAILSPGA
HCV_K1_S3	IGLGKVLVDI	LAGYGAGVAG	ALVDFKIMSG	EMPSAEDIVN	LLPAILSPGA
HCV_L2	IGLGKVLVDI	LAGYGAGVAG	ALVAFKIMSG	EMPSTEDLVN	LLPAILSPGA
HCV_N	IGLGKVLVDI	LAGYGAGVAG	ALVAFKIMSG	EAPSAEDLIN	LLPAILSPGA
HCV12083	IRLGRVLVDV	LAGYGAGVSG	ALVAFKIMSG	ECPSTEDMVN	LLPAILSPGV
HCV1480	IGLGRVLIDI	LAGYGTGAGV	ALVAFKIMCG	ERPTAEDLVN	LLPSILCPGA
HCVPOLYP	IGLGKVLVDI	LAGYGAGVAG	ALVAFKIMSG	EMPSTEDLVN	LLPAILSPGA
HD_1	IGLGKVLVDI	LAGYGAGVAG	ALVAFKIMSG	EVPSTEDLIN	LLPAILSPGA
HPCCGAA	VGLGKVLVDI	LAGYGAGVAG	ALVAFKIMSG	EVPSTEDLVN	LLPAILSPGA
HPCFG	IGLGRVLLDV	LAGYGAGVSG	ALVAFKIMGG	ELPTTEDMVN	LLPAILSPGA
HPCGENANTI	IGLGKVLVDM	VAGYGAGVAG	ALVAFKIMSG	EMPSTEDLVN	LLPAILSPGA
HPCGENOM	IGLGKVLVDI	LAGYGAGVAG	ALVAFKIMSG	EMPSTEDLVN	LLPAILSPGA
HPCHUMR	IGLGKVLVDI	LAGYGAGVAG	ALVAFKIMSG	EMPSTEDLVN	LLPAILSPGA
HPCJ	IGLGKVLVDI	LAGYGAGVAG	ALVAFKIMSG	EVPSTEDLVN	LLPAILSPGA
HPCJCG	IGLGKVLVDI	LAGYGAGVAG	ALVAFKIMSG	EMPSTEDLVN	LLPAILSPGA
HPCJK046	IGLGKIVIDI	LAGYGAGVSG	ALVAFKIMSG	ETPSVEDMVN	LLPAILSPGA
HPCJK049	IGLGKVLLDI	LAGYGAGVAG	ALVAFKIMGG	EMPSTEDMVN	LLPAILSPGA
HPCJTA	IGLGKVLVDI	LAGYGAGVAG	ALVAFKIMSG	EAPSAEDLVN	LLPAILSPGA
HPCJTB	IGLGKVLVDI	LAGYGAGVAG	ALVAFKIMSG	EAPSAEDLVN	LLPAILSPGA
HPCK3A	IGLGRVLLDI	LAGYGAGVSG	ALVAFKIMGG	EPPTTEDMVN	LLPAILSPGA
HPCPLYPRE	VGLGKVLIDI	LAGYGAGVAG	ALVAFKIMSG	EVPSTEDLVN	LLPAILSPGA
HPCPOLP	IGLGKVLVDI	LAGYGAGISG	ALVAFKIMSG	EKPSMEDVNV	LLPGILSPGA
HPCPP	IGLGKVLVDI	LAGYGAGVAG	ALVAFKIMSG	DMPSTEDLVN	LLPAILSPGA
HPCUNKCD	IGLGKVLVDI	LAGYGAGVAG	ALVAFKIMSG	EMPSAEDMVN	LLPAILSPGA
MKC1A	IGLGKVLVDI	LAGYGAGVAG	ALVAFKIMSG	DMPSTEDLVN	LLPAILSPGA
NDM59	IGLGKVLVDI	LAGYGAGISG	ALVAFKIMSG	EKPSMEDVIN	LLPGILSPGA
NZLI	IGLGRVLLDI	LAGYGAGVSG	ALVAFKIMGG	ECPTAEDMVN	LLPAILSPGA
SA13	IGLGRVLIDI	LAGYGAGVAG	ALVAFKIMCG	EKPTAEDLVN	LLPSILCPGA
Th580	IGLGRVIVDI	LAGYGAGVAG	ALVAFKIMSG	ECPSTEDMVN	LLPAILSPGA
Type_3a_CB	IGLGRVLLDI	LAGYGAGVSG	ALVAFKIMGG	ELPTAEDMVN	LLPAILSPGA
TypeV_D	IGLGRVLLDI	LAGYGAGVSG	ALVAFKIMGG	ELPTTEDLVN	LLPAILSPGA
VN004	IGLGRVIVDV	LAGYGAGVSG	ALVAFKIMCG	ETPSAEDMVN	LLPAILSPGA
VN235	IGLGKVIIDI	LAGYGAGVSG	ALVAFKIMSG	EAPAVEDMVN	LLPAILSPGA
VN405	IGLGRVLVDI	IAGYGAGVSG	ALVAFKIMSG	ETPSAEDMVN	LLPAILSPGA

	1901				1950
BEBE1	LVVGVICAAI	LRRHVGQEG	AVQWMNRLIA	FASRGNHVAP	THYVAESDAS
D89815	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
ED43type_4	LVVGVVCPAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HC_C2	LVVGVVCAAI	QRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HC_G9	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAS
HCU16326	LVVGVIVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	RHYVPESEPA
HCV_H_CMV	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA



HCV_J1	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HCV_J483	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HCV_J8	LVVGVICAAI	LRRHVGQEG	AVQWMNRLIA	FASRGNHVAP	THYVPESDAS
HCV_JK1	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HCV_JS	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HCV_K1_R1	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HCV_K1_R2	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HCV_K1_R3	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HCV_K1_S1	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HCV_K1_S2	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HCV_K1_S3	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HCV_L2	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHDSP	THYVPESDAA
HCV_N	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HCV12083	ALVGVVCAAI	LRRHVGPAEG	ANQWMNRLIA	FASRGNHVSP	THYVPETDAS
HCV1480	LVVGVICAAV	LRRHIGPGEG	AVQWMNRLIA	FASRGNHGSP	THYVPETDAS
HCVPOLYP	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HD_1	LVVGVVCAAI	LRGHVGPGEG	AVQWMNRLIA	FAFAGNHVSP	THYVPESDAA
HPCCGAA	LAVGVVFASI	LRRRVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HPCFG	LVVGVICAAV	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HPCGENANTI	LVVGVVCAAI	LRRHVDPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HPCGENOM	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HPCHUMR	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HPCJ	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HPCJCG	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HPCJK046	LVVGVVRAAI	LRRHVGPGEG	AAQWMNRLIA	FASRGNHVSP	THYVPETDAS
HPCJK049	LVVGVICAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVAP	THYVPESDAA
HPCJTA	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HPCJTB	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HPCK3A	LVVGVICAAI	LRRHVGPGEG	PVQWMNRLIA	FASRGNHVSP	AHYVPESDAA
HPCPLYPRE	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HPCPOLP	LVVGVICAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVAP	THYVTESDAS
HPCPP	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HPCUNKCD	LVVGIVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	RHYVPESEPA
MKC1A	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
NDM59	LVVGVICAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVAP	THYVTESDAS
NZLI	LVVGVICAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
SA13	LVVGVICAAV	LRRHIGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPETDAS
Th580	LVVGVVCAAI	LRRHVGPGEG	ANQWMNRLIA	FASRGNHVSP	THYVPETDAS
Type_3a_CB	LVVGVICAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
TypeV_D	LVVGVICAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
VN004	LVVGVVCAAI	LRRHAGPSEG	ATQWMNRLIA	FASRGNHVSP	THYVPETDTS
VN235	LVVGVVCAAV	LRRHVGPGEG	ATQWMNRLIA	FASRGNHVSP	THYVPETDAS
VN405	LVVGVVCAAI	LRRHAGPAEG	ATQWMNRLIA	FASRGNHVSP	THYVPETDTS

	1951		2000		
BEBE1	QRVTQLLGSL	TITSLRLRLH	QWITEDCPVP	CSGSWLRDVW	DWVCSILIDF
D89815	ARVTQILSNL	TITQLLKRLH	QWINEDCSTP	CSGSWLRDVW	DWICTVLADF
ED43type_4	RRVTTLSSL	TVTSLRLRLH	KWINEDCSTP	CAESWLWEVW	DWVLHVLSDF
HC_C2	ARVTQILSSL	TITQLLKRLH	QWINEDCSTP	CSGSWLRDIW	DWICSVLTDF
HC_G9	VRVTHILTSL	TVTQLLKRLH	VWISSDCTAP	CAGSWLKDVW	DWICEVLSDF
HCU16326	ARVTQILSSL	TITQLLKRLH	QWINEDCSTP	CSSSWLREIW	DWICTVLTFD
HCV_H_CMR	ARVAILSSL	TVTQLLRLH	QWISSECTTP	CSGSWLRDIW	DWICEVLSDF
HCV_J1	ARVTAILSSL	TVTQLLRLH	QWLSSESTTP	CSGSWLRDIW	DWICEVLSDF
HCV_J483	ARVTQILSSL	TITQLLKRLH	QWINEDCSTP	CSGSWLRDVW	DWICTVLTFD
HCV_J8	QRVTQVLSSL	TITSLRLRLH	AWITEDCPVP	CSGSWLQDIW	DWVCSILTDF
HCV_JK1	ARVTQILSSL	TITQLRLRLH	QWINEDCSTP	CSGSWLRDVW	DWICTVLTFD
HCV_JS	ARVTQILSSL	TITQLLKRLH	QWINEDCSTP	CSGSWLRDIW	DWICTVLTFD
HCV_K1_R1	ARVTQILSSL	TITQLLRLH	QWINEDCSTP	CSGSWLRDVW	DWICTVLTFD
HCV_K1_R2	ARVTQILSSL	TITQLLKRLH	QWINEDCSTP	CSGSWLRDVW	DWICTVLSDF
HCV_K1_R3	VRVTQILSNL	TITQLLKRLH	QWISEDCTP	CSGSWLRDVW	DWICTVLTFD

HCV_K1_S1	ARVTQILSSL	TITQLLRRRLH	QWINEDCSTP	CSGSWLRDVW	DWICTVLTF
HCV_K1_S2	ARVTQILSSL	TITQLLKRLH	QWINEDCSTP	CSGSWLRDVW	DWICTVLTF
HCV_K1_S3	VRVTQILSSL	TITQLLKRLH	QWINEDCSTP	CSGSWLRDVW	DWICTVLTF
HCV_L2	ARVTQILSSL	TITQLLKRLH	QWINEDCSTP	CSGSWLRDVW	DWICTVLTF
HCV_N	ARVTQILSSL	TITQLLKRLH	QWINEDCSTP	CSGSWLRDVW	DWICTVLTF
HCV12083	KNVTQILSSL	TITQLLKRLH	QWINEDCSTP	CSGSWLRDVW	DWICTVLTF
HCV1480	AKVTQILSSL	TVTSLLRRLH	QWINEDCSTP	CSGSWLRDVW	DWICTVLTF
HCVPOLYP	ARVTQILSSL	TITQLLKRLH	QWINEDCSTP	CSGSWLRDVW	DWICTVLTF
HD_1	ARVTQILSSL	TITQLLKRLH	QWINEDCSTP	CSGSWLRDVW	DWICTVLTF
HPCCGAA	ARVTAILSSL	TVTQLLRRRLH	QWINEDCSTP	CSGSWLRDIW	DWICEVLSDF
HPCFG	AKVTALLSSL	TVTRLRRLH	QWINEDCSTP	CNGDWLHDIW	DWICIVLSDF
HPCGENANTI	ARVTQILSSL	TITQLLKRLH	QWINEDCSTP	CSGSWLRDVW	DWICTVLADF
HPCGENOM	ARVTQILSSL	TITQLLKRLH	QWINEDCSTP	CSGSWLRDVW	DWICTVLADF
HPCHUMR	ARVTQILSSL	TITQLLKRLH	QWINEDCSTP	CSGSWLRDVW	DWICTVLADF
HPCJ	QRVTQILSSL	TITQLLKRLH	QWINEDCSTP	CSGSWLRDVW	DWICTVLADF
HPCJCG	ARVTQILSSL	TITQLLKRLH	QWINEDCSTP	CSGSWLRDVW	DWICTVLADF
HPCJK046	RAVTNILSSL	TITQLLKRLH	QWINEDCSTP	CSGSWLRDVW	DWICTVLADF
HPCJK049	AKVTALLSSL	TVTQLLRRRLH	QWINEDCSTP	CSGSWLRDVW	DWICTVLADF
HPCJTA	ARVTQILSSL	TITQLLKRLH	QWINEDCSTP	CSGSWLRDVW	DWICTVLADF
HPCJTB	ARVTQILSSL	TITQLLKRLH	QWINEDCSTP	CSGSWLRDVW	DWICTVLADF
HPCK3A	ARVTALLSSL	TVTQLLRRRLH	QWINEDCSTP	CSGSWLRDIW	DWICEVLSDF
HPCPLYPRE	ARVTAILSSL	TVTQLLRRRLH	QWINEDCSTP	CSGSWLRDIW	DWICEVLSDF
HPCPOLP	QRVTQILSSL	TITQLLKRLH	QWINEDCSTP	CSGSWLRDVW	DWICTVLADF
HPCPP	ARVTQILSSL	TITQLLKRLH	QWINEDCSTP	CSGSWLRDVW	DWICTVLADF
HPCUNKCD	ARVTQILSSL	TITQLLKRLH	QWINEDCSTP	CSGSWLRDIW	DWICEVLSDF
MKC1A	ARVTQILSSL	TITQLLKRLH	QWINEDCSTP	CSGSWLRDVW	DWICTVLADF
NDM59	QRVTQILSSL	TITQLLKRLH	QWINEDCSTP	CSGSWLRDVW	DWICTVLADF
NZLI	ARVTALLSSL	TVTQLLRRRLH	QWINEDCSTP	CSGSWLRDIW	DWICEVLSDF
SA13	AKVTQILSSL	TVTQLLRRRLH	QWINEDCSTP	CSGSWLRDIW	DWICEVLSDF
Th580	KNVTQILSSL	TITQLLKRLH	QWINEDCSTP	CSGSWLRDVW	DWICTVLADF
Type_3a_CB	ARVTALLSSL	TVTQLLRRRLH	QWINEDCSTP	CSGSWLRDIW	DWICEVLSDF
TypeV_D	AKVTALLSSL	TVTQLLRRRLH	QWINEDCSTP	CSGSWLRDIW	DWICEVLSDF
VN004	RQIMTILSSL	TVTQLLRRRLH	QWINEDCSTP	CSGSWLRDIW	DWICEVLSDF
VN235	RAVTILSSL	TITQLLKRLH	QWINEDCSTP	CSGSWLRDIW	DWICEVLSDF
VN405	RQVMAILSSL	TVTQLLRRRLH	QWINEDCSTP	CSGSWLRDIW	DWICEVLSDF

	2001			2050	
BEBE1	KNWLSAKLFP	RLPGIPFISC	QKGYRGVWAG	TGIMTTRCPC	GANITGNVRL
D89815	KTWLQSKLLP	RLPGVPFFSC	QKGYRGVWAG	DGIMYTTCPC	GAQITGHVKN
ED43type_4	KTCLKAKFVP	LMPGIPLLSW	PRGYKGEWRG	DGVMHTTCPC	GADLAGHIKN
HC_C2	KTWLQSKLLP	RLPGVPFFSC	QKGYRGVWAG	DGIMQTTCPC	GAQITGHVKN
HC_G9	KSWLKAKLMP	QLPGIPFVSC	QKGYRGVWAG	EGIMHARCPC	GADITGHVKN
HCU16326	KTWLQSKLLP	RLPGVPFFSC	QKGYRGVWAG	DGIMHTTCPC	GAQITGHVKN
HCV_H_CMUR	KTWLKAKLMP	QLPGIPFVSC	QKGYRGVWAG	DGIMHTRCHC	GAEITGHVKN
HCV_J1	KTWLKTKLMP	HLPGIPLLSW	QKGYRGVWAG	DGIMHTRCHC	GAEITGHVKN
HCV_J483	KTWLQSKLLP	RLPGVPFFSC	QKGYRGVWAG	DGIMQTTCPC	GAQIAGHVKN
HCV_J8	KNWLSAKLFP	KMPGIPLLSW	QKGYRGVWAG	TGVMTTRCPC	GANISGHVKN
HCV_JK1	KTWLQSKLLP	RLPGDPFFSC	QKGYRGVWAG	DGVMQTTCPC	GAQITGHVKN
HCV_JS	KTWLKSKLMP	RLPGVPFFSC	QKGYRGVWAG	DGIMHTTCPC	GAQITGHVKN
HCV_K1_R1	KTWLQSKLLP	RLPGVPFFSC	QKGYRGVWAG	DGIMQTTCPC	GAQITGHVKN
HCV_K1_R2	KTWLQSKLLP	RLPGVPFFSC	QKGYRGVWAG	DGIMQTTCPC	GAQITGHVKN
HCV_K1_R3	KTWLQSKLLP	RLPGIPFISC	QKGYRGVWAG	DGVMHTTCPC	GAQIAGHVKN
HCV_K1_S1	KTWLQSKLLP	RLPGVPFFSC	QKGYRGVWAG	DGIMQTTCPC	GAQITGHVKN
HCV_K1_S2	KTWLQSKLLP	RLPGVPFFSC	QKGYRGVWAG	DGIMQTTCPC	GAQITGHVKN
HCV_K1_S3	KTWLQSKLLP	RLPGIPFISC	QKGYRGVWAG	DGVMHTTCPC	GAQIAGHVKN
HCV_L2	KTWLQSKLLP	RLPGVPFFSC	QKGYRGVWAG	DGIMQTTCPC	GAQITGHVKN
HCV_N	KTWLQSKLLP	RLPGVPFFSC	QKGYRGVWAG	DGIMHTTCPC	GAQIAGHVKN
HCV12083	KVWLQAKLFP	RLPGIPFISC	QKGYRGVWAG	DGVCHTTCTC	GAVIAGHVKN
HCV1480	KAWLQAKLFP	QLPGVPFFSC	QKGYRGVWAG	DGVNSTKCPC	GATISGHVKN
HCVPOLYP	KTWLQSKLLP	RLPGIPFISC	QKGYRGVWAG	DGIMQTTCPC	GAQITGHVKN

HD_1	KTWLQSKLLP	RLPGVPFLSC	QRGYRGVWRG	DGIMHTTCPC	GAQMAGHVKN
HPCCGAA	KTWLKAKLMP	QLPGIPFVSC	QRGYRGVWRG	DGIMHTRCHC	GAEITGHVKN
HPCFG	KTWLSAKIMP	KVPGIPFLSC	QKGYKGVWRG	DGVMTTTCPC	GEDFTGHVKN
HPCGENANTI	KTWLQSKLLP	RLPGVPFFSC	QKGYKGVWRG	DGIMQTTTCPC	GAQLTGHVKN
HPCGENOM	KTWLQSKLLP	RLPGVPFLSC	QKGYKGVWRG	DGIMQTTTCPC	GAQITGHVKN
HPCHUMR	KTWLQSKLLP	QLPGVPFFSC	QKGYKGVWRG	DGIMQTTTCPC	GAQITGHVKN
HPCJ	KTWLQSKLLP	RLPGVPFFSC	QKGYKGVWRG	EGIMQTTTCPC	GAQIAGHVKN
HPCJCG	KTWLQSKLLP	RLPGLPFLSC	QKGYKGVWRG	DGIMQTTTCPC	GAQITGHVKN
HPCJK046	RVWLKSKLMP	SLPGVPFFSC	QRGYRGVWRG	DGICNTTCPC	GASIAGHVKN
HPCJK049	KLWLGAAILP	KMPGIPFLSC	QKGYRGVWRG	DGVVSTRCPC	GALLSGHVKN
HPCJTA	KTWLQSKLLP	KLPGVPPFSC	QKGYKGVWRG	DGIMQTTTCPC	GAQITGHVKN
HPCJTB	KTWLQSKLLP	QLPGVPFFSC	QKGYKGVWRG	DGIMQTTTCPC	GAQITGHVKN
HPCK3A	KTWLSAKIMP	ALPGLPFISC	QKGYKGVWRG	DGVMSTRCPC	GASIAGHVKN
HPCPLYPRE	KTWLKAKLMP	QLPGIPFVSC	QKGYKGVWRV	DGIMHTRCHC	GAEITGHVKN
HPCPOLP	KNWLTSKLFP	KMPGLPFISC	QKGYKGVWAG	TGIMTTTCPC	GANISGNVRL
HPCPP	KTWLQSKLLP	RLPGVPFFSC	QKGYKGVWRG	DGIMYTTTCPC	GAQITGHVKN
HPCUNKCD	KTWLQSKLLP	RLPGVPFFSC	QKGYKGVWRG	DGIMHTTCPC	GAQITGHVKN
MKC1A	KTWLQSKLLP	RLPGVPFFSC	QKGYKGVWRG	DGIMYTTTCPC	GAQITGHVKN
NDM59	KNWLTSKLFP	KMPGLPFISC	QKGYRGVWAG	TGIMTTTCPC	GANISGNVRL
NZLI	KAWLSAKIMP	ALPGLPFISC	QKGYKGVWRG	DGVMSTRCPC	GAAITGHVKN
SA13	KAWLQAKLLP	QLPGVPFLSC	QRGYRGVWRG	DGVNSTKCPC	GATISGHVKN
Th580	KTWLKAKITP	RIPGIPFISC	QAGYRGVWAG	DGVCHTTTCSC	GAQIAGHVKN
Type_3a_CB	KSWLSAKIMP	ALPGLPFISC	QKGYKGVWRG	DGVMSTRCPC	GATITGHVKN
TypeV_D	KTWLSAKIMP	ALPGLPFISC	QKGYKGVWRG	DGVTTRTCPC	GATITGHVKN
VN004	KTWLKAKLVP	ALPGVPFLSC	QKGYRGVWRG	DGICHTTCPC	GSEITGHVKN
VN235	KTWLRAKLVP	TLPGIPFISC	QKGYRGVWRG	DGVNYTTTCSC	GANITGHVKN
VN405	KVWLKSKLVP	ALPGVPFLSC	QKGYRGVWRG	DGICRTTCPC	GADIVGHVKN

	2051		2100		
BEBE1	GTMRIISGPKT	CLNTWQGTFF	INCYTEGSCV	PKPAPNFKTA	IWRVAASEYA
D89815	GSMRIVGPRT	CSNTWHGTFF	INAYTTGPCT	PSPAPNYSRA	LWRVAAEEYV
ED43type_4	GSMRITGPKT	CSNTWHGTFF	INAYTTGPGV	PIPAPNYKFA	LWRVSAEDYV
HC_C2	GSMRIVGPKT	CSNTWHGTFF	INAYTTGPCT	PSPAPNYSRA	LWRVAAEEYV
HC_G9	GSMRIVGPKT	CSNTWRGSFF	INAHTTGPCT	PSPAPNYTFA	LWRVSAEEYV
HCU16326	GSMRIVGPKT	CSNTWYGTFF	INAYTTGPCT	PSPAPNYSKA	LWRVAAEEYV
HCV_H_CMV	GTMRIISGPKT	CRNMWSGTFF	INAYTTGPCT	PLPAPNYKFA	LWRVSAEEYV
HCV_J1	GTMRIISGPKT	CRNMWSGTFF	INAYTTGPCT	PLPAPNYTFA	LWRVSAEEYV
HCV_J483	GSMRIVGPRT	CSNTWHGTFF	INAYTTGPCT	PSPAPNYSRA	LWRVAAEEYV
HCV_J8	GTMKITGPKT	CLNLWQGTFF	INCYTEGPCV	PKPPPNYKTA	IWRVAASEYV
HCV_JK1	GSMRIVGPKT	CSNTWHGTFF	INAYTTGPCT	PSPAPNYSRA	LWRVAAEEYV
HCV_JS	GSMRIVGPKT	CSNTWHGTFF	INAYTTGPCT	PSPAPNYSRA	LWRVAAEEYV
HCV_K1_R1	GSMRIVGPKT	CSNTWHGTFF	INAYTTGPCT	PSPAPNYSRA	LWRVAAEEYV
HCV_K1_R2	GSMRIVGPKT	CSNTWHGTFF	INAYTTGPCT	PSPAPNYSRA	LWRVAAEEYV
HCV_K1_R3	GSMKIVGPKT	CSNTWDGTFF	INGYTTGSST	PTPASNYSKA	LWRVVFEEYV
HCV_K1_S1	GSMRIVGPKT	CSNTWHGTFF	INAYTTGPCT	PSPAPNYSRA	LWRVAAEEYV
HCV_K1_S2	GSMRIVGPKT	CSNTWHGTFF	INAYTTGPCT	PSPAPNYSRA	LWRVAAEEYV
HCV_K1_S3	GSMKIVGPKT	CSNTWDGTFF	INGYTTGSST	PTPASNYSKA	LWRVVFEEYV
HCV_L2	GSMRIVGPKT	CSNTWHGTFF	INAYTTGPCT	PAPTPNYSRA	LWRVAAEEYV
HCV_N	GSMRIISGPKT	CSNTWHGTFF	INAYTTGPCT	PSPAPNYSKA	LWRVAAEEYV
HCV12083	GTMKITGPKT	CSNTWHGTFF	INATTTGPST	PRPAPNYQRA	LWRVSAEDYV
HCV1480	GTMRIISGPKT	CSNTWQGTFF	INATTTGPSV	PAPAPNYKFA	LWRVGAADYA
HCVPOLYP	GSMRIVGPKT	CSNTWHGTFF	INAYTTGPCT	PSPAPNYSRA	LWRVAAEEYV
HD_1	GSMRIVGPKT	CSNTWYGSFF	INAYTTGPCT	PSPAPNYSRA	LWRVAAEEYV
HPCCGAA	GTMRIISGPKT	CKNMWSGTFF	INAYTTGPCT	PLPAPNYKFA	LWRVSAEEYV
HPCFG	GSMRIISGGL	CANMWHGTFF	INEYTTGPST	PVPAHNYKFA	LWRVTSDSYV
HPCGENANTI	GSMRIISGPKT	CSNTWHGTFF	INAYTTGPCT	PSPAPNYSRA	LWRVAAEEYV
HPCGENOM	GSMRIVGPKT	CSNTWHGTFF	INAYTTGPCT	PSPAPNYSRA	LWRVAAEEYV
HPCHUMR	GSMRIVGPKT	CSNTWHGTFF	INAYTTGPCT	PSPAPNYSRA	LWRVAAEEYV
HPCJ	GSMRIVGPRT	CSNTWHGTFF	INAYTTGPCT	PSPAPNYSRA	LWRVAAEEYV
HPCJCG	GSMRIVGPKT	CSNTWHGTFF	INAYTTGPCT	PSPAPNYSRA	LWRVAAEEYV

HPCJK046	GTMRIVGPR	CSNVWNGTFP	INATTTGPSI	PIPAPNYKKA	LWRVSATEYV
HPCJK049	GTMRLVGPRW	CANTWHGTFP	INGYTTGPST	PAPSYAYSRA	LWRVASDSYV
HPCJTA	GSMRIVGPKT	CSNTWHGTFP	INAYTTGPCT	PSPAPNYSRA	LWRVAAEEYV
HPCJTB	GSMRIVGPKT	CSNMWHGTFP	INAYTTGPCT	PSPAPNYSRA	LWRVAAEEYV
HPCK3A	GSMRLAGPRT	CANMCHGTFP	INEYTTGPST	PCPPPNYTRA	LWRVAANSYV
HPCPLYPRE	GTMRIVGPR	CRNMWSGTFP	INAYTTGPCT	PLPAPNYTFA	LWRVSAEEYV
HPCPOLP	GSMRITGPKT	CMNIWQGTFF	INCYTEGQCV	PKPAPNFKIA	IWRVAASEYA
HPCPP	GSMRIVGPR	CSNTWHGTFP	INAYTTGPCT	PSPAPNYSRA	LWRVAAEEYV
HPCUNKCD	GSMRIVGPKT	CSNTWYGTFF	INAYTTGPCT	PSPAPNYSKA	LWRVAAEEYV
MKC1A	GSMRIVGPR	CSNTWHGTFP	INAYTTGPCT	PSPAPNYSRA	LWRVAAEEYV
NDM59	GSMRITGPKT	CMNTWQGTFF	INCYTEGQCV	PKPAPNFKTA	IWRVAASEYA
NZLI	GSMRLAGPRT	CANMWHGTFP	INEYTTGPST	PCPSPNYTRA	LWRVAANSYV
SA13	GTMRIVGPKL	CSNTWHGTFP	INATTTGPSV	PAPAPNYKFA	LWRVGAADYA
Th580	GSMKITGPRM	CSNTWHGTFP	INATTTSPSV	PVPAPNYKRA	LWRVSAEEYV
Type_3a_CB	GSMRLAGPRT	CANMWHGTFP	INEYTTGPST	PCPSPNYTRA	LWRVAANSYV
TypeV_D	GSMRLAGPRT	CANMWHGTFP	INEYTTGPST	PCPSPNYTRA	LWRVAANSYV
VN004	GTMKISGPRW	CSNVSHRTFF	INATTTGPSV	PIPEPNYTRA	LWRVSAEEYV
VN235	GSMKIVGPKM	CSNVWNNRFP	INAITTTGPSV	PVPEPNYHKA	LWRVSAEDYV
VN405	GSMRISGSRW	CSNIWHGTFP	INATTTGPSV	PIPEPNYKRA	LWRVSAEEYV

	2101			2150		
	BEBE1	EVTQHDSHAY	VTGLTADNLK	VPCQLPCPEF	FSWVDGVQIH	RFAPTPKAFM
	D89815	EVTRVGDFHY	VTGMTTDNVK	CPCQVPAPPEF	FTELDGVRLH	RYAPACKPLL
ED43type_4		EVRRVGDFHY	VTGVTQDNK	FPCQVPAPPEL	FTEVDGIRIH	RHAPCKPPLL
HC_C2		EVTRVGDFHY	ITGMTTDNIK	CPCQVPAPPEF	FTEVDGVRLH	RYAPACKPVL
HC_G9		EVRRVGDFHY	ITGVTTDKIK	CPCQVPSPEF	FTEVDGVRLH	RYAPPCKPLL
HCU16326		EVTRVGDFHY	VTGMTTDNVK	CPCQVPAPPEF	FTEVDGVRLH	RYAPACKPPLL
HCV_H_CM		EIRRVGDFHY	VSGMTTDNLK	CPCQIPSPPEF	FTELDGVRLH	RFAPPCKPLL
HCV_J1		EIRRVGDFHY	VTGMTTDNLK	CPCQVPSPEF	FTELDGVRLH	RFAPPCKPLL
HCV_J483		EVTRVGDFHY	VTGMTTDNVK	CPCQVPAPPEF	FTEVDGVRLH	RYAPACKPPLL
HCV_J8		EVTQHGSFSY	VTGLTSDNLK	VPCQVPAPPEF	FSWVDGVQIH	RFAPVPGPFF
HCV_JK1		EVTRVGDFHY	VTGMTTDNVK	CPCQVPAPPEF	FTEVDGVRLH	RYAPACKPPLL
HCV_JS		EVTRVGDFHY	VTGMTTDNVK	CPCQVPAPPEF	FTEVDGVQLH	RYAPACKPPLL
HCV_K1_R1		EVTRVGDFHY	VTGMTTDNVK	CPCQVPPPEF	FTEVDGVRLH	RNAPACGPLL
HCV_K1_R2		EVTRVGDFHY	VTGMTTDNLK	CPCQVPAPPEF	FKELDGVRLLH	RYAPACKPPLL
HCV_K1_R3		EVTRVGDFHY	VTGMTTDNVK	CPCQVPPPEF	FTELDGVRLH	RYAPVSKPPLL
HCV_K1_S1		EVTRVGDFHY	VTGMTTDNVK	CPCQVPPPEF	FTEVDGVRLH	RNAPACGPLL
HCV_K1_S2		EVTRVGDFHY	VTGMTTDNLK	CPCQVPAPPEF	FKELDGVRLLH	RYAPACKPPLL
HCV_K1_S3		EVTRVGDFHY	VTGMTTDNVK	CPCQVPPPEF	FTELDGVRLH	RYAPVSKPPLL
HCV_L2		EVTRVGDFHY	VTGMTTDNVK	CPCQVPAPPEF	FTEVDGVRLH	RYAPACKTLL
HCV_N		EVTRVGDFHY	VTGITTDNVK	CPCQVPAPPEF	FTEVDGVRLH	RYAPVCKPPLL
HCV12083		EVRRVGDFHY	VVGVTAEGLK	CPCQVPAPPEF	FTEVDGVRLH	RYAPPCKPLL
HCV1480		EVRRVGDFHY	ITGVTQDNK	CPCQVPSPEF	FTELDGVRLH	RFAPPCKPPLL
HCVPOLYP		EVTRVGDFHY	VTGMTTDNVK	CPCQVPAPPEF	FTEVDGVRLH	RYAPACKPPLL
HD_1		EVTRVGDFHY	VTGMTTDNIK	CPCQVPAPPEF	FTEVDGVRLH	RYAPACKPPLL
HPCCGAA		EIRRVGDFHY	VSGMTTDNLK	CPCQIPSPPEF	FTELDGVRLH	RFAPPCKPLL
HPCFG		EVRRVGDFHY	VVGATNDGLK	IPCQVPAPPEF	FTELDGVRLH	RYAPPCKPLL
HPCGENANTI		EVRRVGDFHY	VTGMTTDNVK	CPCQVPAPPEF	FTEVDGVRLH	RYAPACKPPLL
HPCGENOM		EVTRVGDFHY	VTGMTTDNVK	CPCQVPAPPEF	FTEVDGVRLH	RYAPACKPPLL
HPCHUM		EVTRVGDFHY	VTGMTTDNVK	CPCQVPAPPEF	FSEVDGVRLH	RYAPACKPPLL
HPCJ		EVTRVGDFHY	VTGVTQDNK	CPCQVPAPPEF	FTELDGVRLH	RYAPACKPPLL
HPCJCG		EVTRVGDFHY	VTGMTTDNVK	CPCQVPAPPEF	FTEVDGVRLH	RYAPVCKPPLL
HPCJK046		EVRRVGDSHY	ITGVTAENTK	CPCQVPAPPEF	FTEVDGVRLH	RYAPECKPIL
HPCJK049		EVRRVGDFHY	VTGTTDDGLK	CPCQVPLPEF	FTELDGVRLH	RYAPVCRPPLL
HPCJTA		EITRVGDFHY	VTGMTTDNVK	CPCQVPAPPEF	FTELDGVRLH	RYAPACKPPLL
HPCJTB		EITRVGDFHY	VTGXTTDNVK	CPCQVPAPPEF	FTELDGVRLH	RYAPACKPPLL
HPCK3A		EVRRVGDFHY	ITGATEDGLK	CPCQVPATEF	FTEVDGVRLH	RYAPPCKPPLL
HPCPLYPRE		EIRQVGDFHY	VTGMTTDNLK	CPCQVPSPEF	FTELDGVRLH	RFAPPCKPPLL
HPCPOLP		EVTQHGSYHY	ITGLTTDNK	VPCQLPSPEF	FSWVDGVQIH	RFAPIPKPF
HPCPP		EVTRVGDFHY	VTGMTTDNVK	CPCQVPAPPEF	FTELDGVRLH	RYAPACKPPLL

HPCUNKCD	EVTRVGDFHY	VTGMTTDNVK	CPCQVPAPF	FTEVDGVRH	RYAPACRPLL
MKC1A	EVTRVGDFHY	VTGMTTDNVK	CPCQVPAPF	FTELDGVRH	RYAPACKPLL
NDM59	EVTQHGSYSY	ITGLTTDSLK	VPCQLPSPEF	FSWVDGVQIH	RFAPTPKPF
NZLI	EVRRVGDFHY	ITGATEDELK	CPCQVPAAEF	FTEVDGVRH	RYAPPCKPLL
SA13	EVRRVGDYHY	ITGVTQDNLK	CPCQVPSPEF	FTELDGVRIH	RYAPPCNPLL
Th580	EVERHGDRHY	VVGVTADGLK	CPCQVPGPEF	FTEVDGVRIH	RYAPPCKPLL
Type_3a_CB	EVRRVGDFHY	ITGATEDELK	CPCQVPAAEF	FTEVDGVRH	RYAPPCKPLL
TypeV_D	EVRRVGDFHY	ITGATEDELK	CPCQVPAAEF	FTEVDGVRH	RYAPPCKPLL
VN004	EVKRVGDSHF	VVGATTDNLK	CPCQVPAPF	FTEVDGVRH	RYAPRCKPLL
VN235	EVVRVNDHHY	IVGATADNLK	CPCQVPAPF	FTEVDGVRH	RFAPPCRPLM
VN405	EVARVGDSHF	VVGATNQDLK	CPCQVPAPF	FTEVDGVRH	RFAPACKPLL

	2151			2200	
BEBE1	RDEVFSFVGL	NSYVVGSQLP	CEPEPDTEVL	ASMLTDPSHI	TAEAAARRLA
D89815	RDEVTFQVGL	NQYTVGSQPL	CEPEPDVTVV	TSMLTDPSHI	TAEAAARRLA
ED43type_4	RDEVFSFVGL	NSFVVGSQLP	CEPEPDVAVL	TSMLTDPSHI	TAESARRRLA
HC_C2	REEVDFQVGL	NQYPVGSQPL	CEPEPDVAVL	TSMLTDPSHI	TAEAAKRRLA
HC_G9	RDEVTFSIGL	NEYLVGSQLP	CEPEPDVAVL	TSMLTDPSHI	TAETAARRLN
HCU16326	REEVVFQVGL	HQYLVGSQPL	CEPEPDVAVL	TSMLTDPSHI	TAETAKRRLA
HCV_H_CM	REEVSFRVGL	HEYPVGSQLP	CEPEPDVAVL	TSMLTDPSHI	TAEAAARRLA
HCV_J1	REEVSFRVGL	HDYPVGSQLP	CEPEPDVAVL	TSMLTDPSHI	TAAAGARRLA
HCV_J483	REDVAFQVGL	NQYLVGSQPL	CEPEPDVTVL	TSMLTDPSHI	TAETAKRRLA
HCV_J8	RDEVTFQVGL	NSFVVGSQLP	CDPEPDTEVL	ASMLTDPSHI	TAEAAARRLA
HCV_JK1	RDEVTFQVGL	NQFPVGSQLP	CEPEPDVTVL	TSMLTDPSHI	TAETAKRRLA
HCV_JS	RDEVTFQVGL	NQYLVGSQPL	CEPEPDVAVL	TSMLTDPSHI	TAEAAKRRLA
HCV_K1_R1	REEVTFQVGL	NQYLVGSQPL	CEPEPDVTVL	TSMLTDPSHI	TGEAAKRRLA
HCV_K1_R2	RDEVTFQVGL	NQYVVGSQLP	CEPEPDVAVL	TSMLTDPSHI	TAETAKRRLA
HCV_K1_R3	RDEVTFQVGL	NRYPVGSQLP	CEPEPDVAVL	TSMLTDPSHI	TAETAKRRLA
HCV_K1_S1	REEVTFQVGL	NQYLVGSQPL	CEPEPDVAVL	TSMLTDPSHI	TGETAKRRLA
HCV_K1_S2	RDEVTFQVGL	NQYVVGSQLP	CEPEPDVAVL	TSMLTDPSHI	TAEAAKRRLA
HCV_K1_S3	RDEVTFQVGL	NRYAVGSQPL	CEPEPDVTVI	TSMLTDPSHI	TAETAKRRLA
HCV_L2	REEVTFQVGL	NQYLVGSQPL	CEPEPDVAVL	TSMLTDPSHI	TAETAKRRLA
HCV_N	REEVVFQVGL	NQYLVGSQPL	CEPEPDVAVL	TSMLTDPSHI	TAEAAKRRLA
HCV12083	RDEVTFSVGL	SNYAVGSQPL	CEPEPDVTVV	TSMLTDPSHI	TAETAARRLK
HCV1480	REEVTFSVGL	HSYVVGSQLP	CEPEPDVTVL	TSMLSDPAHI	TAETAKRRLN
HCVPOLYP	RDEVTFQVGL	NQYVVGSQLP	CEPEPDVVV	TSMLTDPSHI	TAETAKRRLD
HD_1	RDEVSFQVGL	NHYPVGSQLP	CEPEPDVAVL	TSMLTDPSHI	TAETAKRRLA
HPCCGAA	REEVSFRVGL	HEYPVGSQLP	CEPEPDVAVL	TSMLTDPSHI	TAEAGARRLA
HPCFG	RDEITFSVGL	HSYANGSQLS	CEPEPDVAVL	TSMLRDPahi	TAATAARRLA
HPCGENANTI	REEVSFQVGL	NQYVVGSQLP	CEPEPDVAVL	TSMLTDPSHI	TAETAKRRLA
HPCGENOM	REEVVFQVGL	NQYLVGSQPL	CEPEPDVTVL	TSMLTDPSHI	TAETAKRRLA
HPCHUMR	REEVTFQVGL	NQYLVGSQPL	CEPEPDVAVL	TSMLTDPSHI	TAETAKRRLA
HPCJ	RDEVSFQVGL	NQYLVGSQPL	CEPEPDVAVL	TSMLTDPSHI	TAETAKRRLA
HPCJCG	REEVVFQVGL	NQYLVGSQPL	CEPEPDVAVL	TSMLTDPSHI	TAETAKRRLA
HPCJK046	RDEVTFQVGL	STYVVGSQLP	CEPEPDVLV	TSMLRDPDHI	TAEASARRLK
HPCJK049	RDDVTFQVGL	NSYVIGSQLP	CEPEPDVAV	TSMLQDPSHI	TVETAKRRLD
HPCJTA	REDVTFQVGL	NQYLVGSQPL	CEPEPDVAVL	TSMLTDPSHI	TAETAKRRLA
HPCJTB	REDVTFQVGL	NQYLVGSQPL	CEPEPDVAVL	TSMLTDPSHI	TAETAKRRLA
HPCK3A	RDEITFMVGL	NSYAIGSQLP	CEPEPDVSVL	TSMLRDPDHI	TAETAARRLA
HPCPLYPRE	REEVSFRVGL	HEYPVGSQLP	CEPEPDVAVL	TSMLTDPSHI	TAEAGARRLA
HPCPOLP	RDEVSFQVGL	NSFVVGSQLP	CDPEPDADVL	TSMLTDPSHI	TAETAARRLA
HPCPP	RDEVTFQVGL	NQYTVGSQPL	CEPEPDVTVV	TSMLTDPSHI	TAEAAARRLA
HPCUNKCD	REEVVFQVGL	HQYLVGSQPL	CEPEPDVAVL	TSMLTDPSHI	TAETAKRRLA
MKC1A	RDEVTFQVGL	NQYTVGSQPL	CEPEPDVTVV	TSMLTDPSHI	TAEAAARRLA
NDM59	RDEVSFQVGL	NSFVVGSQLP	CDPEPDADVL	TSMLTDPSHI	TAEAAARRLA
NZLI	RDDITFMVGL	HSYTIGSQLP	CEPEPDVSVL	TSMLRDPDHI	TAETAARRLA
SA13	REEVCFQVGL	HSFVVGSQLP	CEPEPDVTVL	TSMLSDPAHI	TAETAKRRLD
Th580	RDEVFSFVGL	LEFVVGSQLP	CEPEPDVTVV	TSMLTDPSHI	TAETASARRLK
Type_3a_CB	REEITFSVGL	NSYTIGSQLP	CEPEPDVSVL	TSMLRDPDHI	TAETAARRLA
TypeV_D	RDDITFMVGL	NSYAIGSQLP	CEPEPDVSVL	TSMLRDPDHI	TAETAARRLA

VN004	RDEVFSFSVGL	SSYAVGSQLP	CEPEPDVTVV	TSMLIDPSHV	TAEAAAARRLA
VN235	RDDITFSVGL	STYVVGSQLP	CEPEPDVVIL	TSMLTDPDHI	TAETAARRLA
VN405	RDEISFLVGL	NSYAIGSQLP	CEPEPDVTVV	TSMLVDPSHL	TAEAAAARRLA
			2201	2250	
BEBE1	RGSPPSAASS	SASQLSAPSL	RATCTTHAK.	...CPDIDMV	DANLFCWCTM
D89815	RGSPPSLAGS	SASQLSALS	KATCTTHHG.	...APDTDLI	EANLLWRQEM
ED43type_4	RGSRPSLASS	SASQLSPRL	QATCTAPHD.	...SPGTDLL	EANLLW...
HC_C2	RGSPPSLASS	SASQLSAPSL	KATCTTHHD.	...SPDADLI	EANLLWRQEM
HC_G9	RGSPPSLASS	SASQLSAPSL	KATCTTHHD.	...SPDADLI	TANLLWRQEM
HCU16326	RGSPPSLASS	SASQLSAPSL	KATCTTHHD.	...SPDADLI	EANLLWRQEM
HCV_H_CMR	RGSPPSMASS	SASQLSAPSL	KATCTANHD.	...SPDAELI	EANLLWRQEM
HCV_J1	RGSPPEASS	SASQLSAPSL	KATCTINH.	...SPDAELI	EANLLWRQEM
HCV_J483	RGSPPSLASS	SASQLSAPSL	KATCTTHHD.	...SPDADLI	EANLLWRQEM
HCV_J8	RGSPPSQASS	SASQLSAPSL	KATCTTHKT.	...AYDCDMV	DANLF...M
HCV_JK1	RGSPPSLASS	SASQLSAPSL	KATCTTRHD.	...SPDADLI	EANLLWRQEM
HCV_JS	RGSPPSLASS	SASQLSAPSL	KATCTTHHD.	...SPDADLI	EANLLWRQEM
HCV_K1_R1	RGSPPSLASS	SASQLSAPSL	KATCTTHHD.	...SPDADLI	EANLLWRQEM
HCV_K1_R2	RGSPPSLASS	SASQLSAPSL	KATCTTHHD.	...SPDADLI	EANLLWRQEM
HCV_K1_R3	RGSPPSLASS	SASQLSAPSL	KATCTTHHD.	...SPDADLI	EANLLWRQEM
HCV_K1_S1	RGSPPSLASS	SASQLSAPSS	KATYITQYD.	...SPDFDLI	EANLLWRQEM
HCV_K1_S2	RGSPPSLASS	SASQLSAPSL	KATCTTRHD.	...SPDADLI	EANLLWRQEM
HCV_K1_S3	RGSPPSLASS	SASQLSAPSL	KATCTTCHD.	...SPDADLI	EANLLWRQEM
HCV_L2	RGSPPSLASS	SASQLSAPSL	KATCTTHHD.	...SPDADLI	EANLLWRQEM
HCV_N	RGSPPSLASS	SASQLSAPSL	RATCTTHSSY	NLDSPDVLI	EANLLWRQEM
HCV12083	KGSPPSLASS	SANQLSAPSL	RATCTTSQK.	...HPMEMEL	QANLLWKHEM
HCV1480	RGSPPSLANS	SASQLSAPSL	KATCTIQGH.	...HPDADLI	KANLLWRQCM
HCVPOLYP	RGSPPSLASS	SASQLSAPSL	KATCTTRHD.	...SPDADLI	EANLLWRQEM
HD_1	RGSPPSLASS	SASQLSAPSL	KATCTTRHD.	...SPDADLI	EAHLLWRQEM
HPCCGAA	RGSPPSMASS	SASQLSAPSL	KATCTANHD.	...SPDAELI	EANLLWRQEM
HPCFG	RGSPPEASS	SASQLSAPSL	KATCQTHRP.	...HPDAELI	DANLLWRQEM
HPCGENANTI	RGSPPSLASS	SASQLSALS	KAACCTTRHT.	...PPDADLI	EANLLWRQEM
HPCGENOM	RGSPPSLASS	SASQLSAPSL	KATCTTHHD.	...SPDADLI	EANLLWRQEM
HPCHUMR	RGSPPSLASS	SASQLSAPSL	KATCTTHHV.	...SPDADLI	EANLLWRQEM
HPCJ	RGSPPSLASS	SASQLSAPSL	KATCTIHHD.	...SPDADLI	EANLLWRQEM
HPCJCG	RGSPPSLASS	SASQLSAPSL	KATCTTHHD.	...SPDADLI	EANLLWRQEM
HPCJK046	RGSPPSLASS	SASQLSAPSL	KATCTTHAD.	...HPDAELV	EANLLWRQEM
HPCJK049	RGSPPSLASS	SASQLSAPSR	KATCTTHGR.	...HPDAELI	TANLLWRQEM
HPCJTA	RGSPPSLASS	SASQLSAPSL	KATCTTHHD.	...SPDADLI	EANLLWRQEM
HPCJTB	RGSPPSLASS	SASQLSAPSL	KATCTTHHD.	...SPDADLI	EANLLWRQEM
HPCK3A	RGSPPEASS	SASQLSAPSL	KATCQTHRP.	...HPDAELV	DANLLWRQEM
HPCPLYPRE	RGSPPSVASS	SASQLSAPSL	KATCTANHD.	...SPDAELI	EANLLWRQEM
HPCPOLP	RGSPPEASS	SASQLSAPSL	RATCTTHGK.	...AYDVDMV	DANLF...M
HPCPP	RGSPPSLASS	SASQLSALS	KATCTTHHG.	...APDTDLI	EANLLWRQEM
HPCUNKCD	RGSPPSLASS	SASQLSAPSL	KATCTTHHD.	...SPDADLI	EANLLWRQEM
MKC1A	RGSPPSLASS	SASQLSALS	KATCTTHHG.	...APDTDLI	EANLLWRQEM
NDM59	RGSPPEASS	SASQLSAPSL	RATCTTHGK.	...AYDVDMV	DANLF...M
NZLI	RGSPPEASS	SASQLSAPSL	KATCQTHRP.	...HPDAELV	DANLLWRQEM
SA13	RGSPPSLASS	SASQLSAPSL	KATCTTQGH.	...HPDADLI	EANLLWRQCM
Th580	RGSPPSLASS	SASQLSAPSL	KATCTANGD.	...HPDAELI	EANLLWRQEM
Type_3a_CB	RGSPPEASS	SASQLSAPSL	KATCQTHRP.	...HPDAELV	NANLLWRQEM
TypeV_D	RGSPPEASS	SASQLSAPSL	KATCQTHRP.	...HPDAELV	DANLLWRQEM
VN004	RGSPPSLASS	SASQLSAPSL	KATCTMHGA.	...HPDAELI	EANLLWRQEM
VN235	RGSPPSLASS	SASQLSAPSL	KATCTTAGK.	...HPDAELI	EANLLWRQEV
VN405	RGSPSCASS	LASQLSAPSL	KATCTTHCA.	...HPDADLI	EANLLWRQEV
			2251	2300	
BEBE1	GGNMTRIESE	SKVLMVDSFD	PVVDKE.DER	EPSIPSEYLL	PKS.RFPPAL
D89815	GGNITRVESE	NKIVILDSFE	PLRAEE.DER	EVSAAAEILR	KTR.KFPAAM
ED43type_4	GSTATRVETD	EKVIIILDSFE	SCVAEQNDDR	EVSVAAEILR	PTK.KFPPAL

HC_C2	GGNITRVESE	NKVVILDSFE	PLRAEE.DER	EVSVA AEILR	KTR.RFPPAM
HC_G9	GGNITRVESE	NKIVILDSFD	PLVAEE.DDR	EISVPAEILL	KSK.KFPPAM
HCU16326	GGNITRVESE	NKVVILDSFD	PLRAED.DEG	EISVPAEILR	KSR.KFPPAL
HCV_H_CM	GGNITRVESE	NKVVILDSFD	PLVAEE.DER	EVSVPAEILR	KSR.RFARAL
HCV_J1	GGNITRVESE	NKVVILDSFD	PLVAEE.DER	EISVPAEILR	KSR.RFTQAL
HCV_J483	GGNITRVESE	NKVVILDSFE	PLHAEG.DER	EISVAAEILR	KSR.KFPSAL
HCV_J8	GGDVTRIESE	SKVIVLDSLD	SMTEVE.DDR	EPSVPSEYLI	KRR.KFPPAL
HCV_JK1	GGNITRVESE	NKVVILDSFE	PLRAEE.DER	EVSVA AEILR	KSR.KFPPAL
HCV_JS	GGNITRVESE	NKVVILDSFD	PLHAEE.DER	EVSVA AEILR	KSR.KFPPAL
HCV_K1_R1	GGNITRVESE	NKVIILDSFD	PLRAEE.DER	EVSIPAEILR	KSK.KFPPAL
HCV_K1_R2	GGNITRVESE	NKVVILDSFE	PLRAEE.DER	EVSLPAEILR	KSR.KFPPAM
HCV_K1_R3	GGNITRVESE	NKVVILDSFD	PLRAEE.DER	EVSVA AEILR	KTR.KFPPAL
HCV_K1_S1	GGNITRVESE	NKVVTLDSFD	PLRAEE.DER	EVSIPAEILR	KSK.KFPSAL
HCV_K1_S2	GGNITRVESE	NKVVILDSFE	PLRAEE.DER	EVSLPAEILR	KSR.KFPPAM
HCV_K1_S3	GGNITRVESE	NKVVILDSFD	PLRAEE.DER	EVSVA AEILR	KTK.KFPPAL
HCV_L2	GGNITRVESE	SKVVILDSFD	PLRAEE.GEG	EVSVA AEILR	KSK.KFPPAL
HCV_N	GGNITRVESE	NKVVVILDSFE	PLRAEG.DEN	EISIAAEILR	KSK.KFPAAI
HCV12083	GSHIPRVQSE	NKVVVILDSFE	LYPLEY.EER	EISVSVECHR	QPRCKFPVPF
HCV1480	GGNITRVEAE	NKVEILDCFK	PLKEEE.DDR	EISVSADCFK	KGP.AFPPAL
HCVPOLYP	GGNITRVESE	NKVVILDSFD	PLRAEE.DER	EVSVA AEILR	KSR.RFPPAM
HD_1	GGNITRVESE	NKVVILDSFD	PLRAEE.DER	EVSVPAEILR	KSR.KFPPAM
HPCCGAA	GGNITRVESE	NKVVILDSFD	PLVAEE.DER	EVSVPAEILR	KSR.RFAPAL
HPCFG	GSNITRVESE	TKVVILDSFE	PLRAEE.DDT	ELSIPAECFK	KPP.KYPPAL
HPCGENANTI	GGNITRVESE	NKVVILDSFD	PLRAEE.DER	EVSVPAEILR	KSR.KFPPAL
HPCGENOM	GGNITRVESE	NKVVILDSFD	PLRAEE.DER	EVSVA AEILR	KSR.KFPSAL
HPCHUMR	GGNITRVESE	NKVVVILDSFD	PLRAEE.DER	EVSVPAEILR	KSK.KFPAAM
HPCJ	GGNITRVESE	NKVVILDSFE	PIRAEE.DER	EVSVPAEILR	RSR.KFPAAM
HPCJCG	GGNITRVESE	NKVVILDSFD	PIRAVE.DER	EISVPAEILR	KPR.KFPPAL
HPCJK046	GGNITRVESE	NKIVILDSFE	PLKAEE.DDR	EISVAAECHR	PPRFKYPPAL
HPCJK049	GSNITRVESE	SKVVILDSFE	PLRACD.DED	ELSVAAECFK	KPP.KYPPAL
HPCJTA	GGNITRVESE	NKVVILDSFD	PLRAEE.DER	EVSVA AEILR	KSK.KFPPAL
HPCJTB	GGNITRVESE	NKVVILDSFD	PLRAEE.DER	EVSVA AEILR	KSK.KFPPAL
HPCK3A	GSNITRVESE	TKVVILDSFE	PLRAET.DDA	ELSAAAECKF	KPP.KYPPAL
HPCPLYPRE	GGNITRVESE	NKVVILDSFD	PLVAEE.DER	EISVPAEILR	KSR.RFAQAL
HPCPOLP	GGDVTRIESE	SKVVVILDSLD	PMVEER.SDL	EPSIPSEYML	PKK.RFPPAL
HPCPP	GGNITRVESE	NKIVILDSFE	PLRAEE.DER	EVSVA AEILR	KTR.KFPAAM
HPCUNKCD	GGNITRVESE	NKVVILDSFD	PLRAED.DEG	EISVPAEILR	KSR.KFPPAL
MKC1A	GGNITRVESE	NKIVILDSFE	PLRAEE.DER	EVSVA AEILR	KTR.KFPAAM
NDM59	GGDVTRIESE	SKVVVILDSLD	PMAEER.SDL	EPSIPSEYML	PRN.RFPPAL
NZLI	GSNITRVESE	TKVVVILDSFE	PLRAET.DDV	EPSVAAECFK	KPP.KYPPAL
SA13	GGNITRVEAE	NKVVILDSFE	PLKADD.DDR	EISVSADCFR	RGP.AFPPAL
Th580	GSNITRVESE	TKVVILDSFD	PLVAEE.DDR	EISVSAECHR	PPRPKFPPAL
Type_3a_CB	GSNITRVESE	NKVVILDSFE	PLRAET.DDA	ELSVAAECFK	KPP.KYPPAL
TypeV_D	GSNITRVESE	TKVVILDSFE	PLRAQT.DDA	ELSVAAECFK	KPP.KYPPAL
VN004	GGNITRVESE	NKVVILDSFD	PLVPEF.EER	EMSVPAECHR	PPRPKFPPAL
VN235	GGNITRVESE	NKIVILDSFD	PLIAET.DDR	EISVGAECFN	PPRPKFPPAL
VN405	GGNITRVESE	NKIVILDSFD	PLVPEY.DDR	EPSVPAECHR	PNRPKFPPAL

2301			2350		
BEBE1	PPWARPDYNP	PLLETWKRPD	YQPPVVAGCA	LPPPGTTPVP	PPRRRR.AVV
D89815	PVWARPDYNP	PLLESWKNDP	YVPPVVHGCP	LPPTKAPPIP	PPRRKR.TVV
ED43type_4	PIWARPDYNP	PLTETWKQD	YQAPTVMGCA	LPPAKQPPVP	SPRRKR.TVQ
HC_C2	PVWARPDYNP	PLLESWKDPD	YVPPVVHGCP	LPPTKAPPIP	PPRRKR.TVV
HC_G9	PIWARPDYNP	PLVEPWKRPD	YEPPLVHGCP	LPPPKPTPVP	PPRRKR.TVV
HCU16326	PIWAPPDYNP	PLLESWKDPD	YVPPVVHGCP	LPPTKAPPIP	PPRRKR.TVV
HCV_H_CM	PVWARPDYNP	PLVETWKKPD	YEPVVVHGCP	LPPPRSPPVP	PPRKKR.TVV
HCV_J1	PIWARPDYNP	PLIETWKKPN	YEPVVVHGCP	LPPQSPPVP	PPRKKR.TVV
HCV_J483	PIWARPDYNP	PLLESWKDPD	YVPPVVHGCP	LPPTKAPPIP	PPRRKR.TVV
HCV_J8	PPWARPDYNP	VLIETWKRPD	YEPPTVLGCA	LPPTPQTPVP	PPRRRR.AKV
HCV_JK1	PIWARPSYNP	PLLESWKDPD	YVPPVVHGCP	LPPTMAPPIP	PPRRKR.TVV

HCV_JS	PIWARPDYNP	PLLESWKDPD	YVPPVVHGCP	LPPTKAPPPI	Pprrkr.TVv
HCV_K1_R1	PIWARPDYNP	PLLESWKDPD	YVPPVVHGCP	LPPAKAPPPI	Pprrkr.TVv
HCV_K1_R2	PIWARPDYNP	PLIESWKDPD	YVPPVVHGCP	LPPTKAPPPI	Pprrkr.TVv
HCV_K1_R3	PIWARPDYNP	PLLEPWDRPD	YAPPVVHGCP	LPPAKDPPPI	Pprrkr.TVv
HCV_K1_S1	PIWARPDYNP	PLLEPWKDPD	YVPPVVHGCP	LPPAKAPPPI	Pprrkr.TVv
HCV_K1_S2	PIWARPDYNP	PLIESWKDPD	YVPPVVHGCP	LPPTKAPPPI	Pprrkr.TVv
HCV_K1_S3	PIWARPDYNP	PLLESWRAPD	YAPPVVHGCP	LPPAKDPPPI	Pprrkr.TVv
HCV_L2	PEWARPDYNP	PLLESWKDPD	YVPPVVHGCP	LPPAKAPPPI	Pprrkr.TVv
HCV_N	PIWARPDYNP	PLLESWKDPD	YVPPVVHGCP	LPPVKAPPPI	Pprrkr.TVv
HCV12083	PVWARPDNNP	PFIQAWQMPG	YEPPVVS GCA	VAPPKPAPVP	Pprrkr.LVh
HCV1480	PVWARPGYDP	PLLETWKRPD	YDPPQVWGCP	IPPAGPPVP	LprrkrkPME
HCVPOLYP	PIWARPDYNP	PLLESWKDPD	YVPPVVHGCP	LPPTKAPPPI	Pprrkr.TVv
HD_1	PIWARPDYNP	PLLESWKDPD	YVPPVVHGCP	LPPTKAPPPI	Pprrkr.TVv
HPCCGAA	PVWARPDYNP	LLVETWKKPD	YEPPVVHGCP	LPPRSPPVP	Pprrkr.TVv
HPCFG	PIWARPDYNP	PLLPSWKDPT	YEPPAVHGCA	LPPTRPAPVP	Pprrkr.TIK
HPCGENANTI	PVWARPDYNP	PLLEPWKDPD	YVPPVVHGCP	LPPVKAPPPI	Pprrkr.TVv
HPCGENOM	PIWARPDYNP	PLLESWKDPD	YVPPVVHGCP	LPPTTAPPVP	Pprrkr.TVv
HPCHUMR	PIWARPDYNP	PLLESWKDPD	YVPPVVHGCP	LPPIKAPPPI	Pprrkr.TVv
HPCJ	PIWARPDYNP	PLLESWKDPD	YVPPVVHGCP	LPPTKAAPPI	Pprrkr.TIV
HPCJCG	PIWARPDYNP	PLLESWKDPD	YVPPVVHGCP	LPSTKAPPPI	Pprrkr.TVv
HPCJK046	PVWARPDYNP	PLLETWKAPD	YDPPVVS GCA	LPPQGLPPVP	Pprrkr.LVQ
HPCJK049	PIWARPDYNP	PLVEPWKDPD	YVPPTVHGCA	LPPQKLPPVP	Pprrkr.TIV
HPCJTA	PIWARPDYNP	PLLESWKSPD	YVPPAVHGCP	LPPTTGPPPI	Pprrkr.TVv
HPCJTB	PIWARPDYNP	PLLESWKSPD	YVPPAVHGCP	LPPTTGPPPI	Pprrkr.TVv
HPCK3A	PIWARPDYNP	PLLDRWKSPD	YVPPTVHGCA	LPPKGAPPVP	Pprrkr.TIQ
HPCPLYPRE	PVWARPDYNP	PLVETWKKPD	YEPPVVHGCP	LPPPKSPPVP	Pprrkr.TVv
HPCPOLP	PAWARPDYNP	PLVESWKRPD	YQPATVAGCA	LPPPKKTPTP	Pprrrr.TVG
HPCPP	PVWARPDYNP	PLLESWKDPD	YVPPVVHGCP	LPPTKAPPPI	Pprrkr.TVv
HPCUNKCD	PIWAPPDYNP	PLLESWKDPD	YVPPVVHGCP	LPPTKAPPPI	Pprrkr.TVv
MKC1A	PVWARPDYNP	PLLESWKDPD	YVPPVVHGCP	LPPTKAPPPI	Pprrkr.TVv
NDM59	PAWARPDYNP	PLVESWKRPD	YQPTTVAGCA	LPPPKKTPTP	Pprrrr.TVG
NZLI	PIWARPDYNP	PLLDRWKAPD	YVPPTVHGCA	LPPRGAPPVP	Pprrkr.TIQ
SA13	PIWARPGYDP	PLLETWKQPD	YDPPQVSGCP	LPPAGLPPVP	PprrkrkPVP
Th580	PIWARPDYNP	PLLQKWQMPG	YEPPVVS GCA	LPPAKPTPI	Pprrkr.LIQ
Type_3a_CB	PIWARPDYNP	PLLDRWKAPD	YVPPTVHGCA	LPPRGAPPVP	Pprrkr.TIQ
TypeV_D	PIWARPDYNP	PLLDRWKTPD	YVPPTVHGCA	LPPRGAPPVP	Pprrkr.TIQ
VN004	PIWATPGYNP	PVLETWKSPT	YEPPVVHGCA	LPPSGPPPPI	Pprrkr.VVQ
VN235	PVWARPDYNP	PLLQPWKAPD	YEPLLVHGCA	LPPKGLPPVP	Pprrkr.VVQ
VN405	PIWARPDYNP	PLLETWKKPD	YAPPLVHGCA	LPSPVQPPVP	Pprrks.VVh

	2351				2400
BEBE1	LDQSNVGEAL	KELAIKSFGC	PPPSGDPGHS	TGGGTTGETS	KSPPD.EPDD
D89815	LTESTVSSAL	AELATKTFGG	SGS.SAVDSG	TATGPPDQAS	AE....GDAG
ED43type_4	LTESTVSSAL	AELAAKTFGQ	SEP.SSDRDT	DLTTPTETTD	SGPIV.VDDA
HC_C2	LTESTVSSAL	AELATKTFGS	SGS.SAVDSG	TATAPPDQTS	ND....GDRE
HC_G9	LDESTVSSAL	AELATKTFGS	STT.SGVTSG	EAAESSPAPS	CD....GELD
HCU16326	LTESTVSSAL	AELATKTFGS	SGS.SAIDSG	TATAPPDQAS	GD....GDRE
HCV_H_CM	LTESTLPTAL	AELATKSFGS	SST.SGITGD	NMTTSSEPAP	SG....CPPD
HCV_J1	LTESTLSTAL	AELAAKSFGS	SST.SGITGD	NTTSSEPAP	SG....CSPD
HCV_J483	LTESTVSSAL	AELATKTFS	SGS.SAVDSG	TATALPDQAS	DD....GDKG
HCV_J8	LTQDNVEGVL	REMADKVLSP	LQDNND SGHS	TGADTGGDIV	QQPSD.ETAA
HCV_JK1	LTESTVSSAL	AELATKTFGS	SGS.SAVDSG	TATAPPDQPS	DD....GDRG
HCV_JS	LTESTVSSAL	AELATKTFGS	SGS.SAADSG	TATAPPDQAS	DD....GDKG
HCV_K1_R1	LTESTVSSAL	AELATKTFGS	SGS.SAADRG	TATAPPDQAS	ND....GDAG
HCV_K1_R2	LTESTVSSAL	AELATKTFGS	SES.SAADSG	TATAPPDQPS	SD....GDAG
HCV_K1_R3	LTESTVSSAL	AELATKTFGS	SGS.SAVDSG	TATAPPDQTS	ND....GDTG
HCV_K1_S1	LTESTVSSAL	AELATKTFGS	SES.SAADRG	TATAPPDQTS	ND....GDAG
HCV_K1_S2	LTESTVSSAL	AELATKTFGS	SES.SAADSG	TATAPPDQPS	ND....GDAG
HCV_K1_S3	LTESTVSSAL	AELATKTFGS	SGS.SAVDSG	TATAPPDQPS	ND....GDTG
HCV_L2	LTESTVSSAL	AELAVKTFGS	SES.SAVDSG	TATAPPDQVS	DN....GDKG



HCV_N	LTDSTVSSVL	AELATKTFGS	SEL.SAADSG	TATAPPDQTS	DN....GGKD
HCV12083	LDESTVSHAL	AQLADKVFVE	SSNDPGPSSD	SGLSITSPVP	PDPTTPEDAG
HCV1480	LSDSTVSQVM	ADLADARFKV	DTP.SIEGQD	SALGTSSQHD	SGPEEKRDDN
HCVPOLYP	LTESTVSSAL	AELATKTFGS	SES.SAVDSG	TATAPPDQPP	DN....DDTG
HD_1	LTESTVSSAL	AELATKTFGS	SES.SAVDSG	TATAPPGQSS	DD....VDTG
HPCCGAA	LTESTLPTAL	AELATKSFGS	SST.SGITGD	NTTTSSEPAP	SG....CPPD
HPCFG	LDGSNVSAAL	LALAERSFPS	TKPEGTGTSS	SGVGTESTAE	SGDSPETGEE
HPCGENANTI	LTESTVSSAL	AELATKTFGS	SES.SAAGSG	TATAPPDQPS	DD....GDAG
HPCGENOM	LTESTVSSAL	AELATKTFGS	SES.SAVDSG	TATAPPDEAS	GG....GDKG
HPCHUMR	LTESTVSSAL	AELATKTFGS	SES.SAVDSG	TATALPDQAS	DD....GDKG
HPCJ	LTESTVSSAL	AELATKTFGG	SGS.SAADSG	TATAPPDQTS	DD....GDKE
HPCJCG	LTESTVSSAL	AELATKTFGS	SGS.SAVDSG	TATGPPDQAS	DD....GDKG
HPCJK046	LDDSVVGHVL	AQLAEKSFFA	TPDQPQTNSD	SGHGTNGAAS	LPSAE.DDDA
HPCJK049	LDGSNVSKAL	ASLAEKSFPO	PTCSAEDEST	SGVGTQSGSL	TGPVQLDDDD
HPCJTA	LTESTVSSAL	AELATKTFGS	SGS.SAVDSG	TATAPPDQTS	DD....GDKE
HPCJTB	LTESTVSSAL	AELATKTFGS	SGS.SAVDSG	TATAPPDQTS	DD....GDKE
HPCK3A	LDGSNVSAAL	AALAEKSFPS	SKPQEENSSS	SGVDTQSSTA	SKVLPSPGEE
HPCPLYPRE	LTESTLSTAL	AELATRSFGS	SST.SGITGD	NTTTSSEPAP	SG....CPPD
HPCPOLP	LSESIADAL	QQLAIKSFGQ	PPPSGDSGLS	TGADAADSGS	RTPPD.ELAL
HPCPP	LTESTVSSAL	AELATKTFGS	SGS.SAVDSG	TATGPPDQAS	AE....GDAG
HPCUNKCD	LTESTVSSAL	AELATKTFGS	SGS.SAIDSG	TATAPPDQAS	GD....GDRE
MKC1A	LTESTVSSAL	AELATKTFGS	SGS.SAVDSG	TATGPPDQAS	AE....GDAG
NDM59	LNENTIGDAL	QQLAIKAFGQ	PPLSGDSGLS	TGADAADSGS	RTPPD.ESAL
NZLI	LDGSNVSAAL	AALAEKSFPS	SKPQEENSSS	SGVDTQSSTT	SKVPPSPGGE
SA13	LSDSNVSQVL	ADLAHARFKA	DTQ.SIEGQD	SAVGTSSQPD	SGPEEKRDDDD
Th580	LDESAVSQAL	QQLADKVFVE	DTSTSEPSSG	LGGSIAGPSS	PDPTTADDTTC
Type_3a_CB	LDGSNVSAAL	RALAEKSFPS	LKPQEENNSS	SGVDTQSSTT	SKVPPSPGGE
TypeV_D	LDGSNVSAAL	AALAKKSFPS	VNPQDENSSS	SGVDTQSSTT	SKVPPSPGGE
VN004	LDSSNVSAAL	AQLAAKTFFET	PSS.PTTGYG	SDQPDHSTES	SEHDRDDGVA
VN235	LDEGSAKRAL	AELAQTSFPP	STATLSEDSG	RETSTLSSDM	TPPREEADRA
VN405	LDDSTVATAL	AELAEKSFFT	QPA.STPDS	SGHPTTSKSS	DQADEGEDTP

	2401			2450	
BEBE1	SEAGSVSSMP	PLEGEPGDPD	LEPEQVEHPA	PPQEGGAAPG	SDSGSWSTCS
D89815	SDAESYSSMP	PLEGEPGDPD	LS.....	.....	..DGSWSTVS
ED43type_4	SDDGSYSSMP	PLEGEPGDPD	LT.....	.....	..SDSWSTVS
HC_C2	SDAESYSSMP	PLEGEPGDPD	LS.....	.....	..DGSWSTVS
HC_G9	SEAESYSSMP	PLEGEPGDPD	LS.....	.....	..DGSWSTVS
HCU16326	SDVESFSSMP	PLEGEPGDPD	LS.....	.....	..DGSWSTVS
HCV_H_CMV	SDVESYSSMP	PLEGEPGDPD	FS.....	.....	..DGSWSTVS
HCV_J1	SDAESYSSMP	PLEGEPGDPD	LS.....	.....	..DGSWSTVS
HCV_J483	SDVESYSSMP	PLEGEPGDPD	LS.....	.....	..DGSWSTVS
HCV_J8	SEAGSLSSMP	PLEGEPGDPD	LEFEPVGSAP	PSEGECEVID	SDSKSWSTVS
HCV_JK1	SDDESYSMP	PLEGEPGDPD	LS.....	.....	..DGSWSTVS
HCV_JS	SDVESYSSMP	PLEGEPGDPD	LS.....	.....	..DGSWSTVS
HCV_K1_R1	SDVGSYSSMP	PLEGEPGDPD	LS.....	.....	..DGSWSTVS
HCV_K1_R2	SDVESYSSMP	PLEGEPGDPD	LS.....	.....	..DGSWSTVS
HCV_K1_R3	SDVGSYSSMP	PLEGEPGDPD	LS.....	.....	..DGSWSTVS
HCV_K1_S1	SDVESYSSMP	PLEGEPGDPD	LS.....	.....	..DGSWSTVS
HCV_K1_S2	SDVESYSSMP	PLEGEPGDPD	LS.....	.....	..DGSWSTVS
HCV_K1_S3	SDVGSYSSMP	PLEGEPGDPD	LS.....	.....	..DGSWSTVS
HCV_L2	SDAESYSSMP	PLEGEPGDPD	LS.....	.....	..DGSWSTVS
HCV_N	SDAESCSSMP	PLEGEPGDPD	LS.....	.....	..DGSWSTVS
HCV12083	SEAESYSSMP	PLEGEPGDPD	LS.....	.....	..SGSWSTVS
HCV1480	SDAASYSSMP	PLEGEPGDPD	LS.....	.....	..SGSWSTVS
HCVPOLYP	SDVESCSSMP	PLEGEPGDPD	LS.....	.....	..DGSWSTVS
HD_1	SDVESYSSMP	PLEGEPGDPD	LS.....	.....	..DGSWSTVS
HPCCGAA	SDVESYSSMP	PLEGEPGDPD	LS.....	.....	..DGSWSTVS
HPCFG	SDVESYSSMP	PLEGEPGDPD	LD.....	.....	..ADSWSTVS
HPCGENANTI	SDVESCSSMP	PLEGEPGDPD	LS.....	.....	..DGSWSTVS

HPCGENOM	SDVESYSSMP	PLEGEPGDPD	LS.....	.....	..DGSWSTVS
HPCHUMR	SDVESYSSMP	PLEGEPGDPD	LS.....	.....	..DGSWSTVS
HPCJ	SDVESYSSMP	PLEGEPGDPD	LS.....	.....	..DGSWSTVS
HPCJCG	SDVESYSSMP	PLEGEPGDPD	LS.....	.....	..DGSWSTVS
HPCJK046	SDADSYSSMP	PLEGEPGDPD	LSDG.....	.....	GGSGSWSTVS
HPCJK049	SDNESHSSMP	PLEGEPGDPD	LS.....	.....	..SGSWSTVS
HPCJTA	SDVESYSSMP	PLEGEPGDPD	LS.....	.....	..DGSWSTVS
HPCJTB	SDVESYSSMP	PLEGEPGDPD	LS.....	.....	..DGSWSTVS
HPCK3A	SDSESCSSMP	PLEGEPGDPD	LS.....	.....	..CDSWSTVS
HPCPLYPRE	SDAESYSSMP	PLEGEPGDPD	LS.....	.....	..DGSWSTVS
HPCPOLP	SETGSISSMP	PLEGEPGDPD	LEPEQVELQP	PPQGGVVTPG	SGSGSWSTCS
HPCPP	SDAESYSSMP	PLEGEPGDPD	LN.....	.....	..DGSWSTVS
HPCUNKCD	SDVESFSSMP	PLEGEPGDPD	LS.....	.....	..DGSWSTVS
MKC1A	SDAESYSSMP	PLEGEPGDPD	LN.....	.....	..DGSWSTVS
NDM59	SETGSISSMP	PLEGEPGDPD	LEPEQVELQP	PPQGEVVP	SDSGSWSTCS
NZLI	SDSESCSSMP	PLEGEPGDPD	LS.....	.....	..CDSWSTVS
SA13	SDAASYSSMP	PLEGEPGDPD	LS.....	.....	..SGSWSTVS
Th580	SDAGSFSSMP	PLEGEPGDPD	LS.....	.....	..TGSWSTVS
Type_3a_CB	SDSESCSSMP	PLEGEPGDPD	LS.....	.....	..CDSWSTVS
TypeV_D	SDSESCSSMP	PLEGEPGDPD	LS.....	.....	..CDSWSTVS
VN004	SEAESYSSMP	PLEGEPGDPD	LS.....	.....	..SGSWSTVS
VN235	SDDGSYSSMP	PLEGEPGDPD	LS.....	.....	..SGSWSTVS
VN405	SEAGSYSSMP	PLEGEPGDPD	LS.....	.....	..SGSWSTVS

	2451				2500
BEBE1	DVD..DSVVC	CSMSYSWTGA	LITPCSPEEE	KLPINPLSNS	LLRYHNKVYC
D89815	EEA.SEDVVC	CSMSYTWGTGA	LITPCAAEES	KLPINALSNS	LLRHHNMVYS
ED43type_4	GSE...DVVC	CSMSYSWTGA	LVTPCAAEES	KLPISPLSNS	LLRHHNMVYA
HC_C2	EEA.SGDVVC	CSMSYTWGTGA	LITPCAAEES	KLPINPLSNS	LLRHHNMVYA
HC_G9	SDGGTEDVVC	CSMSYSWTGA	LITPCAAEET	KLPINALSNS	LLRHHNLVYS
HCU16326	EEA.SEDVVC	CSMSYTWGTGA	LITPCAAEES	KLPINPLSNS	LLRHHNMVYA
HCV_H_CMV	SGADTEDVVC	CSMSYTWGTGA	LVTPCAAEEQ	KLPINALSNS	LLRHHNLVYS
HCV_J1	SEAGTEDVVC	CSMSYTWGTGA	LITPCAAEEQ	KLPINALSNS	LLRHHNLVYS
HCV_J483	EEA.SEDVVC	CSMSYTWGTGA	LITPCAAEES	KLPINPLSNS	LLRHHNMVYA
HCV_J8	DQE..DSVIC	CSMSYSWTGA	LITPCGPEEE	KLPINPLSNS	LMRFHNKVYS
HCV_JK1	EEA.SEDVAC	CSMSYTWGTGA	LITPCAAEES	KLPINPLSNS	LLRHHNMVYA
HCV_JS	EEA.SEDVVC	CSMSYTWGTGA	LITPCAAEES	KLPINPLSNS	LLRHHNMVYA
HCV_K1_R1	EEA.GEDVVC	CSMSYTWGTGA	LITPCAAEES	KLPINALSNS	LLRHHNMVYA
HCV_K1_R2	EEA.GEDVVC	CSMSYTWGTGA	LITPCAAEES	KLPINALSNS	LLRHHNMVYA
HCV_K1_R3	EEA.GEDVVC	CSMSYTWGTGA	LITPCAAEES	KLPINALSNS	LLRHHNMVYA
HCV_K1_S1	EEA.GEDVVC	CSMSYTWGTGA	LITPCAAEES	KLPINALSNS	LLRHHNMVYA
HCV_K1_S2	EEA.GEDVVC	CSMSYTWGTGA	LITPCAAEES	KLPINALSNS	LLRHHNMVYA
HCV_K1_S3	EEA.GEDVVC	CSMSYTWGTGA	LITPCAAEES	KLPINALSNS	LLRHHNMVYA
HCV_L2	EEA.SEDVVC	CSMSYSWTGA	LITPCAAEES	KLPINALSNS	LLRHHNMVYA
HCV_N	EEA.GESVVC	CSMSYTWGTGA	LITPCAAEES	KLPINALSNS	LLRHHNMVYA
HCV12083	DEDD...VVC	CSMSYSWTGA	LITPCAAEEE	KLPINPLSNS	LVRHHNMVYS
HCV1480	GED...NVVC	CSMSYTWGTGA	LITPCSAEEE	KLPINPLSNT	LLRHHNLVYS
HCVPOLYP	EEA.SEDVVC	CSMSYTWGTGA	LITPCAAEES	KLPINALSNS	LLRHHNMVYA
HD_1	EEA.NEDVVC	CSMSYTWGTGA	LITPCAAEES	KLPINALSNS	LLRHHNMVYA
HPCCGAA	SGADTEDVVC	CSMSYSWTGA	LVTPCAAEEQ	KLPINALSNS	LLRHHNLVYS
HPCFG	DSE.EQSVVC	CSMSYSWTGA	IITPCSAEEE	KLPISPLSNS	LLRHHNLVYS
HPCGENANTI	EED.GEGVIC	CSMSYTWGTGA	LITPCAAEES	KLPINALSNS	LLRHHNMVYA
HPCGENOM	EEA.SEDVVC	CSMSYTWGTGA	LITPCAAEES	KLPINPLSNS	LLRHHNMVYA
HPCHUMR	EEA.SEDVVC	CSMSYTWGTGA	LITPCAAEES	KLPINALSNS	LLRHHNMVYA
HPCJ	EEA.SEDVVC	CSMSYTWGTGA	LITPCAAEES	KLPINPLSNS	LLRHHNMVYA
HPCJCG	GEA.GEDVVC	CSMSYTWGTGA	LITPCAAEES	KLPINPLSNS	LLRHHNMVYS
HPCJK046	SEETS..VVC	CSMSYSWTGA	LITPCAAEEE	KLPISPLSNT	LIRHHNMVYS
HPCJK049	.GE.EQSVVC	CSMSYSWTGA	LITPCAAEEE	KLPISPLSNS	LLRHHNLVYS
HPCJTA	GEA.SDDIVC	CSMSYTWGTGA	LITPCAAEES	KLPINALSNS	LLRHHNMVYA
HPCJTB	GEA.SDDIVC	CSMSYTWGTGA	LITPCAAEES	KLPINALSNS	LLRHHNMVYA

HPCCK3A	DSE.EQSVVC	CSMSYSWTGA	LITPCSAEEEE	KLPISPLSNS	LLRHHNLVYS
HPCPLYPRE	SEANAEDVVC	CSMSYSWTGA	LVTPCAAEEQ	KLPINALSNS	LLRHHNLVYS
HPCPOLP	EED..DSVVC	CSMSYSWTGA	LITPCSPEEE	KLPINPLSNS	LLRYHNKVYC
HPCPP	EEA.SEDVVC	CSMSYTWGTA	LITPCAAEES	KLPINALSNP	LLRHHNMVYA
HPCUNKCD	EEA.SEDVVC	CSMSYTWGTA	LITPCAAEES	KLPINPLSNS	LLRHHNMVYA
MKC1A	EEA.SEDVVC	CSMSYTWGTA	LITPCAAEES	KLPINALSNP	LLRHHNMVYA
NDM59	EED..DSVVC	CSMSYSWTGA	LITPCSPEEE	KLPINPLSNS	LLRYHNKVYC
NZLI	DSE.EQSVVC	CSMSYSWTGA	LITPCSAEEEE	KLPISPLSNS	LLRHHNLVYS
SA13	DED...SVVC	CSMSYSWTGA	LITPCSAEEEE	KLPINPLSNT	LLRHHNLVYS
Th580	EEDD...VVC	CSMSYTWGTA	LITPCAAEEEE	KLPINPLSNS	LIRHHNMVYS
Type_3a_CB	DSE.EQSVVC	CSMSYSWTGA	LITPCSAEEEE	KLPISPLSNS	LLRHHNLVYS
TypeV_D	DSE.EQSVVC	CSMSYSWTGA	LITPCSAEEEE	KLPISPLSNS	LLRHHNLVYS
VN004	EEGDS..VVC	CSYSYSWTGA	LVTPCAAEEEE	KLPINPLSNS	LIRHHNLVYS
VN235	EDHDS..VVC	CSMSYSWTGA	LITPCAAEEEE	KLPISPLSNA	LIRHHNLVYS
VN405	EEGDS..VVC	CSMSYSWTGA	LVTPCAAEEEE	KLPINPLSNS	LIRHHNLVYS

	2501				2550
BEBE1	TTSRASQRA	KKVTFDRVQL	LDSHYESVLK	DVKQAATKVS	AKLLSIEEAC
D89815	TTSRASLRQ	KKVTFDRMQV	LDDHYRDVLK	EMKAKASTVK	AKLLSVEEAC
ED43type_4	TTTRSAVTRQ	KKVTFDRLQV	VDSTYNEVLK	EIKARASRVK	PRLLTTEEAC
HC_C2	TTSRASLRQ	KKVTFDRLQV	LDDHYRDVLK	EMKAKASTVK	AKLLSIEEAC
HC_G9	TTSRASQQRQ	KKVTFDRLQV	LDDHYRDVLK	EAKAKASTVK	AKLLSVEEAC
HCU16326	TTSRASGLRQ	KKVTFDRLQV	LDDHYRDVLK	EMKAKASTVK	AKLLSVEEAC
HCV_H_CMR	TTSRASQQRQ	KKVTFDRLQV	LDSDHYQDVLK	EVKAAASKVK	ANLLSVEEAC
HCV_J1	TTSRASQQRQ	KKVTFDRLQV	LDSDHYQDVLK	EVKAAASKVK	ANLLSVEEAC
HCV_J483	TTSRASLRQ	KKVTFDRLQV	LDDHYRDVLK	EMKAKASTVK	AKLLSIEEAC
HCV_J8	TTSRASLRA	KKVTFDRVQV	LDADHYDSVLQ	DVKRAASKVS	ARLLTVEEAC
HCV_JK1	TTSRASGLRQ	KKVTFDRLQV	PDDHYRDVLK	EMKAKASTVK	AKLLSVEEAC
HCV_JS	TTSRASGLRQ	KKVTFDRLQV	LDDHYRDVLK	EMKAKASTVK	AKLLSIEEAC
HCV_K1_R1	TTSRASQQRQ	KKVTFDRLQV	LDDHYRDVLK	EMKAKASTVK	AKLLSVEEAC
HCV_K1_R2	TTSRASQQRQ	KKVTFDRLQV	LDDHYRDVLK	EMKAKASTVK	ARLLSVEEAC
HCV_K1_R3	TTSRASQQRQ	KKVTFDRLQV	LDDHYRDVLK	EMKAKASTVK	AKLLSVEEAC
HCV_K1_S1	TTSRASQQRQ	KKVTFDRLQV	LDDHYRDVLK	EMKAKASTVK	AKLLSVEEAC
HCV_K1_S2	TTSRASQQRQ	KKVTFDRLQV	LDDHYRDVLK	EMKAKASTVK	ARLLSVEEAC
HCV_K1_S3	TTSRASQQRQ	KKVTFDRLQV	LDDHYRDVLK	EMKAKASTVK	AKLLSVEEAC
HCV_L2	TTSRASGLRQ	KKVTFDRLQV	LDDHYRDVLK	EMKAKASTVK	AKLLSVEEAC
HCV_N	TTSRASGLRQ	KKVTFDRLQV	LDDHYRDVLK	EMKAKASTVK	AKLLSIEEAC
HCV12083	TTSRASLRQ	KKVTFDRVQV	FDQHYQDVLK	EIKLRASVQ	AKLLSIEEAC
HCV1480	TSSRSAGLRQ	KKVTFDRLQV	LDDHYREVVD	EMKRLASKVK	ARLLPLEEAC
HCVPOLYP	TTSRASQQRQ	KKVTFDRLQV	LDDHYRDVLK	EMKAKASTVK	AKLLSVEEAC
HD_1	TTSRASQQRQ	KKVTFDRQQV	QDDHYRDVLK	EMKAKASTVK	ARLLSVEEAC
HPCCGAA	TTSRASQQRQ	KKVTFDRLQV	LDSDHYQDVLK	EVKAAASKVK	ANLLSVEEAC
HPCFG	TSSRSAAARQ	KKVTFDRLQV	LDDHYKNVLK	EVKERASGVK	GRLLSFEEAC
HPCGENANTI	TTSRASQQRQ	KKVTIDRLQV	LDDHYRDVLK	EMKAKASTVK	AKLLSVEEAC
HPCGENOM	TTSRASLRQ	KKVAFDRMQV	LDDHYRDVLK	EMKAKASTVK	AKLLSIEEAC
HPCHUMR	TTSRASGLRQ	KKVTFDRLQV	LDDHYRDVLK	EMKAKASTVK	AKLLSVEEAC
HPCJ	TTSRASLRQ	KKVTFDRLQV	LDDHYRDVLK	EMKAKASTVK	AKLLSVEEAC
HPCJCG	TTSRASLRQ	KKVTFDRLQV	LDDHYRDVLK	EMKAKASTVK	ARLLSIEEAC
HPCJK046	TTSRSAALRQ	KKVTFDRQQV	VDQHYDYLK	EMKARASTVS	AKLLSVEEAC
HPCJK049	TSSRSAAQQRQ	KKVTFDRLQV	LDDHYNTTLK	EIKELASGVK	AELLSVEEAC
HPCJTA	TTSRASLRQ	KKVTFDRLQV	LDDHYRDVLK	EMKAKASTVK	AKLLSVEEAC
HPCJTB	TTSRASLRQ	KKVTFDRLQV	LDDHYRDVLK	EVKAKASTVK	AKLLSVEEAC
HPCCK3A	TSSRSASQQRQ	KKVTFDRLQV	LDDHYKTALQ	EVKERASRVK	ARMLSIEEAC
HPCPLYPRE	TTSRASQQRQ	KKVTFDRLQV	LDSDHYQDVLK	EVKAAASKVK	ANLLSVEEAC
HPCPOLP	TTSKSASLRA	KKVTFDRMQA	LDADHYDSVLK	DIKLAASKVT	ARLLTLEEAC
HPCPP	TTSRASQQRQ	KKVTFDRLQV	LDDHYRDVLK	DMKAKASTVK	AKLLSVEEAC
HPCUNKCD	TTSRASGLRQ	KKVTFDRLQV	LDDHYRDVLK	EMKAKASTVK	AKLLSVEEAC
MKC1A	TTSRASQQRQ	KKVTFDRLQV	LDDHYRDVLK	DMKAKASTVK	AKLLSVEEAC
NDM59	TTSKSASLRA	KKVTFDRMQV	LDADHYDSVLK	DIKLAASKVS	ARLLTLEEAC
NZLI	TSSRSASQQRQ	KKVTFDRLQV	LDDHYKTALK	EVKERASRVK	ARMLTIEEAC

SA13	TSSRSAGQRQ	KKVTFDRLQV	LDDHYREVVD	EMKRLASKVK	ARLLPLEEAC
Th580	TTSRSAGLRQ	KKVTFDRLQV	VDQHYQDVLK	EIKLRASVH	ARLLSTEEAC
Type_3a_CB	TSSRSASQRQ	RKVTFDRLQV	LDDHYKTVLK	EVKERASRVK	ARMLTIEEAC
TypeV_D	TSSRSASQRQ	KKVTFDRLQV	LDDHYKTALK	EVKERASRVK	ARMLTIEEAC
VN004	TSSRSAATRQ	KKVTFDRVQL	LDQHYDVTVK	EIKLRASHVK	AQLLSTEEAC
VN235	TTSRSASLRQ	KKVTFDRVQV	VDQHYDVLK	EIKTKASGVS	AKLLSVEEAC
VN405	TTTRSAAMRQ	KKVTFDRLQI	LDQHYNNVVK	EVKLASGVT	AKLLSVEEAC

	2551			2600	
BEBE1	ALTTPPHSARS	KYGFGAKEVR	SLSRRAVDHI	KSVWEDLLED	HCSPIDTTIM
D89815	KLTPPHSAKS	KFGYGAKDVR	SLSSRAVNHI	RSVWKDLLED	TDTPIQTTIM
ED43type_4	DLTPPHSARS	KFGYGKKDVR	SHSRKAINHI	SSVWKDLLED	NNTPIPTTIM
HC_C2	KLTPPHSAKS	KFGYGAKDVR	NLSSKAVNHI	RSVWKDLLED	TETPIDTTIM
HC_G9	SLTPPHSARS	KFGYGAKDVR	SHSSKAIRHI	NSVWQDLLED	NTPIDTTIM
HCU16326	KLTPPHSAKS	KFGYGAKDVR	SLSSRAVTHI	RSVWKDLLED	TETPISTTIM
HCV_H_CMV	SLTPPHSAKS	KFGYGAKDVR	CHARKAVAH	NSVWKDLLED	SVTPIDTIIM
HCV_J1	SLTPPHSAKS	KFGYGAKDVR	CHARKAVNHI	NSVWKDLLED	SVTPIQTTIM
HCV_J483	KLTPPHSAKS	KFGYGAKDVR	NLSSRAVNHI	RSVWEDLLED	TETPIDTTIM
HCV_J8	ALTTPPHSAKS	RYGFGAKEVR	SLSRRAVNHI	RSVWEDLLED	QHTPIDTTIM
HCV_JK1	KLTPPHSARS	KFGYGAKDVR	NLSSKAVNHI	HSVWKDLLED	TETPIDTTIM
HCV_JS	KLTPPHSAKS	KYGYGAKDVR	NLSSRAVNHI	RSVWEDLLED	TETPIDTTIM
HCV_K1_R1	RLTPPHSARS	KFGYGAKDVR	NLSSGAVNHI	RSVWKDLLED	TETPIDTTIM
HCV_K1_R2	KLTPPHSARS	KFGYGAKDVR	NLSSRAINHI	RSVWKDLQED	TETPIDTTIM
HCV_K1_R3	KLTPPHSAKS	KFGYGGKDVR	NLSSKAVNHI	RSVWKDLLED	TETPIDTTVM
HCV_K1_S1	RLTPPHSARS	KFGYGAKDVR	NLSSGAVNHI	RSVWKDLLED	TETPIDTTIM
HCV_K1_S2	KLTPPHSARS	KFGYGAKDVR	NLSSRAINHI	RSVWKDLLED	TETPIDTTIM
HCV_K1_S3	KLTPPHSAKS	KFGYGGKDVR	NLSSKAVNHI	RSVWKDLLED	TETPIDTTVM
HCV_L2	KLTPPHSAKS	KFGYGAKDVR	NLSSRAVNHI	RSVWKDLLED	TETPIDTTIM
HCV_N	RLTPPHSAKS	KFGYGAKDVR	NLSSRAINHF	RSVWEDLLED	TVTPIDTTVM
HCV12083	DLTPSHSARS	KYGYGAQDVR	SRASKAVDHI	PSVWEGILLED	SDTPIPTTIM
HCV1480	GLTPPHSARS	KYGYGAKEVR	SLDKKALKHI	EGVWQDLLED	SDTPLPTTIM
HCVPOLYP	KLTPPHSARS	KFGYGAKDVR	NLSSKAVNHI	RSVWKDLLED	TETPIDTTIM
HD_1	KLTPPLSARS	KFGYGAKDVR	NLSSKAVNHI	RSVWEDLLED	NVTPIIDTTIM
HPCCGAA	SLAPPHSAKS	KFGYGAKDVR	CHARKAVAH	NSVWKDLLED	SVTPIDTTIM
HPCFG	SLVPPHSGRS	KYGYSAKDVR	SLSSKAMNHI	RSVWEDLLED	NSTPIPTTIM
HPCGENANTI	KLTPPHSARS	KFGYGAKDVR	NLSSKAINHI	RSVWKDLLED	TETPIDTTIM
HPCGENOM	KLTPPHSAKS	KFGYGAKDVR	NLSSKAVNHI	RSVWKDLLED	NETPINTTIM
HPCCHUMR	KLTPPHSAKS	KFGYGAKDVR	NLSSKAVNHI	HSVWKDLLED	TVTPIDTTIM
HPCJ	KLTPPHSAKS	KFGYGAKDVR	SLSSRAVNHI	TSVWKDLLED	TKTPIDTTIM
HPCJCG	KLTPPHSAKS	KFGYGAKDVR	SLSSRAVNHI	RSVWEDLLED	TETPIDTTIM
HPCJK046	DLTPAHSARS	KFGYGAKDVR	GRTSKALNHI	NSVWEDLLED	NVTPIPTTIM
HPCJK049	RLVPSHSARS	KFGYGAKDVR	SLSSKAINHI	NSVWEDLLED	NTPIDTTIM
HPCJTA	KLTPPHSAKS	KFGYGAKDVR	NLSSKAINHI	RSVWKDLLED	TETPIDTTIM
HPCJTB	KLTPPHSAKS	KFGYGAKDVR	NLSSKAINHI	RSVWKDLLED	TETPIDTTIM
HPCK3A	ALVPPHSARS	KFGYSAKDVR	SLSSKAINHI	RSVWEDLLED	TTTPIPTTIM
HPCPLYPRE	SLTPPHSAKS	KFGYGAKDVR	CHARKAVTHI	NSVWKDLLED	NVTPIIDTTIM
HPCPOLP	QLTPPHSARS	KYGFGAKEVR	SLSGRAVNHI	KSVWKDLLED	TQTPIPTTIM
HPCPP	KLTPPHSARS	KFGYGAKDVR	SLSSKAVNHI	RSVWKDLLED	TETPIDTTIM
HPCUNKCD	KLTPPHSAKS	KFGYGAKDVR	SLSSRAVTHI	RSVWKDLLED	TETPISTTIM
MKC1A	KLTPPHSARS	KFGYGAKDVR	SLSSKAVNHI	RSVWKDLLED	TETPIDTTIM
NDM59	QLTPPHSARS	KYGFGAKEVR	SLSGRAVNHI	KSVWKDLLED	SQTPIPTTIM
NZLI	ALVPPHSARS	KFGYSAKDVR	SLSSRAINHI	RSVWEDLLED	TTTPIPTTIM
SA13	GLTPPHSARS	KYGYGAKEVR	SLDKKALNHI	KGWQDLLED	SDTPLPTTIM
Th580	SLTPPHSARS	RYGYGARDVR	SHTSKAVKHI	DSVWEDLLED	NATPIPTTIM
Type_3a_CB	ALVPPHSARS	KFGYSAKDVR	SLSSRAINHI	RSVWEDLLED	TTTPIPTTIM
TypeV_D	ALVPPHSARS	KFGYSAKDVR	SLSSRAIDHI	RSVWEDLLED	TTTPIPTTIM
VN004	DLTPPHSARS	KFGYGAKDVR	SHASKAINHI	NSVWADLLED	TQTPIPTTIM
VN235	ALTTPPHSARS	KFGYGAKDVR	GLASKAVNHI	NSVWEDLLED	NSTPIPTTIM
VN405	SLTPPHSARS	KFGYGAKDVR	SHTSKAINHI	NSVWEDLLED	NQTPIPTTIM

	2601				2650	
	BEBE1	AKNEVFCVDP	TKGGKKPARL	IVYPDLGVRV	CEKMALYDIT	QKLPAVAVMGQ
	D89815	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGS
ED43type_4	AKNEVFAVNP	EKGGRKPARL	IVYPDLGSRV		CEKRALHDVI	KKTALAVMGA
	HC_C2	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGS
	HC_G9	AKNEVFCVKP	EKGGRKPARL	IVYPDLGVRV	CEKRALYDVV	KQLPIAVMGT
	HCU16326	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGS
	HCV_H_CM	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	SKLPLAVMGS
	HCV_J1	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	SKLPPAVMGS
	HCV_J483	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGS
	HCV_J8	AKNEVFCIDP	TKGGKKPARL	IVYPDLGVRV	CEKMALYDIA	QKLPKAIMGP
	HCV_JK1	AKNEVFCVQP	EKGGRKPARL	IVFPELGVRV	CEKMALYDVV	STLPQAVMGS
	HCV_JS	AKSEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGS
	HCV_K1_R1	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGS
	HCV_K1_R2	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGA
	HCV_K1_R3	AKNEVFCVQP	EKGGRKAARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGS
	HCV_K1_S1	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGS
	HCV_K1_S2	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGP
	HCV_K1_S3	AKNEVFCVQP	EKGGRKAARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGS
	HCV_L2	AKSEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGP
	HCV_N	AKNEVFCVQP	EKGQKPARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGS
	HCV12083	AKNEVFCVDP	SKGGRKPARL	IVYPDLGVRV	CEKMALYDVT	QKLPAVAVMGP
	HCV1480	AKNEVFAVEP	SKGGKKPARL	IVYPDLGVRV	CEKRALYDVA	QKLPTALMGP
	HCVPOLYP	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGP
	HD_1	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPHTVMGS
	HPCCGAA	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	SKLPLAVMGS
	HPCFG	AKNEVFSVNP	AKGGRKPARL	IVYPDLGVRV	CEKRALYDVI	QKLSIATMGP
HPCGENANTI	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGS	
HPCGENOM	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGS	
HPCHUMR	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGS	
HPCJ	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGS	
HPCJCG	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGP	
HPCJK046	AKNEVFCVDV	SKGGRKPARL	IVYPDLGVRV	CEKRALYDVT	RKLPAVAVMGA	
HPCJK049	AKNEVFAVAP	HKGGRKPARL	IVYPDLGVRV	CEKRALYDVI	QKLPSAIMGS	
HPCJTA	AKSEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGS	
HPCJTB	AKSEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGS	
HPCK3A	AKNEVFCVDP	AKGGRKAARL	IVYPDLGVRV	CEKRALYDVI	QRLSIETMGS	
HPCPLYPRE	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	TKLPLAVMGS	
HPCPOLP	AKNEVFCVDP	TKGGKKAARL	IVYPDLGVRV	CEKMALYDIT	QKLPAVAVMGA	
HPCPP	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGS	
HPCUNKCD	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGS	
MKC1A	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGS	
NDM59	AKNEVFCVDP	AKGGKKAARL	IVYPDLGVRV	CEKMALYDVT	QKLPAVAVMGA	
NZLI	AKNEVFCVDP	AKGGRKPARL	IVYPDLGVRV	CEKRALYDVI	QKLSIETMGP	
SA13	AKNEVFAVEP	SKGGKKPARL	IVYPDLGVRV	CEKRALYDIA	QKLPTALMGP	
Th580	AKNEVFCVDP	SKGGRKPARL	IVYPDLGVRV	CEKMALYDVT	QKLPKTVMGS	
Type_3a_CB	AKNEVFCVDP	AKGGRKPARL	IVYPDLGVRV	CEKRALYDVI	QKLAIETIGS	
TypeV_D	AKNEVFCVDP	ARGGRKRARL	IVYPDLGVRV	CEKRVLYDVI	QKLSIETMGT	
VN004	AKNEVFCVDA	SKGGRKSARL	IVYPDLGVRV	CEKRALFDVT	RKLPTAIMGD	
VN235	AKNEVFCVDA	QKGGRKPARL	IVYPDLGVRV	CEKRALYDVT	QKLPIAVMGA	
VN405	AKNEVFCADV	SKGGRKPARL	IVYPDLGVRV	CEKRALYDVT	RKLPTAIMGD	

	2651				2700	
	BEBE1	SYGFQYSPAQ	RVDFLQAWK	EKKTPMGFSY	DTRCFDSTVT	ERDIRTEESI
	D89815	SYGFQYSPKQ	RVEFLVNTWK	AKKCPMGFSY	DTRCFDSTVT	ENDIRVEESI
ED43type_4	AYGFQYSPAQ	RVEFLLTAWK	SKNDPMGFSY		DTRCFDSTVT	EKDIRVEEEV
	HC_C2	SYGFQYSPGQ	RVEFLVNTWK	SKKCPMGFSY	DTRCFDSTVT	ENDIRIEESI
	HC_G9	SYGFQYSPAQ	RVDFLLNAWK	SKKNPMGFSY	DTRCFDSTVT	EADIRTEEDL
	HCU16326	SYGFQYSPKQ	RVEFLVNTWK	SKKCPMGFSY	DTRCFDSTVT	ENDIRVEESI
	HCV_H_CM	SYGFQYSPGQ	RVEFLVQAWK	SKKTPMGFPY	DTRCFDSTVT	ESDIRTEEAI

HCV_J1	SYGFQYSPGQ	RVEFLVQAWK	SKRTPMGFSY	DTRCFDSTVT	ESDIRTEEEAI
HCV_J483	SYGFQYSPKQ	RVEFLVNTWK	SKKCPMGFSY	DTRCFDSTVT	ESDIRVEESI
HCV_J8	SYGFQYSPAE	RVDFLKAWG	SKKDPMGFSY	DTRCFDSTVT	ERDIRTEESI
HCV_JK1	SYGFQYSPGQ	RVEFLVNAWK	SKKNPMGFAY	CTRCFDSTVT	ESDIRVEESI
HCV_JS	SYGFQYSPKQ	RVEFLVNTWK	SKKCPMGFSY	DTRCFDSTVT	ENDIRVEESI
HCV_K1_R1	SYGFQYSPGQ	RVEFLVNAWK	SKKCPMGFAY	DTRCFDSTVT	ESDIRVEESI
HCV_K1_R2	SYGFQYSPGQ	RVEFLVNAWK	SKKCPMGFAY	DTRCFDSTVT	ENDIRVEESI
HCV_K1_R3	SYGFQYSPGQ	RVEFLVNAWK	SKKSPMGFAY	DTRCFDSTVT	ENDIRTEESI
HCV_K1_S1	SYGFQYSPGQ	RVEFLVNAWK	SKKCPMGFAY	DTRCFDSTVT	ESDIRVEESI
HCV_K1_S2	SYGFQYSPGQ	RVEFLVNAWK	SKKCPMGFAY	DTRCFDSTVT	ESDIRVEESI
HCV_K1_S3	SYGFQYSPGQ	RVEFLVNAWK	SKKSPMGFAY	DTRCFDSTVT	ENDIRVEESI
HCV_L2	SYGFQYSPGQ	RVEFLVNAWK	SKKCPMGFSY	DTRCFDSTVT	ESDIRTEESI
HCV_N	SYGFQYSPGQ	RVEFLVKAWK	SKKNPMGFSY	DTRCFDSTVT	ENDIRVEESI
HCV12083	AYGFQYSPNQ	RVEYLLKMWR	SKKVPMGFSY	DTRCFDSTVT	ERDIRTENDI
HCV1480	SYGFQYSPAQ	RVDFLKAWK	SKKIPMAFSY	DTRCFDSTIT	EHDIMTEESI
HCVPOLYP	SYGFQYSPGQ	RVEFLVNAWK	SKKCPMGFAY	DTRCFDSTVT	ESDIRVEESI
HD_1	SYGFQYSPGQ	RVEFLVNTWK	SKKCPMGFAY	DTRCFDSTVT	ENDIRVEESI
HPCCGAA	SYGFQYSPGQ	RVEFLVQAWK	SKKTPMGLSY	DTRCFDSTVT	ESDIRTEEEAI
HPCFG	AYGFQYSPKQ	RVEHLLKMWT	SKKTPMGFSY	DTRCFDSTVT	EHDIRTEEGI
HPCGENANTI	SYGFQYSPGQ	RVEFLVNAWK	SKKCPMGFSY	DTRCFDSTVT	ESDIRVEESI
HPCGENOM	SYGFQYSPGQ	RVEFLVNAWK	SKKNPMGFSY	DTRCFDSTVT	QNDIRVEESI
HPCHUMR	SYGFQYSPGQ	RVEFLVNTWK	SKKNPMGFSY	DTRCFDSTVT	ENDIRVEESI
HPCJ	SYGFQYSPGQ	RVEFLVKTWK	SKKCPMGFSY	DTRCFDSTVT	ENDIRTEESI
HPCJCG	SYGFQYSPGQ	RVEFLVNTWK	SKKCPMGFSY	DTRCFDSTVT	ENDIRTEESI
HPCJK046	AYGFQYSPSQ	RVEYLLKIWR	SKKTPMGFSY	DTRCFDSTVT	ERDIRTEESI
HPCJK049	AYGFQYSPKQ	RVEYLLKMWN	SKKTPMGFSY	DTRCFDSTVT	EQDIRVEESI
HPCJTA	SYGFQYSPGQ	RVEFLVNAWK	SKKSPMGFSY	DTRCFDSTVT	ESDIRVEESI
HPCJTB	SYGFQYSPGQ	RVEFLVNAWK	SKKSPMGFSY	DTRCFDSTVT	ESDIRVEESI
HPCK3A	AYGFQYSPRQ	RVERLLKMWT	SKKTPMGFSY	DTRCFDSTVT	GQDIRVEEAV
HPCPLYPRE	SYGFQYSPGQ	RVEFLVQAWK	SKKTPMGFSY	DTRCFDSTVT	ESDIRTEEEAI
HPCPOLP	SYGFQYSPAQ	RVEFLKAWA	EKKDPMGFSY	DTRCFDSTVT	ERDIRTEESI
HPCPP	SYGFQYSPGQ	RVEFLVNAWK	SKKSPMGFAY	DTRCFDSTVT	ENDIRTEESI
HPCUNKCD	SYGFQYSPKQ	RVEFLVNTWK	SKKCPMGFSY	DTRCFDSTVT	ENDIRVEESI
MKC1A	SYGFQYSPGQ	RVEFLVNAWK	SKKSPMGFAY	DTRCFDSTVT	ENDIRTEESI
NDM59	SYGFQYSPAQ	RVEFLKAWA	EKKDPMGFSY	DTRCFDSTVT	ERDIRTEESI
NZLI	AYGFQYSPQQ	RVERLLKMWT	SKKTPMGFSY	DTRCFDSTVT	EQDIRVEEEI
SA13	SYGFQYSPAQ	RVEFLKAWA	SKKTPMAFSY	DTRCFDSTVT	EHDIMTEESI
Th580	AYGFQYSPSQ	RVEYLLKMWR	SKKTPMGFSY	DTRCFDSTVT	ERDIRTEEDI
Type_3a_CB	AYGFQYSPQQ	RVERLLKMWT	SKKTPMGFSY	DTRCFDSTVT	EQDIRVEEEI
TypeV_D	AYGFQYSPQQ	RVERLLKMWT	SKKTPMGFSY	DTRCFDSTVT	EQDFRVEEEI
VN004	AYGFQYSPQQ	RVDRLKMW	SKKTPMGFSY	DTRCFDSTVT	ERDIRTEQDI
VN235	AYGFQYSPKQ	RVDYLLKMWR	SKKTPMGFSY	DTRCFDSTVT	ERDIRTEEDI
VN405	AYGFQYSPKQ	RVDQLKMW	SKKTPMGFSY	DTRCFDSTVT	EHDIKTERDV

	2701			2750	
BEBE1	YLSCSLPEEA	RTAIHSLTER	LYVGGPMTNS	KGQSCGYRRC	RASGVLTTSM
D89815	YQCCDLAPEA	RQAIRSLTER	LYIGGPMTNS	KGQNCGYRRC	RASGVLTTSC
ED43type_4	YQCCDLEPEA	RKVITALTDR	LYVGGPMHNS	KGDLGCGYRRC	RATGVYTTSF
HC_C2	YQCCDLAPEA	KQAIKSLTER	LYIGGPLTNS	KGQNCGYRRC	RASGVLTTSC
HC_G9	YQSCDLVPEA	RAAIRSLTER	LYIGGPLTNS	KGQNCGYRRC	RASGVLTTSC
HCU16326	YQCCDLAPEA	KLAIKSLTER	LYIGGPLTNS	KGQNCGYRRC	RASGVLTTSC
HCV_H_CM	YQCCDLDPQA	RVAIKSLTER	LYVGGPLTNS	RGENCYRRC	RASGVLTTSC
HCV_J1	YQCCDLDPQA	RVAIRSLTER	LYVGGPLTNS	RGENCYRRC	RASGVLTTSC
HCV_J483	YQCCDLAPEA	RQAIRSLTER	LYIGGPLTNS	KGQNCGYRRC	RASGVLTTSC
HCV_J8	YQACSLPQEA	RTVIHSLTER	LYVGGPMTNS	KGQSCGYRRC	RASGVFTTSM
HCV_JK1	YQCCDLAPEA	RQVIRSLTER	LYIGGPLTNS	KGQNCGYRRC	RASGVLTTNC
HCV_JS	YQCCDLAPEA	KLAIRSLTER	LYIGGPLTNS	KGQNCGYRRC	RASGVLTTSC
HCV_K1_R1	YQCCDLAPEA	RQAIRSLTER	LYIGGPLTNS	KGQNCGYRRC	RASGVLTTSC
HCV_K1_R2	YQCCDLAPEA	RQAIRSLTER	LYIGGPLTNS	KGQNCGYRRC	RASGVLTTSC
HCV_K1_R3	YQCCDLAPEA	RQVIRSLTER	LYVGGPLTNS	KGQNCGYRRC	RASGVLTTSC

HCV_K1_S1	YQCCDLAPEA	RQAIRSLTER	LYIGGPLTNS	KGQNCGYRRC	RASGVLTTSC
HCV_K1_S2	YQCCDLAPEA	RQAIRSLTER	LYIGGPLTNS	KGQNCGYRRC	RASGVLTTSC
HCV_K1_S3	YQCCDLAPEA	RQVIRSLTER	LYIGGPLTNS	KGQNCGYRRC	RASGVLTTSC
HCV_L2	YQCCDLAPEA	RQAIKSLTER	LYIGGPLTNS	KGQNCGYRRC	RASVVLTTSC
HCV_N	YQCCDLAPEA	RQAIKSLTER	LYIGGPLTNS	KGQSCGYRRC	RASGVLTTSC
HCV12083	YQSCQLDPVA	RRVVSSLTER	LYVGGPMANS	KGQSCGYRRC	RASGVLPTSM
HCV1480	YQSCDLQPEA	RVAIRSLTQR	LYCGGPMYNS	KGQOCGYRRC	RASGVFTTSM
HCVPOLYP	YQCCDLAPEA	RQAIKSLTER	LYIGGPLTNS	KGQNCGYRRC	RASGVLTTSC
HD_1	YQCCDLGPEA	RQAIRSLTER	LYIGGPLTNS	KGQNCGYRRC	RASGVLTTSC
HPCCGAA	YQCCDLDPQA	RVAIKSLTER	LYVGGPLTNS	RGENCYRRC	RASRVLTTSF
HPCFG	YQCCDLEPEA	RKAISALTER	LYIGGPMYNS	KGLQCGYRRC	RASGVLPTSF
HPCGENANTI	YQCCDLAPEA	RQAIRSLTER	LYIGGPLTNS	KGQNCGYRRC	RASGVLTTSC
HPCGENOM	YQCCDLAPEA	RRAIKSLTER	LYIGGPLTNS	KGQNCGYRRC	RASGVLTTSC
HPCHUMR	YQCCDLAPEA	RQAIKSLTER	LYIGGPLTNS	KGQNCGYRRC	RASGVLTTSC
HPCJ	YQCCDLAPEA	RQVIRSLTER	LYIGGPLTNS	KGQNCGYRRC	RASGVLTTSC
HPCJCG	YQCCDLAPEA	RQAIRSLTER	LYVGGPLTNS	KGQNCGYRRC	RASGVLTTSC
HPCJK046	YQCCDLDPVA	RKAISLTER	LYVGGPMYNS	KGQSCGYRRC	RASGVLPTSM
HPCJK049	YQACDLKDEA	RRVITSLTER	LYCGGPMFNS	KGQHCYRRC	RASGVLPTSF
HPCJTA	YQCCDLAPEA	RQAIKSLTER	LYIGGPLTNS	KGQNCGYRRC	RASGVLTTSC
HPCJTB	YQCCDLAPEA	RQAIKSLTER	LYIGGPLTNS	KGQNCGYRRC	RASGVLTTSC
HPCK3A	YQCCNLEPEP	RKAISLTER	LYCGGPMNNS	KGAQCGYLRC	RASGVLPTSF
HPCPLYPRE	YQCCDLDPQA	RVAIKSLTER	LYVGGPLTNS	RGENCYRRC	RASGVLTTSC
HPCPOLP	YRACSLPEEA	HTAIHSLTER	LYVGGPMFNS	KGQTCGYRRC	RASGVLTTSM
HPCPP	YQCCDLDPQA	RQAIRSLTER	LYIGGPLTNS	KGQNCGYRRC	RVSGVLTTSC
HPCUNKCD	YQCCDLAPEA	KLAIKSLTER	LYIGGPLTNS	KGQNCGYRRC	RASGVLTTSC
MKC1A	YQCCDLDPQA	RQAIRSLTER	LYIGGPLTNS	KGQNCGYRRC	RVSGVLTTSC
NDM59	YRACSLPEEA	HTAIHSLTER	LYVGGPMFNS	KGQTCGYRRC	RASGVLTTSM
NZLI	YQCCNLEPEA	RKVISSLTER	LYCGGPMFNS	KGAQCGYRRC	RASGVLPTSF
SA13	YQSCDLQPEA	RAAIRSLTQR	LYCGGPMYNS	KGQOCGYRRC	RASGVFTTSM
Th580	YQSCQLDPTA	RKAISLTER	LYCGGPMFNS	KGESCGYRRC	RASGVLTTSL
Type_3a_CB	YQCCNLEPEA	RKVISSLTER	LYCGGPMFNS	KGAQCGDRRC	RASGVLPTSF
TypeV_D	YQCCNLEPEA	RKVISSLTER	LYCGGPMFNS	KGAQCGYRRC	RASGVLPTSF
VN004	YLSCQLDPVA	RKVIESLTER	LYVGGPMYNS	KGQLCGQRR	RASGVLPTSM
VN235	YQCCQLDPVA	KKAITSLTER	LYCGGPMYNS	RGQSCGYRRC	RASGVLTTSL
VN405	YLSCQLDPVA	RKAIESLTER	LYIGGPMYNS	RGQLCGTRRC	RASGVLTTSL

2751

2800

BEBE1	GNTLTCTYVKA	KAACNAAGIV	APTMLVCGDD	LVVISESQGV	EEDERNLRVF
D89815	GNTLTCTYLKA	AAACRAAKLQ	DCTMLVCGDD	LVVICDSAGT	QEDAASLRVF
ED43type_4	GNTLTCTYLKA	TAAIRAAALR	DCTMLVCGDD	LVVIAESDGV	EEDNRALRAF
HC_C2	GNTLTCTYLKA	SAACRAAKLQ	DCTMLVNGDD	LVVICESAGT	QEDAASLRVF
HC_G9	GNTITCTYLKA	SAACRAAKLR	DCTMLVCGDD	LVVICESAGV	QEDAANLRAF
HCU16326	GNTLTCTYLKA	TAACRAAKLR	DCTMLVNGDD	LVVICESAGT	QEDAASLRVF
HCV_H_CMR	GNTLTCTYIKA	RAARRAAGLQ	DCTMLVCGDD	LVVICESAGV	QEDAASLRAF
HCV_J1	GNTLTCTYIKA	RAACRAAGLQ	DCTMLVCGDD	LVVICESAGV	QEDAASLRAF
HCV_J483	GNTLTCTYLKA	TAACRAAKLQ	DCTMLVNGDD	LVVICESAGT	QEDAAALRVF
HCV_J8	GNTMTCTYIKA	LAACKAAGIV	DPVMLVCGDD	LVVISESQGN	EEDERNLRAF
HCV_JK1	GNTLTCTYLKA	SAACRAAKLQ	DCTMLVCGDD	LVVICESAGT	QEDAASLRVF
HCV_JS	GNTLTCTYLKA	SAACRAAKLQ	DCTMLVNGDD	LVVICESAGT	QEDAASLRVF
HCV_K1_R1	GNTLTCTYLKA	SAACRAAKLQ	DCTMLVCGDD	LVVICESAGT	QEDAASLRVF
HCV_K1_R2	GNTLTCTYLKA	TAACRAAKLQ	DCTMLVCGDD	LVVICESAGT	QEDAASLRVF
HCV_K1_R3	GNTLTCTYLKA	AAACRAAKLQ	DCTMLVCGDD	LVVICESAGT	QEDAASLRVF
HCV_K1_S1	GNTLTCTYLKA	SAACRAAKLQ	DCTMLVCGDD	LVVICESAGT	QEDAASLRVF
HCV_K1_S2	GNTLTCTYLKA	TAACRAAKLQ	DCTMLVCGDD	LVVICESAGT	QEDAASLRVF
HCV_K1_S3	GNTLTCTYLKA	AAACRAAKLQ	DCTMLVCGDD	LVVICESAGT	QEDAASLRVF
HCV_L2	GNTLTCTYLKA	SAACRAAKLQ	DCTMLVNGDD	LVVICESAGT	QEDAANLRAF
HCV_N	GNTLTCTYLKA	SAACRAAKLQ	DCTMLVNGDD	RVVICESAGT	QEDAASLRVF
HCV12083	GNTLTCTYLKA	QAACRAANIK	DCDMLVCGDD	LVVICESAGV	QEDTASLRAF
HCV1480	GNTMTCTYIKA	LASCRAAKLR	DCTLLVCGDD	LVAICESQGT	HEDEASLRAF
HCVPOLYP	GNTLTCTYLKA	SAACRAAKLQ	DCTMLVCGDD	LVVICESAGT	QEDAASLRVF

HD_1	GNTLTCTYLKA	TAACRAAKLQ	DCTMLVCGDD	LVVICESAGT	QEDAANLRVF
HPCCGAA	GNTLTCTYIKA	RAACRAAGLQ	DCTMLVCGDD	LVVICESAGV	QEDAASLRAF
HPCFG	GNTITCTYIKA	TAASRAAGLK	NPSFLVCGDD	LVVISESCGV	EEDRTALRAF
HPCGENANTI	GNTLTCTYLKA	SAACRAAKLQ	DCTMLVCGDD	LVVICESAGT	QEDAASLRVF
HPCGENOM	GNTLTCTYLKA	SAACRAAKLQ	DCTMLVNGDD	LVVICESAGT	QEDAASLRVF
HPCHUMR	GNTLTCTYLKA	SAACRAAKLQ	DCTMLVNGDD	LVVICESAGT	QEDAASLRVF
HPCJ	GNTLTCTYLKA	SAACRAAKLQ	DCTMLVNGDD	LVVICESAGT	QEDAASLRVF
HPCJCG	GNTLTCTYLKA	TAACRAAKLQ	DCTMLVNGDD	LVVICESAGT	QEDAAALRAF
HPCJK046	GNTLTCTYLKA	MAACKAAGLK	NFDMLVCGDD	LVVISESLGV	SEDASALRAF
HPCJK049	GNTVTCYLKA	KAATKAAGIK	DPSFLVCGDD	LVVIAESAGI	DEKDSALRAF
HPCJTA	GNTLTCTYLKA	TAACRAAKLQ	DCTMLVNGDD	LVVICESAGT	QEDAASLRVF
HPCJTB	GNTLTCTYLKA	TAACRAAKLQ	DCTMLVNGDD	LVVICESAGT	QEDAASLRVF
HPCK3A	GNTITCTYIKA	TAAARAAGLR	NPDFLVCGDD	LVVVAESDGV	DEDRTALRAF
HPCPLYPRE	GNTLTCTYIKA	RAACRAAGLQ	DCTMLVCGDD	LVVICESAGV	QEDAASLRAF
HPCPOLP	GNTITCTYVKA	LAACKAAGII	APTMLVCGDD	LVVISESQGT	EEDERNLRAF
HPCPP	GNTLTCTYLKA	SAACRAAKLQ	DCTMLVCGDD	LVVICDSAGT	QEDAASLRVF
HPCUNKCD	GNTLTCTYLKA	TAACRAAKLR	DCTMLVNGDD	LVVICESAGT	QEDAASLRVF
MKC1A	GNTLTCTYLKA	SAACRAAKLQ	DCTMLVCGDD	LVVICDSAGT	QEDAASLRVF
NDM59	GNTITCTYIKA	LAACKAAGIV	APTMLVCGDD	LVVISESQGT	EEDERNLRAF
NZLI	GNTITCTYIKA	TAAAKAANLR	NPDFLVCGDD	LVVVAESDGV	DEDRAALRAF
SA13	GNTMTCTYIKA	LASCRAAKLR	DCTLLVCGDD	LVAICESQGT	HEDEASLRAF
Th580	GNTLTCTYLKA	QAACRAANIK	NFDMLVCGDD	LVVICESAGV	QEDVVALRAF
Type_3a_CB	GNTITCTYIKA	TAAANGAGLR	DPDFLVCGDD	LVVVAESDGV	DEDGAALRAF
TypeV_D	GNTITCTYIKA	TAAAKAAGLR	NPDFLVCGDD	LVVVAESDGV	DEDRTALRAF
VN004	GNTVTCFLKA	TAACRAAGFT	DYDMLVCGDD	LVVVTESAGV	NEDIANLRAF
VN235	GNTLTCTYLKA	QAACRAAKLK	DFDMLVCGDD	LVVISESMGV	AEDASALRAF
VN405	GNTMTCTFIKA	EAACRAAGLT	NYDMLVCGDD	LVVIAESAGV	QEDASNLRVF

	2801		2850		
BEBE1	TEAMTRYSAP	PGDPPKAEYD	LELITSCSSN	VSVALDPRGR	RRYYLTRDPT
D89815	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSAHDASGK	RVYYLTRDPT
ED43type_4	TEAMTRYSAP	PGDAPQPAYD	LELITSCSSN	VSAHDVTGK	KVYYLTRDPE
HC_C2	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSAHDASGK	RVYYLTRDPT
HC_G9	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSAHDGAGK	RVYYLTRDPE
HCU16326	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSAHDASGK	RVYYLTRDPT
HCV_H_CMV	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSAHDGAGK	RVYYLTRDPT
HCV_J1	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSAHDGTGK	RVYYLTRDPT
HCV_J483	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSAHDASGK	RVYYLTRDPT
HCV_J8	TEAMTRYSAP	PGDLPQPEYD	LELITSCSSN	VSVALDSRGR	RRYFLTRDPT
HCV_JK1	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSAHDASGK	RVYYLTRDPT
HCV_JS	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSAHDASGK	RVYYLTRDPT
HCV_K1_R1	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSAHDASGK	RVYYLTRDPT
HCV_K1_R2	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSAHDASGK	RVYYLTRDPT
HCV_K1_R3	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSAHDASGK	RVYYLTRDPT
HCV_K1_S1	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSAHDASGK	RVYYLTRDPT
HCV_K1_S2	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSAHDASGK	RVYYLTRDPT
HCV_K1_S3	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSAHDASGK	RVYYLTRDPT
HCV_L2	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSAHDASGK	RVYYLTRDPT
HCV_N	TEAMTRYSAP	PGDLPQPEYD	LELITSCSSN	VSAHDASGK	RVYYLTRDPT
HCV12083	TDAMTRYSAP	PGDAPQPTYD	LELITSCSSN	VSAHEGNGK	KYYLTRDCT
HCV1480	TEAMTRYSAP	PGDPPVPAYD	LELITSCSSN	VSVARDASGN	RIYYLTRDPQ
HCVPOLYP	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSAHDASGK	RVYYLTRDPT
HD_1	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSAHDASGK	RVYYLTRDPT
HPCCGAA	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSAHDGAGK	RVYYLTRDPT
HPCFG	TEAMTRYSAP	PGDAPQPTYD	LELISSCSSN	VSVACDGAGK	RYYYLTRDPE
HPCGENANTI	TEAMTRYSAP	PGDLPQPEYD	QELITSCSSN	VSAHDASGK	RVYYLTRDPT
HPCGENOM	TEAMTRYSAP	PGDLPQPEYD	LELITSCSSN	VSAHDASGK	RVYYLTRDPT
HPCHUMR	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSAHDASGK	RVYYLTRDPT
HPCJ	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSAHDASGK	RVYYLTRDPT
HPCJCG	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSAHDASGK	RVYYLTRDPT



HPCJK046	TDAMTRYSAP	PGDEPHPEYD	LEHITSCSSN	VSVAHDHGTGQ	RYYYYLTRDPT
HPCJK049	TEAMTRYSAP	PGDPPQPTYD	LELITSCSSN	VSVAHDGAGK	RYYYYLTRDPE
HPCJTA	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSVAHDASGK	RVYYLTRDPT
HPCJTB	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSVAHDASGK	RVYYLTRDPT
HPCK3A	TEAMTRYSAP	PGDAPQPTYD	LELITSCSSN	VSVARDDKGK	RYYYYLTRDAT
HPCPLYPRE	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSVAHDGAGK	RVYYLTRDPT
HPCPOLP	TEAMTRYSAP	PGDPPRPEYD	LELITSCSSN	VSVALGPQGR	RRYYLTRDPT
HPCPP	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSVAHDASGK	RVYYLTRDPT
HPCUNKCD	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSVAHDASGK	RVYYLTRDPT
MKC1A	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSVAHDASGK	RVYYLTRDPT
NDM59	TEAMTRYSAP	PGDPPRPEYD	LELITSCSSN	VSVAXGPQGR	RRYYLTRDPT
NZLI	TEAMTRYSAP	PGDAPQATYD	LELITSCSSN	VSVARDDKGR	RYYYYLTRDAT
SA13	TEAMTRYSAP	PGDPPVPAYD	LELITSCSSN	VSVAHDASGN	RVYYLTRDPQ
Th580	TDAMIRYSAP	PGDAPQPTYD	LELITSCSSN	VSVAHDGTGQ	RYYYYLTRDCT
Type_3a_CB	TEAMTRYSAP	PGDAPQPTYD	LELITSCSSN	VSVARDDKGR	RYYYYLTRDAT
TypeV_D	TEAMTRYSAP	PGDAPQPTYD	LELITSCSSN	VSVALDNKGK	RYYYYLTRDAT
VN004	TEAMTRYSAT	PGDEPSPTYD	LELITSCSSN	VSVAHGDGGR	RYYYYLTRDPV
VN235	TEAMTRYSAP	PGDDPQPEYD	LELITSCSSN	VSVAHDGAGQ	RYYYYLTRDPL
VN405	TEAMTRYSAP	PGDEPHPAYD	LELITSCSSN	VSVAHDHGTGQ	RYYYYLTRDPT

	2851				2900	
	BEBE1	TPLARAAWET	ARHSPVNSWL	GNI IQYAPT V	WVRMVLMT HF	FSVLMAQDTL
	D89815	TPLARAAWET	ARHTPVNSWL	GNI IMYAPT L	WARMILMT HF	FSILLAQEQL
ED43type_4	TPLARAVWET	VRHTPVNSWL	GNI IVYAPT I	WVRMILMT HF		FSILQSQEAL
HC_C2	TPLARAAWET	ARHTPVNSWL	GNI IMYAPT L	WARMILMT HF		FSILLAQEQL
HC_G9	TPLARAAWET	ARHTPVNSWL	GNI IMFAPT L	WVRMVLMT HF		FSILLAQEHL
HCU16326	TPLARAAWET	ARHTPVNSWL	GNI IMYAPT L	WARMILMT HF		FSILLAQEQL
HCV_H_CM R	TPLARAAWET	ARHTPVNSWL	GNI IMFAPT L	WARMILMT HF		FSVLIARDQL
HCV_J1	TPLARAAWET	ARHTPVNSWL	GNI IMFAPT L	WARMILMT HF		FSVLIARDQL
HCV_J483	IPLARAAWET	ARHTPVNSWL	GNI IMYAPAL	WARMILMT HF		FSILLAQEQL
HCV_J8	TPITRAAWET	VRHSPVNSWL	GNI IQYAPT I	WVRMVIMT HF		FSILLAQDTL
HCV_JK1	TPLARAAWET	ARHTPVNSWL	GNI IMYAPT L	WARMILMT HF		FSILLAQEQL
HCV_JS	TPIARAAWET	ARHTPVNSWL	GNI IMYAPT L	WARMILMT HF		FSILLAQEQL
HCV_K1_R1	TPLARAAWET	AKSTPVNSWL	GNI IMFAPT L	WVRMILMT HF		FSILLAQEQL
HCV_K1_R2	TPLARAAWET	ARHTPVNSWL	GNI IMYAPT L	WARMILMT HF		FSILLAQEQL
HCV_K1_R3	TPLARAAWET	ARHTPVNSWL	GNI IMYGPT L	WARMILMT HF		FSNLLAQEYL
HCV_K1_S1	TPLARAAWET	ARSTPVNSWL	GNI IMFAPT L	WVRMILMT HF		FSILLAQEQL
HCV_K1_S2	TPLARAAWET	ARHTPVNSWL	GNI IMYAPT L	WARMILMT HF		FSILLAQEQL
HCV_K1_S3	TPLARAAWET	ARHTPVNSWL	GNI IMYGPT L	WARMILMT HF		FSNLLAQEYL
HCV_L2	TPLARAAWET	ARHTPVNSWL	GNI IMYAPT L	WARMILMT HF		FSILLAQEQL
HCV_N	TPIARAAWET	ARHTPVNSWL	GNI IMYAPT L	WARMILMT HF		FSILLAQEQL
HCV12083	TPLARAAWET	ARHTPVNSWL	GNI IMFAPT I	WVRMVLMT HF		FSILQSQEQL
HCV1480	VPLAKAAWET	AKHSPVNSWL	GNI IMYAPT L	WARIVLMT HF		FSVLQSQEQL
HCVPOLYP	TPLARAAWET	ARHTPVNSWL	GNI IMYAPT L	WARMILMT HF		FSILLAQEQL
HD_1	TPLARAAWET	ARHTSVNSWL	GNI IMYAPT L	WARMILMT HF		FSILLAQEQL
HPCCGAA	TPLARAAWET	ARHTPVNSWL	GNI IMFAPT L	WARMILMT HF		FSVLIARDQL
HPCFG	TPLARAAWET	ARHTPVNSWL	GNI IMFAPT I	WVRMVLIT HF		FSILQAQEQL
HPCGENANTI	TPLARAAWAT	ARHTPVNSWL	GNI IMYAPT L	WARMILMT HF		FSILLAQEQL
HPCGENOM	IPLARAAWET	ARHTPVNSWL	GNI IMYAPT L	WARMILMT HF		FSILLAQEQL
HPCHUMR	TPLARAAWET	ARHTPVNSWL	GNI IMYAPT L	WARMILMT HF		FSILLAQEQL
HPCJ	TPLARAAWET	ARHTPVNSWL	GNI IMYAPT L	WARMILMT HF		FSILLAQEQL
HPCJCG	TPLARAAWET	VRHTPVNSWL	GNI IMYAPT L	WARMILMT HF		FSILLAQEQL
HPCJK046	NVLARAAWET	ARHTPVNSWL	GNI IMYAPT I	WVRMVLMT HF		FGILQPQEQL
HPCJK049	TPLARAAWET	ARHTPVNSWL	GNI IMYAPT I	WVRMVIMT HF		FSILQAQEQL
HPCJTA	TPLARAAWET	ARHTPVNSWL	GNI IMYAPT L	WARMILMT HF		FSILLAQEQL
HPCJTB	TPLARAAWET	ARHTPVNSWL	GNI IMYAPT L	WARMILMT HF		FSILLAQEQL
HPCK3A	TPLARAAWET	ARHTPVNSWL	GSIMYAPT I	WVRMVMMT HF		FSILQSQEIL
HPCPLYPRE	TPLARAAWET	ARHTPVNSWL	GNI IMFAPT L	WARMILMT HF		FSVLIARDQL
HPCPOLP	TPIARAAWET	VRHSPVNSWL	GNI IQYAPT I	WARMVLMT HF		FSILMAQDTL
HPCPP	TPLARAAWET	ARHTPVNSWL	GNI IMYAPT L	WARMILMT HF		FSILLAQEQL

HPCUNKCD	TPLARAAWET	ARHTPVNSWL	GNIIMYAPTL	WARMILMTHF	FSILLAQEQ
MKC1A	TPLARAAWET	ARHTPVNSWL	GNIIMYAPTL	WARMILMTHF	FSILLAQEQ
NDM59	TPLSRAAWET	VRHSPVNSWL	GNI IQYAPTI	WVRMVLMTFH	FSILMAQDTL
NZLI	TPLARAAWET	ARHTPVNSWL	GNIIMYAPTI	WVRMVMTHF	FSILQSQEIL
SA13	VPLARAAWET	AKHSPVNSWL	GNIIMYAPTL	WARIVLMTFH	FSVLQSQEIL
Th580	TPLARAAWET	ARHTPVNSWL	GNIIMYAPTI	WVRMVLMTFH	FSILQCQEIL
Type_3a_CB	TPLARAAWET	ARHTPVNSWL	GNIIMYAPTI	WVRMVMTHF	FSILQSQEIL
TypeV_D	TPLARAAWET	ARHTPVNSWL	GNIIMYAPTI	WVRMVMTHF	FSILQSQEIL
VN004	TPLARAAWET	ARHTPVNSWL	GNIIMYAPTI	WVRMVLMTFH	FQILQAQETL
VN235	TPLSRAAWET	ARHTPVNSWL	GNIIMYAPTI	WVRMVLMTFH	FAILQSQEIL
VN405	TPLSRAAWET	ARHTPVNSWL	GNIIMYAPAI	WVRMVLMTFH	FQILQAQEQ

	2901				2950
BEBE1	DQDLNFEMYG	AVYSVSPLDL	PAIERLHGL	EAFLSHSYSP	HELTRVAAAL
D89815	EKALDCQIYG	ATYSIEPLDL	PQIIQRLHGL	SAFLSHSYSP	GEINRVASCL
ED43type_4	EKALDFDMYG	VTYSITPLDL	PAIIQRLHGL	SAFTLHGYS	HELN RVAGAL
HC_C2	EKALECQIYG	ACYSIEPLDL	PQIIERLHGL	SAFLSHSYSP	GEINRVASCL
HC_G9	EKALDCEIYG	AVHSVQPLDL	PEIIQRLHGL	SAFLSHSYSP	GEINRVAACL
HCU16326	EKTLDCQIYG	ACYSIEPLDL	PQIIERLHGL	SAFLSHSYSP	GEINRVASCL
HCV_H_CMR	EQALNCEIYA	ACYSIEPLDL	PPIIQRLHGL	SAFLSHSYSP	GEVNRVAACL
HCV_J1	EQALDCEIYG	ACYSIEPLDL	PPIIQRLHGL	SAFLSHSYSP	GEINRVAACL
HCV_J483	EQALDCQIYG	ACYSIEPLDL	PQIIERLHGL	SAFLSHSYSP	GEINRVASCL
HCV_J8	NQNLNFEMYG	AVYSVNPLDL	PAIERLHGL	EAFLSHSYSP	HEL SRVAATL
HCV_JK1	EKALGCQIYG	ATYFIEPLDL	PQIIQRLHGL	SAFLSHSYSP	GEINRVASCL
HCV_JS	EKALDCQIYG	ACYSIEPLDL	PQIIERLHGL	SAFLSHSYSP	GEINRVASCL
HCV_K1_R1	EKALDCQIYG	ACYSIEPLDL	PQIIQRLHGL	SAFLSHSYSP	GEINRVASCL
HCV_K1_R2	EKALDCQIYG	ACYSIEPLDL	PQIIQRLHGL	SAFLSHSYSP	GEINRVASCL
HCV_K1_R3	DKALDCQIYE	AIYSIGPLDL	PQVIQRLHGL	SAFLSHSYSP	GEINRVASCL
HCV_K1_S1	EKALDCQIYG	ACYSIEPLDL	PQIIQRLHGL	SAFLSHSYSP	GEINRVASCL
HCV_K1_S2	EKALDCQIYG	ACYSIEPLDL	PQIIQRLHGL	SAFLSHSYSP	GEINRVASCL
HCV_K1_S3	DKALDCQIYE	AIYSIGPLDL	PQVIQRLHGL	SAFLSHSYSP	GEINRVASCL
HCV_L2	EKALECQIYG	ACYSIEPLDL	PQIIERLHGL	SAFLSHSYSP	GEINRVASCL
HCV_N	EKALDCQIYG	ACYSIEPLDL	PQIIERLHGL	SAFLSHSYSP	GEINRVASCL
HCV12083	EKALDFDIYG	VTYSVSPLDL	PAIIQRLHGM	AAFLSHGYS	VELNRVGACL
HCV1480	EKTLAFEMYG	SVYSVTPLDL	PAIIQRLHGL	SAFLSHSYSP	SEINRVASCL
HCVPOLYP	EKALDCQIYG	ACYSIEPLDL	PQIIQRLHGL	SAFLSHSYSP	GEINRVASCL
HD_1	EKALDCQIYG	ACYSIEPLDL	PQIIQRLHGL	SAFLSHSYSP	GEINRVASCL
HPCCGAA	EQALNCEIYG	ACYSIEPLDL	PPIIQRLHGL	SAFLSHSYSP	GEINRVAACL
HPCFG	ERALDFEMYG	ATYSVTPLDL	PAIERLHGL	SAFLSHGYS	TELNRVAGAL
HPCGENANTI	EKALDCQIYG	ACYSIEPLDL	PQIIERLHGL	SAFLSHSYSP	GEINRVASCL
HPCGENOM	EKALDCQIYG	AYYSIEPLDL	PQIIERLHGL	SAFLSHSYSP	GEINRVASCL
HPCHUMR	EKALDCQIYG	ACYSIEPLDL	PQIIERLHGL	SAFLSHSYSP	GEINRVASCL
HPCJ	GKALDCQIYG	ACYSIEPLDL	PQIIERLHGL	SAFLSHSYSP	GEINRVASCL
HPCJCG	EKALDCQIYG	ACYSIEPLDL	PQIIERLHGL	SAFLSHSYSP	GEINRVASCL
HPCJK046	HKALDFDMYG	VTYNITPLDL	PQIIQRLHGM	AAFLSHGYS	GELNRVGACL
HPCJK049	EKALDFEMYG	AVYSVTPLDL	PAIERLHGL	SAFLSHSYSP	VELNRVAGAL
HPCJTA	EKALDCQIYG	ACYSIEPLDL	PQIIQRLHGL	SAFLSHSYSP	GEINRVASCL
HPCJTB	EKALDCQIYG	ACYSIEPLDL	PQIIQRLHGL	SAFLSHSYSP	GEINRVASSL
HPCK3A	DRPLDFEMYG	ATYSVTPLDL	PAIERLHGL	SAFSVHSYSP	VELNRVAGTL
HPCPLYPRE	EQALDCEIYG	ACYSIEPLDL	PPIIQRLHGL	SAFLSHSYSP	GEINRVAACL
HPCPOLP	DQNLNFEMYG	AVYSVSPLDL	PAIERLHGL	DAFLSHYTYP	HELTRVASAL
HPCPP	EKALDCQIYG	ATYSIEPLDL	PQIIQRLHGL	SAFLSHSYSP	GEINRVASCL
HPCUNKCD	EKTLDCQIYG	ACYSIEPLDL	PQIIERLHGL	SAFLSHSYSP	GEINRVASCL
MKC1A	EKALDCQIYG	ATYSIEPLDL	PQIIQRLHGL	SAFLSHSYSP	GEINRVASCL
NDM59	DQNLNFEMYG	XVYSVSPLDL	PAIERLHGL	DAFLSHYTYP	HELTRVASAL
NZLI	DRPLDFEMYG	ATYSVTPLDL	PAIERLHGL	SAFTLHSYSP	VELNRVAGTL
SA13	EKALAFEMYG	SVYSVTPLDL	PAIIQRLHGL	SAFTLHSYSP	SEINRVSSCL
Th580	EAALNFDMYG	VTYSVTPLDL	PAIIQRLHGM	AAFLSHGYS	TELNRVGASL
Type_3a_CB	DRPLDFEMYG	ATYSVTPLDL	PAIERLHGL	SAFTLHSYSP	VELNRVAGTL
TypeV_D	DRPLDFEMYG	ATYSVTPLDL	PAIERLHGL	SAFTLHSYSP	VELNRVAGTL

VN004	DRALDFDIYG	VTYSITPLDL	PVIIQRLHGM	AAFSLHGYS	DELNRVASCL
VN235	HKALDFDMYG	VTYSVTPLDL	PYIIQRLHGM	AAFSLHGYS	GELNRVASCL
VN405	DKVLDFDMYG	VTYSVSPLQL	PAIIQRLHGM	AAFSLHGYS	TELNRVGACL
			2951	3000	
BEBE1	RKLGAPPLRA	WKSRAVRA	SLISRGGSAA	TCGRYLFNWA	VRTKLKLTPL
D89815	RKLGVPPLRV	WRHRARSVRA	KLLSQGGRAA	TCGKYLFNWA	VTKLKLTP
ED43type_4	RKLGVPPLRA	WRHRARAVRA	KLIAQGGRAK	ICGIYLFNWA	VTKLKLTP
HC_C2	RKLGVPPLRV	WRHRARSVRA	KLLSQGGRAA	TCGKYLFNWA	VRTKLKLTPI
HC_G9	RKLGVPPLRA	WRHRARSVRA	TLLSQGGRAA	ICGKYLFNWA	VTKLKLTP
HCU16326	RKLGVPPLRA	WRHRARSVRA	KLLSQGGRAA	TCGKYLFNWA	VRTKLKLTPI
HCV_H_CM	RKLGVPPLRA	WRHRARSVRA	RLLSRGGRAA	ICGKYLFNWA	VRTKLKLTPI
HCV_J1	RKLGVPPLRA	WRHRARSVRA	RLLSRGGRAA	ICGKYLFNWA	VRTKLKLTPI
HCV_J483	RKLGVPPLRV	WRHRARSVRA	KLLSQGGRAA	TCGRYLFNWA	VRTKLKLTPI
HCV_J8	RKLGAPPLRA	WKSRAVRA	SLIAQGARA	ICGRYLFNWA	VTKLKLTP
HCV_JK1	RKLGVPPLRV	WRHRARSVRA	KLLSQGGRAA	TCGKYLFNWA	VRTKLKLTPI
HCV_JS	RKLGVPPLRV	WRHRARSVRA	KLLSQGGRAA	TCGKYLFNWA	VRTKLKLTPI
HCV_K1_R1	RKLGVPPLRT	WRHRARSVRA	KLLSQGGRAA	TCGRYLFNWA	VTKLKLTP
HCV_K1_R2	RKLGVPPLRV	WRHRARSVRA	KLLSQGGRAA	ICGKYLFNWA	VRTKLKLTPI
HCV_K1_R3	RKLGVPPLRV	WRHRARSVRA	KLLSQGGRAA	TCGKYLFNWA	VTKLKLTP
HCV_K1_S1	RKLGVPPLRT	WRHRARSVRA	KLLSQGGRAA	TCGRYLFNWA	VTKLKLTP
HCV_K1_S2	RKLGVPPLRV	WRHRARSVRA	KLLSQGGRAA	ICGKYLFNWA	VRTKLKLTPI
HCV_K1_S3	RKLGVPPLRV	WRHRARSVRA	KLLSQGGRAA	TCGKYLFNWA	VTKLKLTP
HCV_L2	RKLGVPPLRV	WRHRARSVRA	KLLSQGGRAA	TCGKYLFNWA	VRTKLKLTPI
HCV_N	RKLGVPPLRV	WRHRARSVRA	KLLSQGGRAA	TCGKYLFNWA	VTKLKLTP
HCV12083	RKLGVLPSRA	WRHRARAVRA	KLIAQGGKAA	ICGKYLFNWA	VTKLKLTP
HCV1480	RKLGVPPLRA	WRHRARAVRA	KLIAQGGRAA	ICGIYLFNWA	VTKRKLTP
HCVPOLYP	RKLGVPPLRA	WRHRARSVRA	KLLSQGGRAA	TCGRYLFNWA	VTKLKLTP
HD_1	RKLGVPPLRV	WRHRARSVRA	KLLSPGGEGS	TCGKYLFNWA	VRTKLKLTPI
HPCCGAA	RKLGVPPLRA	WRHRARSVRA	RLLARGGKAA	ICGKYLFNWA	VRTKLKLTPI
HPCFG	RKLGIPPLRA	WRHRARAVRA	KLIAQGGKAR	ICGLYLFNWA	VRTKLKLTPI
HPCGENANT	RKLGVPPLRA	WRHRARSVRA	KLLSQGGRAA	TCGRYLFNWA	VTKLKLTP
HPCGENOM	RKLGVPPLRV	WRHRARSVRA	KLLSQGGRAA	TCGKYLFNWA	VTKLKLTP
HPCHUMR	RKLGVPPLRV	WRHRARSVRA	RLLSQGGRAA	TCGKYLFNWA	VTKLKLTP
HPCJ	RKLGVPPLRV	WRHRARSVRA	KLLSQGGRAA	TCGKYLFNWA	VRTKLKLTPI
HPCJCG	RKLGVPPLRV	WRHRARSVRA	KLLSQGGRAA	TCGKYLFNWA	VTKLKLTP
HPCJK046	RKLGAPPLRA	WRHRARAVRA	KLIAQGGKAA	ICGMYLFNWA	VTKLKLTP
HPCJK049	RKLGIPPLRA	WRHRARAVRA	KLISQGGKAK	ICGLYLFNWA	VRTKAKLTPL
HPCJTA	RKLGVPPLRV	WRHRARSVRA	RLLSQGGRAA	TCGKYLFNWA	VRTKLKLTPI
HPCJTB	RKLGVPPLRV	WRHRARSVRA	RLLSQGGRAA	TCGKYLFNWA	VRTKLKLTPI
HPCK3A	RKLGCPPLRA	WRHRARAVRA	KLIAQGGRAK	ICGLYLFNWA	VRTKLKLTPI
HPCPLYPRE	RKLGVPPLRA	WRHRARSVRA	RLLARGGRAA	ICGKYLFNWA	VTKLKLTP
HPCPOLP	RKLGAPPLRA	WKSRAVRA	SLISRGGSAA	VCGRYLFNWA	VTKLKLTP
HPCPP	RKLGVPPLRV	WRHRARSVRA	KLLSQGGRAA	TCGKYLFNWA	VTKLKLTP
HPCUNKCD	RKLGVPPLRA	WRHRARSVRA	KLLSQGGRAA	TCGKYLFNWA	VRTKLKLTPI
MKC1A	RKLGVPPLRV	WRHRARSVRA	KLLSQGGRAA	TCGKYLFNWA	VTKLKLTP
NDM59	RKLGAPPLRA	WKSRAVRA	SLISRGGSAA	ICGRYLFNWA	VTKLKLTP
NZLI	RKLGCPPLRA	WRHRARAVRA	KLIAQGGKAK	ICGLYLFNWA	VRTKTNLTP
SA13	RKLGVPPLRA	WRHRARAVRA	KLIAQGGKAA	ICGIYLFNWA	VTKRKLTP
Th580	RKLGAPPLRA	WRHRARAVRA	KLIAQGGKAA	ICGKYLFNWA	VTKLKLTP
Type_3a_CB	RKLGCPPLRA	WRHRARAGRA	KLIAQGGKAK	ICGLYLFNWA	VRTKLKLTPI
TypeV_D	RKLGCPPLRA	WRHRARAVRA	KLIAQGGKAK	ICGLYLFNWA	VRTKTNLTP
VN004	RKLGAPPLRA	WRHRARAVRA	KLIAQGGKAA	VCGKYLFNWA	IKTKLRLTP
VN235	RKLGAPPLRA	WRHRARAVRA	KLIAQGGKHA	ICGKYLFNWA	VRTKLKLTPI
VN405	RKLGAPPLRA	WRHRARAVRA	KLIAQGGGAA	ICGKYLFNWA	VTKLKLTP
			3001	3050	
BEBE1	PAARLLDLSS	WFTVSAGGGD	IYHSVSRARP	RLLLLGLLLL	CVGVGIFLLP
D89815	PEASQLDLSS	WFWAGYSGGD	IYHSLSRARP	RWFMCCLLLL	SVGVGIYLLP
ED43type_4	PAAAKLDLSS	WFTVGAGGGD	IYHSMHARP	RYLLLCCLLL	TVGVGIFLLP

HC_C2	PAASRLDL	SG	W	F	V	A	G	Y	G	G	D	I	Y	H	S	L	S	R	A	R	P	R	W	F	M	L	C	L	L	L	L	S	V	G	V	G	I	Y	L	L	P	
HC_G9	PSASQLDL	SN	W	F	T	G	G	Y	S	G	G	I	Y	H	S	V	S	H	V	R	P	R	W	F	F	W	C	L	L	L	L	L	S	V	G	V	G	I	Y	L	L	P
HCU16326	PAASRLDL	SG	W	F	V	A	G	Y	S	G	G	I	Y	H	S	L	S	R	A	R	P	R	W	F	M	L	C	L	L	L	L	L	S	V	G	V	G	I	Y	L	L	P
HCV_H_CM	AAAGRLDL	SG	W	F	T	A	G	Y	S	G	G	I	Y	H	S	V	S	H	A	R	P	R	W	F	W	F	C	L	L	L	L	L	A	A	G	V	G	I	Y	L	L	P
HCV_J1	AAAGRLDL	SG	W	F	T	A	G	Y	S	G	G	I	Y	H	S	V	S	H	A	R	P	R	W	F	W	F	C	L	L	L	L	L	A	A	G	V	G	I	Y	L	L	P
HCV_J483	PAASQLDL	SG	W	F	V	A	G	Y	S	G	G	I	Y	H	S	L	S	R	A	R	P	R	W	F	L	L	C	L	L	L	L	L	S	V	G	V	G	I	Y	L	L	P
HCV_J8	PEASRLDL	SG	W	F	T	V	G	A	G	G	G	I	Y	H	S	V	S	H	A	R	P	R	R	L	L	L	L	C	L	L	L	L	S	V	G	V	G	I	F	L	L	P
HCV_JK1	PAASQLDL	SG	W	F	V	A	G	Y	S	G	G	I	Y	H	S	L	S	R	A	R	P	R	W	F	M	W	C	L	L	L	L	L	S	V	G	V	G	I	Y	L	L	P
HCV_JS	PAASRLDL	SG	W	F	V	A	G	Y	S	G	G	I	Y	H	S	L	S	R	A	R	P	R	W	F	M	W	C	L	L	L	L	L	S	V	G	V	G	I	Y	L	L	P
HCV_K1_R1	PAASQLDL	SN	W	F	V	A	G	Y	S	G	G	I	Y	H	S	L	S	R	A	R	P	R	W	F	M	L	C	L	L	L	L	L	S	V	G	V	G	I	Y	L	L	P
HCV_K1_R2	PAASQLDL	SG	W	F	V	A	G	Y	S	G	G	I	Y	H	S	V	S	R	A	R	P	R	W	F	M	W	C	L	L	L	L	L	S	V	G	V	G	I	Y	L	L	P
HCV_K1_R3	PAASQLDL	SS	W	F	V	A	G	Y	S	G	G	I	Y	H	S	L	S	R	A	R	P	R	W	F	M	W	C	L	L	L	L	L	S	V	G	V	G	I	Y	L	L	P
HCV_K1_S1	PAASQLDL	SN	W	F	V	A	G	Y	S	G	G	I	Y	H	S	L	S	R	A	R	P	R	W	F	M	L	C	L	L	L	L	L	S	V	G	V	G	I	Y	L	L	P
HCV_K1_S2	PAASQLDL	SG	W	F	V	A	G	Y	S	G	G	I	Y	H	S	V	S	R	A	R	P	R	W	F	M	W	C	L	L	L	L	L	S	V	G	V	G	I	Y	L	L	P
HCV_K1_S3	PAASQLDL	SS	W	F	V	A	G	Y	S	G	G	I	Y	H	S	L	S	R	A	R	P	R	W	F	M	W	C	L	L	L	L	L	S	V	G	V	G	I	Y	L	L	P
HCV_L2	PAASRLDL	SS	W	F	V	A	G	Y	S	G	G	I	Y	H	S	V	S	H	A	R	P	R	W	F	M	L	C	L	L	L	L	L	S	V	G	V	G	I	Y	L	L	P
HCV_N	PAASQLDL	SG	W	F	V	A	G	Y	S	G	G	I	Y	H	S	L	S	R	A	R	P	R	W	F	M	L	C	L	L	L	L	L	S	V	G	V	G	I	Y	L	L	P
HCV12083	VSASKLDL	SG	W	F	V	A	G	Y	D	G	G	I	Y	H	S	V	S	Q	A	R	P	R	R	F	L	L	L	G	L	L	L	L	T	V	G	V	G	I	F	L	L	P
HCV1480	ADADRLDL	SS	W	F	T	V	G	A	G	G	G	I	Y	H	S	M	S	R	A	R	P	R	R	N	L	L	L	C	L	L	L	L	S	V	G	V	G	I	F	L	L	P
HCVPOLYP	PAASQLDL	SN	W	F	V	A	G	Y	S	G	G	I	Y	H	S	L	S	R	A	R	P	R	W	F	M	W	C	L	L	L	L	L	S	V	G	V	G	I	Y	L	L	P
HD_1	PAAFQLDL	SG	W	F	V	A	G	Y	S	G	G	I	Y	H	S	L	S	R	A	R	P	R	W	F	M	W	C	L	L	L	L	L	S	V	G	V	G	I	Y	L	L	P
HPCCGAA	TAAGRLDL	SG	W	F	T	A	G	Y	S	G	G	I	Y	H	S	V	S	H	A	R	P	R	W	F	W	F	C	L	L	L	L	L	A	A	G	V	G	I	Y	L	L	P
HPCFG	PTAGQLDL	SS	W	F	T	V	G	V	G	G	N	I	Y	H	S	V	S	R	A	R	T	R	R	H	L	L	L	C	L	L	L	L	T	V	G	V	G	I	F	L	L	P
HPCGENANTI	PAASQLDL	SK	W	F	V	A	G	Y	G	G	G	I	Y	H	S	L	S	R	A	R	P	R	W	F	M	L	C	L	L	L	L	L	S	V	G	V	G	I	Y	L	L	P
HPCGENOM	PAASRLDL	SG	W	F	V	A	G	Y	S	G	G	I	Y	H	S	L	S	R	A	R	P	R	W	F	M	L	C	L	L	L	L	L	S	V	G	V	G	I	Y	L	L	P
HPCHUMR	PAASRLDL	SG	W	F	V	A	G	Y	S	G	G	I	Y	H	S	L	S	R	A	R	P	R	W	F	M	L	C	L	L	L	L	L	S	V	G	V	G	I	Y	L	L	P
HPCJ	PAASQLDL	SS	W	F	V	A	G	Y	S	G	G	I	Y	H	S	L	S	R	A	R	P	R	W	F	M	L	C	L	L	L	L	L	S	V	G	V	G	V	Y	L	L	P
HPCJCG	PAASQLDL	SG	W	F	V	A	G	Y	N	G	G	I	Y	H	S	L	S	R	A	R	P	R	W	F	M	L	C	L	L	L	L	L	S	V	G	V	G	I	Y	L	L	P
HPCJK046	RDAHRLDL	SG	W	F	V	A	G	Y	S	G	G	I	F	H	S	V	S	H	A	R	P	R	R	V	L	L	L	C	L	L	L	L	T	V	G	V	G	I	F	L	L	P
HPCJK049	PQAGLLDL	SR	W	F	T	V	G	A	G	G	N	I	Y	H	S	V	S	R	A	R	S	R	R	H	L	L	L	G	L	L	L	L	T	V	G	V	G	I	F	L	L	P
HPCJTA	PAASQLDL	SS	W	F	V	A	G	Y	S	G	G	I	Y	H	S	L	S	R	A	R	P	R	W	F	M	W	C	L	L	L	L	L	S	V	G	V	G	I	Y	L	L	P
HPCJTB	PAASQLDL	SS	W	F	V	A	G	Y	S	G	G	I	Y	H	S	L	S	R	A	R	P	R	W	F	M	W	C	L	L	L	L	L	S	V	G	V	G	I	Y	L	L	P
HPCK3A	PAAGQLDL	SS	W	F	T	V	G	V	G	G	N	I	Y	H	S	V	S	R	A	R	T	R	R	Y	L	L	L	C	L	L	L	L	T	V	G	V	G	I	F	L	L	P
HPCPLYPRE	AAAGQLDL	SG	W	F	T	A	G	Y	S	G	G	I	Y	H	S	V	S	H	A	R	P	R	R	W	I	W	F	C	L	L	L	L	A	A	G	V	G	I	Y	L	L	P
HPCPOLP	PEARLLDL	SS	W	F	T	V	G	A	G	G	G	I	Y	H	S	V	S	R	A	R	P	R	R	L	L	L	L	G	L	L	L	L	F	V	G	V	G	L	F	L	L	P
HPCPP	PEASQLDL	SG	W	F	V	A	G	Y	S	G	G	I	Y	H	S	L	S	R	A	R	P	R	W	F	M	W	C	L	L	L	L	L	S	V	G	V	G	I	Y	L	L	P
HPCUNKCD	PAASRLDL	SG	W	F	V	A	G	Y	S	G	G	I	Y	H	S	L	S	R	A	R	P	R	W	F	M	L	C	L	L	L	L	L	S	V	G	V	G	I	Y	L	L	P
MKC1A	PEASQLDL	SG	W	F	V	A	G	Y	S	G	G	I	Y	H	S	L	S	R	A	R	P	R	W	F	M	W	C	L	L	L	L	L	S	V	G	V	G	I	Y	L	L	P
NDM59	PEARLLDL	SS	W	F	T	V	G	A	G	G	G	I	Y	H	S	V	S	R	A	R	P	R	R	L	L	L	L	S	L	L	L	L	L	V	G	V	G	L	F	L	L	P
NZLI	PAAGQLDL	SS	W	F	T	V	G	V	G	G	N	I	Y	H	S	V	S	R	A	R	T	R	R	H	L	L	L	C	L	L	L	L	T	V	G	V	G	I	F	L	L	P
SA13	ADADRLDL	SS	W	F	T	V	G	A	G	G	G	I	Y	H	S	M	S	R	A	R	P	R	R	C	I	L	L	C	L	L	L	L	T	V	G	V	G	I	F	L	L	P
Th580	AAASQLDL	SG	W	F	V	A	G	Y	D	G	G	I	Y	H	S	V	S	R	A	R	P	R	R	L	L	L	L	G	L	L	L	L	T	V	G	V	G	I	F	L	L	P
Type_3a_CB	PRAGQLDL	SI	W	F	T	V	G	V	G	G	N	I	Y	H	S	V	S	R	A	R	T	R	R	Y	L	L	L	C	L	L	L	L	T	V	G	V	G	I	F	L	L	P
TypeV_D	PATGQLDL	SS	W	F	T	V	G	V	G	G	N	I	Y	H	S	V	S	R	A	R	T	R	R	Y	L	L	L	C	L	L	L	L	T	V	G	V	G	I	F	L	L	P
VN004	RGASALDL	SG	W	F	T	S	G	Y	G	G	G	I	V	H	S	A	S	R	A	R	P	R	R	F	L	L	L	C	L	L	L	L	S	V	G	V	G	I	F	L	L	P
VN235	RGAANLDL	SG	W	F	V	S	G	G	S	G	G	I	F	H	S	V	S	R	A	R	P	R	R	N	L	L	L	C	L	L	L	L	T	V	G	V	G	I	F	L	L	P
VN405	PDAARLDL	SG	W	F	I	S	G	F	S	G	G	I	Y	H	S	V	S	R	A	R	P	R	R	I	F	L	L	C	L	L	L	L	S	V	G	V	G	I	F	L	L	P

3051

BEBE1	AR
D89815	NR
ED43type_4	AR
HC_C2	NR
HC_G9	NR
HCU16326	NR
HCV_H_CM	NR
HCV_J1	NR
HCV_J483	NR
HCV_J8	AR
HCV_JK1	NR

HCV_JS	NR
HCV_K1_R1	NR
HCV_K1_R2	NR
HCV_K1_R3	NR
HCV_K1_S1	NR
HCV_K1_S2	NR
HCV_K1_S3	NR
HCV_L2	NR
HCV_N	N.
HCV12083	AR
HCV1480	AR
HCVPOLYP	NR
HD_1	NR
HPCCGAA	NR
HPCFG	AR
HPCGENANTI	NR
HPCGENOM	NR
HPCHUMR	NR
HPCJ	NR
HPCJCG	NR
HPCJK046	PR
HPCJK049	AR
HPCJTA	NR
HPCJTB	NR
HPCK3A	AR
HPCPLYPRE	NR
HPCPOLP	AR
HPCPP	NR
HPCUNKCD	NR
MKC1A	NR
NDM59	AR
NZLI	AR
SA13	AR
Th580	AR
Type_3a_CB	AR
TypeV_D	AR
VN004	AR
VN235	AR
VN405	AR



Table 23. HIV Fusion Construct

(SEQ ID NO: 1934)

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCCGGATCCAGA  
GGAAAGCTGGTGGGCAAACCTCAACTGGGCCGGAGCTGCAATCCTGAAGGAGCCCGTCCACGG  
GGTGAATGCCGCTTGCCCTAAAGTCAGCTTCGAACCAATTAAGATCCCCATTCTACTGTGC  
ACCTGCCAAAGCTAAGTTTGTGGCCGCTTGGACCCCTCAAGGCCGCTGCAAAAGCCTTCCCAGT  
GAGGCCCCAGGTGCCTCTGGGCGCCGCTAAACTCACACCACTGTGCGTCACTCTGGGAGCCGC  
TGCAGTGCTGGCAGAGGCCATGTCCCAAGTGAAGGTGTATCTGGCTTGGGTGCCCCGCCACAA  
GGGGGCCGCTGCAGCCATCTTTCAGTCTAGCATGACCAAGAAAACAACCTCTGTTCTGTGCCTC  
CGACGCTAAGAACATCCCTTATAATCCACAGTCTCAGGGCGTGGTCAAGCATCCCGTGCACGC  
CGGACCTATTGCTAACGTGACCGTGTACTATGGGGTCCCAGTGTGGAAGAAAGCCGCTGCACA  
GATGGCCGTGTTTATTCACAATTTCAAAAACGCCGCTGCATACCCCCTCGCCAGCCTGAGATC  
CCTCTTCAACCTGACATTTCGGCTGGTGCTTTAAGCTGAACCGGATCCTGCAGCAACTGCTCTTT  
ATCAATGCTAAAATCCAGAACTTCCGCGTCTACTATAGGAAGGCTGCAGTGACTATCAAAATT  
GGCGGACAACTGAAGAAAGTGCCTCTCCAGCTGCCCCCTCTCAAGGCAATGACCAACAATCC  
CCCTATCCCAGTCTGA

EP-HIV-1090 (SEQ ID NO: 1935)

MGMQVQIQSLFLLLLWVPGSRGKLVGKLNWAGAAILKEPVHGVNAACPKVSFEPIKIPHYCAPA  
KAKFVAAWTLKAAAKAFPVRPQVPLGAAKLTPLCVTLGAAAVLAEAMSQVKVYLAWVPAHKG  
AAAAIFQSSMTKKTTLFCASDAKNIPYNPQSQGVVKHVPVHAGPIANVTVYYGVPVWKKAAAQMA  
VFIHNFKNAAA YPLASLRSLFNLTFGWCFKLNRIQLQLFINAKIQNFRVYYRKA AVTIKIGGQLKK  
VPLQLPPLKAMTNNPPIPV

**Table 24. HBV GCR-3697 Fusion Construct**

<p>GCR-3697</p> <p>SEQ ID NO: [[<u>  </u>]] <u>1936</u></p>	<p><i>Polynucleotide</i></p> <p>1 Start ↑***</p> <p><u>ATG</u>GGCATGCAGGTGCAGATCCAGAGCCTGTTCTGCTCCTGCTGTGGGTGCCAGGAAGCAGAGGCTTTCTC CTGTCCCCTGGGCATCCACCTGAACGCCGCTGCAAAGTACACCAGCTTCCCCTGGCTGCTCAACGCCCGCTGCC CGGTTTCAGCTGGCTGTCCCTGCTCGTGCCCTTCAACGCAGCCTTCCCCACTGCCTTTCAGCTACATGA AAGCAGCCCTGGTGGTGCAGTTCTCCAGTTTCAGCCGGGGAGCCATCCTGCTCCTGTGCCTGATCTTTCTGCT CAACGCCCGCTGCCCACACCCTGTGGAAGGCTGGCATCCTGTACAAGAAAGCCTGGATGATGTGGTACTGGG GACCCAGCCTGTACAAGGCATATCCAGCCCTGATGCCCCCTGTACGCCCTGCATCGGAGCTGCCGCATGGCTGA GCCTCCTGGTGGCCTTCGTGAACGCCGCTGCCGGGTTCTGCTGACAAGAATCCTGACCATCAACGCCGCAG CCATTCTATCCCCCTCCAGCTGGGCCCTCAAGGCAGCCGCCGAGTACCTGGTGAGCTTCGGAGTCTGGAACC TGCCCAGCGACTTCTTTCCCAGCGTGAAAGCCGACGCTTCTGCCCTCCGACTTCTTTCCCAGCGTGAAGGC CGCAGCCGATCTCCTGGACACCGCTAGCGCCCTGTACAACAGCTGGCCCAAGTTCGCCGTGCCCAACCTGAA GGCCGAGCCAGCGCCATCTGCAGCGTGGTCAGACGGAAGCTGTCCCTCGATGTGAGCGCCGCTTTCTACAA CGCCGCCGCAAAGTTCGTGGCCGCTGGACCTGAAAGCCGCTGCCAAGGCAGCCAACGTGAGCATCCCCCT GGACCCACAAAGGAGCCGAGGACTGAGCCGCTGTGAGCCAGACTGAAAGCCGCTGCCAAGGCAGCCAACGTGAGCATCCCCCT GAGACCAGTGGTCAGACGGAAGCACCCCGCCGATGCCACCTGCTGAAGGCCGAGCCCGGTGGAT GTGCCTCAGACGGTTCATCATCAACGCTTCTTCTGTGGCAGCCCTACAAGGCCGCTACATGGATGACGT GGTCTGGGAGTGAACGCCCTCTGGTTCCACATCAGCTGCCTGACCTTCAAAGCCGCTGCCACACCCGCAAG AGTGACCGGAGGCGTGTCAAGGCTGCAGCCCTGACCTTGGCCGCGGAGACCGTGGTGGAGTACAAGCAGG CCTTACCTTCAGCCCCACCTACAAGAAGCCGGCACCAGCTTTGTGTACGTCCCAAGCGCCCTGAATCCCG CAGACGGCCCCGGCCCCGACTGTGCCAGGTGTTGCCGATGCCACACCAACCGGATGGGGCCTGGGCCCT GGACCCGGCAGACACTACCTGCATACCCTGTGGAAGGCAGGAATCCTGTACAAAGGCCCGGCCCTGGACC CCATCACACCGCTCTGCCGAGGCCATCCTGTGCTGGGGCGAGTCTATGACTCTGGCAGGACCCGGCCCCGG CGAATCCAGGCTGGTGGTGGACTTTAGCCAGTTCTCCAGAGGCAACGGACCCGGCCAGGACCTTCTGTGCT CGCCAGTTACACAGCCATCTGCAGCGTGGTGGGACCTGGCCAGGACTGGTGCCCTTCGTGCAGTGGTT CGTGGCCTCAGCCCCACCGTCGGACCTGGCCCCGGCCTGCACCTTACAGCCACCTATCATTCTGGGCTT CAGAAAGATCGGACCAGGCCCGGCTCCAGCAACCTGTCTGGCTCAGCCTGGACGTGAGCGCAGCCTTCG GACCCGGCCCTGGCCTGCAGAGCCTGACCAACCTGTCTCAGCAGCAACCTCAGCTGGCTGGGCCAGGACCC GGCGCAGGCTTCTTCTGCTCACCAGAATCCTGACCATCCCTCAGAGCGGCCCGGACCAGGCGTGAGCTTC GGCGTGTGGATTTCGACTCCTCCCGCTACAGACCCCAATGCCCCATCGGCCAGGACCCGGCGTCGGA CCTCTGACTGTGAACGAGAAGCGGAGACTGAAGCTGATCGGCCCGGACCAGGCAACAGTGCTTCAGGAA GCTCCCTGTGAACAGACCTATCGACTGGGGCCCCGACCCGGCGCAGCCAACCTGGATTCTGAGAGGCACCA GCTTCGTGTACGTCCCTGGACCCGGCCCTGGCAAGCAAGCCTTACCTTACGCCCCACCTACAAGGCATTCC TGTGCGGA<u>TAG</u></p> <p>↓ Stop 2232</p>
<p>GCR-3697</p> <p>SEQ ID NO: [[<u>  </u>]] <u>1937</u></p>	<p><i>Polypeptide</i></p> <p>1 ↑</p> <p>MGMQVQIQSLFLLLLWVPGSRGFLLSLGIHLNAAAKYTSFPWLLNAAARFWSLSLLVPFNAAFPHCLAFSYMKA ALVVDIFSQFSRGAILLLCLIFLLNAAHTLWKAGILYKKAWMWYWGPSLYKAYPALMPLYACIGAAAWLSLL VPFVNAAAGFLLTRILTINAAAIPISSWAFKAAAEYLVSFVWNLPSDFPVSVKAAAFPSDFPVSVKAAADLLD TASALYNSWPKFAVPNLKAAASAICSVVRKLSLDVSAAFYNAAAKFVAAWTLKAAAKAANVSIPWTHKGAA GLSRYVARLNAAASTLPETTIVRRKHPAAMPHLLKAAARWMCLRRFIINASFCGSPYKAAAYMDDVVLGVNAL WFHISCLTFKAAATPARVTGGVFKAALTFGRETVLEYKQAFTFSPYKNAGTSFVYVPSALNPADGPGPGLCQ VFADATPTGWGLPGPGRHYLHTLWKAGILYKGP GPHHTALRQAILCWGELMTLAGPGPGESRLVVDIFSQFS RGNGPGPGPFLLAQFTSAICSVVGPGLVPFVQWFGVLSPTVGPGLHLYSHPIILGFRKIGPGGSSNLSWLSL DVSAAFPGPGPGLQSLTNLLSSNLSWLGP GPGAGFFLLTRILTIQSGPGPGVSVFGVWIRTPPAYRPPNAPIGPGPV GPLTVNEKRRLKLIGPGPGKQCFRKLVPNRPIDWGP GPGGAANWILRGTSFVYVPGPGPGKQAFTFSPYKALFCG</p> <p>↓ 744</p>



**Table 25. HBV AOSIb2 Fusion Construct**

<p>HBV AOSIb2</p> <p>SEQ ID NO: [ ] <u>1938</u></p>	<p><i>Polynucleotide</i></p> <p>1 Start ↑ [ATG]GGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCTGTGGGTGCCCGGGTCCAGAGGACACAC CCTGTGGAAGGCCGGAATCCTGTATAAGGCCAAGTTCGTGGCTGCCTGGACCCCTGAAGGCTGCCGCTTTCCT GCCTAGCGATTCTTTCTAGCGTGAACCTCCTGCTGTCCCTGGGAATCCACCTGTATATGGATGACGTGGTG CTGGGAGTGGGACTGTCCAGGTACGTGGCTAGGCTGTTCCTGCTGACCAGAACTCTGACCATCTCCACCCTG CCAGAGACCACCGTGGTGAGGAGGCAGGCCTTCACCTTTAGCCCTACCTATAAGGGAGCCGCTGCCTGGCT GAGCCTGCTGGTGCCCTTTGTGAATATCCCTATCCCTAGCTCCTGGGCTTTCAAGACCCAGCCAGGGTGAC CGGAGGAGTGTTTAAGGTGGGAACTTCACCGGCCTGTATAACCTGCCCAGCGATTCTTTCTAGCGTGAA GACCCTGTGGAAGGCCGGAATCCTGTACAAGAATGTGTCCATCCCTTGGACCCACAAGGGAGCCGCTCTGG TGGTGGACTTTTCCCAGTTCAGCAGAAATCCGCTATCTGCTCCGTGGTGAGGAGAGCTCTGATGCCACTGT ATGCCTGTATC[TGA] ↓ Stop 657</p>
<p>HBV AOSIb2</p> <p>SEQ ID NO: [ ] <u>1939</u></p>	<p><i>Polypeptide</i></p> <p>1 ↑ MGMQVQIQSLFLLLLWVPGSRGHTLWKAGILYKAKFVAAWTLKAAFLPSDFFPSVNFLLSLGIHLYMDDVVL GVGLSRYVARLFLLTRILTISTLPETTVVRRQAFTFSPTYKGAAWLSLLVPFVNIPISSWAFKTPARVTGGVFKV GNFTGLYNLPSDFFPSVKTLWKAGILYKNVSIPWTHKGAALVVDIFSQFSRNSAICSVVRRALMPYACI ↓ 219</p>

**Table 26. HCV Fusion Construct**

HCV 4312(1P) (SEQ ID NO: 1940)

MGMQVQIQSLFLLLLWVPGSRGRLGVRATRKKAAAKTSERSQPRNLPGCSFSIFNDLMGYIPLVK  
YLLPRRGPRNLNLCGFADLMGYRMYVGGVEHRKLLFNILGGWVKAAALADGGCSGGAYRLIVFP  
DLGVKFWAKHMWNFIGVAGALVAFKKQLFTFSPRRNGYLVAYQATVAAALLFLLLADALIFCHS  
KKKYLVRHADVLGFGAYMSKCTCGSSDLYHMWNFISGIFWAKHMWNFKKAAAVLVGGVLAA  
AFLLLADARVLSAFSLHSYILAGYGAGVWMNRLAFANAAKFVAAWTLKAAA

(SEQ ID NO: 1941)

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGG  
GTGCCCCGGCTCCAGAGGAAGGCTGGGCGTGAGAGCCACCCGGAAGAAGGCTGCCGCTAAAAAC  
AAGCGAGCGCTCCCAGCCCAGGAACCTGCCTGGATGCTCTTTCAGCATCTTTAATGACCTCAT  
GGGGTACATTCCACTGGTGAAGTATCTGCTCCCCAGACGGGGCCCTCGCCTGAACACTCTCTG  
TGGATTTGCTGATCTGATGGGGTACAGGATGTATGTCGGCGGAGTCGAACACAGAAAAGTCTGCT  
CTTCAACATCCTGGGCGGATGGGTGAAGGCTGCCGCTCTGGCCGACGGGGGATGCAGCGGCG  
GAGCTTACAGGCTCATTGTCTTTCCCGATCTCGGAGTCAAATTTTGGGCAAAGCACATGTGGA  
ATTTTCATCGGGGTGGCCGGAGCCCTGGTCGCTTTTAAAAAGCAGCTCTTCACCTTCTCCCCAA  
GACGGAACGGATACCTCGTCGCCTACCAGGCCACTGTGGCTGCAGCTCTGCTCTTCCTGCTCC  
TGGCCGATGCACTCATCTTCTGCCATTCCAAGAAAAAGTATCTGGTCACCAGACATGCTGACG  
TGCTGGGGTTTTGGCGCCTACATGAGCAAGTGCACCTGTGGCAGCTCCGACCTGTATCACATGT  
GGAACCTTTATTTCTGGAATCTTTTGGGCCAAGCACATGTGGAATTTTAAGAAAGCCGCTGCAG  
TCCTGGTGGGCGGCGTCCTGGCAGCCGCTTTCCTGCTCCTGGCAGACGCCAGGGTGCTGTCTG  
CCTTCAGCCTCCACTCCTACATCCTCGCAGGGTATGGCGCAGGCGTGTGGATGAATCGGCTGA  
TCGCCTTTGCCAATGCTGCAGCTAAATTCGTGGCAGCCTGGACACTGAAAGCAGCTGCATGAG  
GATCC

**Table 27. *Plasmodium falciparum* Fusion Construct**

Pf33 (SEQ ID NO: 1942)

MGMQVQIQSLFLLLLWVPGSRGRLGVRATRKKAAAKTSERSQPRNLPGCSFSIFNDLMGYIPLVK  
YLLPRRGPRNLNLCGFADLMGYRMYVGGVEHRKLLFNILGGWVKAAALADGGCSGGAYRLIVFP  
DLGVKFWAKHMWNFIGVAGALVAFKKQLFTFSPPRNGYLVAYQATVAAALLFLLLADALIFCHS  
KKKYLVTRHADVLGFGAYMSKCTCGSSDLYHMWNFISGIFWAKHMWNFKKAAAVLVGGVLAA  
AFLLLADARVLSAFSLHSYILAGYGAGVWMNRLAFANAAKFVAAWTLKAAA

(SEQ ID NO: 1943)

GCCGCCACCATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCC  
GGATCCAGAGGATTTATGAAAGCTGTCTGTGTAGAGGTGAATGTAACATGCGGTAACGGAAT  
TCAGGTGAGAAAGGGACTCATCATGGTACTCAGCTTTCTGAACGCAGCCCTGTTCCACATCTT  
TGACGGAGACAATGAAATCAAAGCCGCATTGCTCGCCTGTGCCGGACTAGCCTATAAAAAGA  
GTTTCCTTTTCGTTGAAGCACTATTTAACGCAGCACCCAGTGACGGTAAATGCAACCTATATA  
AAGCAGCTCAGACTAATTTCAAAGCCTGTTAAGAAATCTGCCCTCAGAGAATGAAAGGGGT  
TACAAAGCCGCCGCGGTGTCCGAGAATATTTTCCTGAAGAACGCCGCTGCTTATTTTATACTC  
GTGAATCTACTCATAAAGGCAGCCGCAATCCTTTCAAGGTGCAGCAAAAATACAAGCTTGCCACATCAGTAT  
CATATGCGGGCGAGCCGGCTCCTTTCAAGGCTGCAGCAAAAATACAAGCTTGCCACATCAGTAT  
TGAAAGCAGCTGTGTTTTTGTATATTCTTTGATCTTTTTTTAAACTACTACATACCTCATCAGTCT  
AGTCTTAAAGCAGCCGGGCTACTGGGGAACGTCTCTACTGTGGGGGCCGTCTTACTTGGAGGA  
GTTGGCCTCGTGTTGAACCTCGCGTGCGCAGGTCTGGCCTACAAAAAAGCGAAATTCATCAAG  
TCTCTGTTCCACATTTTTAAAGCCGCATTCTATTTCACTAGTGAACCTTCTCAAAGCTTTCCT  
GATCTTCTTCGATCTATTCCTCGTAAAAGCGCTATTCTTCATTATCTTTAACAAAAATTATTAC  
GGCAAGCAAGAAAATTGGTACTCACTCAAGTTTGTAGAAGCTCTGTTCCAGGAATACAACGCC  
GCTGCTAAATTTCGTTGCAGCTTGGACCCTGAAAGCAGCTGCAAAGATCCTATCGGTCTTCTTTC  
TCGCTAATGCCGTATTAGCAGGACTTCTAGGCAACGTGAACTTTCAAGACGAAGAGAATATAG  
GCATCTACAAAGCCGCAGCACTGTACATTTCACTTCTACTTCATCAAGGCCTTCATACTGGTCAA  
CCTTCTGATATTTTATAATGCAGCACTGCCATATGGGAGAACCAACTTGAAAGCGGCCACGT  
GTTGAGCCACAACCTCCTACGAGAAGAACGCCGCCGCGAAATATCTCGTCATTGTCTTCCTGAT  
TTGA

**Table 28. *Mycobacterium tuberculosis* Fusion Construct**

TB.1 (SEQ ID NO: 1944)

MQVQIQSLFLLLLWVPGSRGRMSRVTTFTVKALVLLMLPVVNL  
MIGTAAAVVKALVLLMLPVGA  
GLMTAVYLVGAAAMALLRLPVKRMFAANLGVNSLYFGGICVGR  
LPLVLPVNA<sup>5</sup>AAAKFVAAWT  
LKAAAKAAARLMIGTAAAGFVVALIPLV<sup>10</sup>NAMTYAAPLFV  
GAAAAMALLRLPLV

(SEQ ID NO: 1945)

ATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGT  
GCCCCGGATCCAGAGGAAGG  
ATGAGCAGAGTGACCACATTCACTGTCAAGGCCCTGGTGCTCCT  
GATGCTCCCCGTCGTGAAC  
CTGATGATCGGCACCGCTGCAGCCGTCGTGAAAGCTCTCGTCCT  
GCTCATGCTCCCTGTGGGA  
GCAGGGCTGATGACAGCCGTGTACCTGGTCGGCGCTGCAGCCAT  
GGCCCTCCTGCGGCTGCCA  
GTGAAGCGCATGTTTGCTGCAAATCTGGGAGTCAACTCCCTCTAT  
TTTCGGGGGCATTTGCGTG  
GGAAGGCTGCCCCCTCGTGCTGCCTGCTGTGAATGCAGCCGCTG  
CCAAATTTGTCGCCGCTTGG  
ACTCTGAAGGCAGCCGCTAAGGCCGCTGCAAGACTGATGATCGGG  
ACCGCCGCTGCCGGCTT  
CGTGGTCGCCCTGATTCCCCTGGTGAACGCCATGACATACGCAG  
CTCCTCTGTTTGTGGGAGC  
CGCTGCAGCCATGGCTCTCCTGCGGCTGCCACTGGTGTGA

**Table 29.      Hepatitis B Virus Core Protein (SEQ ID NO: [ ] 1946)**

MQLFHLCLIISCSCPTVQASKLCLGWLWGMDIDPYKEFGATVELLSFLPSDFFPSVRDLLDTAS  
ALYREALSPEHCSPHHTALRQAILCWGELMTLATWVGVNLEDPASRDLVVS YVNTNMGLKF  
RQLLWFHISCLTFGRET VIEYLVSF G VWIRT PPAYRPPNAPILSTLPETT V VRRRGRSPRR RTP  
SPRRRRSQSPRRRRSQSRESQC

WHAT IS CLAIMED IS:

1. A method for identifying a candidate peptide epitope which induces a HLA class I CTL response against variants of said peptide epitope, comprising
  - a) identifying, from a particular antigen of an infectious agent, variants of a peptide epitope 8-11 amino acids in length, each variant comprising primary anchor residues of the same HLA class I binding motif; and
  - b) determining whether one of said variants comprises only conserved non-anchor residues in comparison to at least one remaining variant, thereby identifying a candidate peptide epitope.
2. A method for identifying a candidate peptide epitope which induces a HLA class I CTL response against variants of said peptide epitope, comprising
  - a) identifying, from a particular antigen of an infectious agent, variants of a peptide epitope 8-11 amino acids in length, each variant comprising primary anchor residues of the same HLA class I binding motif;
  - b) determining whether each of said variants comprises conserved, semi-conserved or non-conserved non-anchor residues in comparison to each of the remaining variants; and
  - c) identifying a variant which comprises only conserved non-anchor residues in comparison to at least one remaining variant.
3. A method for identifying a candidate peptide epitope which induces a HLA class I CTL response against variants of said peptide epitope, comprising
  - a) identifying, from a particular antigen of an infectious agent, a population of variants of a peptide epitope 8-11 amino acids in length, each peptide epitope comprising primary anchor residues of the same HLA class I binding motif;
  - b) choosing a variant selected from the group consisting of:
    - i) a variant which comprises preferred primary anchor residues of said motif; and
    - ii) a variant which occurs with high frequency within the population of variants; and

- c) determining whether the variant of (b) comprises only conserved non-anchor residues in comparison to at least one remaining variant, thereby identifying a candidate peptide epitope.
  
- 4. A method for identifying a candidate peptide epitope which induces a HLA class I CTL response against variants of said peptide epitope, comprising
  - a) identifying, from a particular antigen of an infectious agent, a population of variants of a peptide epitope 8-11 amino acids in length, each peptide epitope comprising primary anchor residues of the same HLA class I binding motif;
  - b) choosing a variant selected from the group consisting of:
    - i) a variant which comprises preferred primary anchor residues of said motif; and
    - ii) a variant which occurs with high frequency within the population of variants; and
  - c) determining whether the variant of (b) comprises conserved, semi-conserved or non-conserved non-anchor residues in comparison to each of the remaining variants; and
  - d) identifying a variant which comprises only conserved non-anchor residues in comparison to at least one remaining variant.
  
- 5. The method of claim 1, wherein (b) comprises identifying a variant which comprises only conserved non-anchor residues in comparison to at least 25%, at least 50%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, or at least 99% of the remaining variants.
  
- 6. The method of claim 2 or 3, wherein (c) comprises identifying a variant which comprises only conservative non-anchor residues in comparison to at least 25%, at least 50%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, or at least 99% of the remaining variants.
  
- 7. The method of claim 4, wherein (d) comprises identifying a variant which comprises only conservative non-anchor residues in comparison to at least 25%, at least 50%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, or at least 99% of the remaining variants.

8. The method of any of claims 1-4, wherein (a) comprises aligning the sequences of said antigens.
9. The method of claim 3 or 4, wherein (b) comprises choosing a variant which comprises preferred primary anchor residues of said motif.
10. The method of claim 3 or 4, wherein (b) comprises choosing a variant which occurs with high frequency within said population.
11. The method of claim 10, wherein (b) comprises ranking said variants by frequency of occurrence within said population.
12. The method of claim 3 or 4 wherein (b) comprises choosing a variant which comprises preferred primary anchor residues of said motif and which occurs with high frequency within said population.
13. The method of claim 12, wherein (b) comprises ranking said variants by frequency of occurrence within said population.
14. The method of any of claims 1-13, wherein the identified variant comprises the fewest conserved anchor residues in comparison to each of the remaining variants.
15. The method of any of claims 1-4, wherein the remaining variants comprise 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 220, 240, 260, 280, or 300 variants.
16. The method of any of claims 1-15, wherein the infectious agent is selected from the group consisting of: HIV, HBV, HCV, HPV, *Plasmodium falciparum*, Influenza virus, and Dengue virus, Epstein-Barr virus, *Mycobacterium tuberculosis*, *Chlamydia*, *Candida albicans*, *Cryptococcus neoformans*, *Coccidoides spp.*, *Histoplasma spp.*, *Aspergillus fumigatis*, *Plasmodium spp.*, *Trypanosoma spp.*, *Schistosoma spp.*, and *Leishmania spp.*
17. The method of claim 16, wherein the infectious agent is selected from the group consisting of: HIV, HBV, HCV, HPV, *Plasmodium falciparum*, Influenza virus, and Dengue virus.
18. The method of claim 16, wherein the infectious agent is HIV and the antigen is selected from the group consisting of: Gag, Env, Pol, Nef, Rev, Tat, Vif, Vpr, and Vpu.



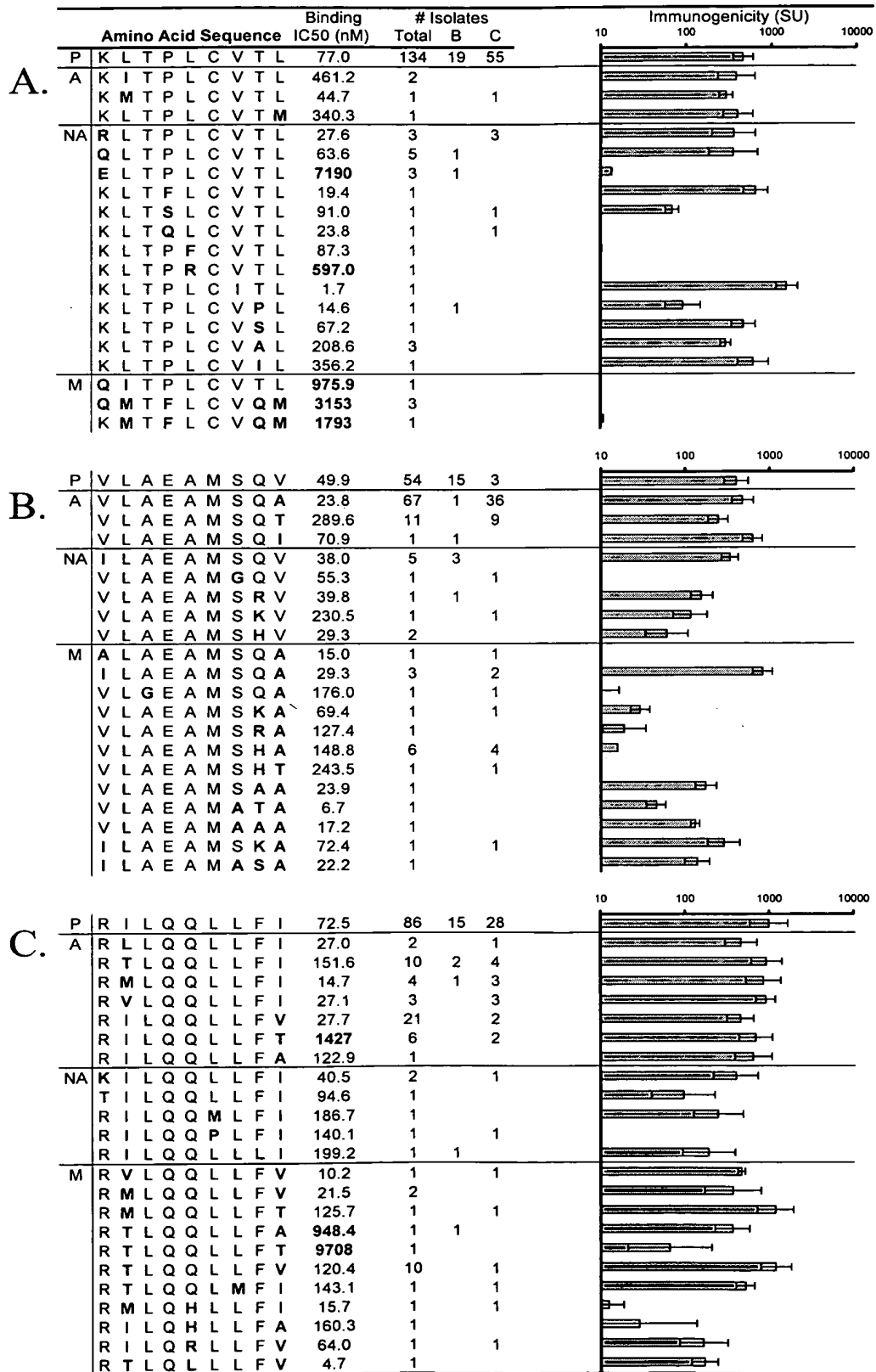
19. The method of claim 16, wherein the infectious agent is HBV and the antigen is selected from the group consisting of: Pol, Env, Core, and NS1/Env2.
20. The method of claim 16, wherein the infectious agent is HCV and the antigen is selected from the group consisting of: Core, E1, E2, NS1, NS2, NS3, NS4, and NS5.
21. The method of claim 16, wherein the infectious agent is HPV and the antigen is selected from the group consisting of: E1, E2, E3, E4, E5, E6, E7, L1, and L2.
22. The method of claim 16, wherein the infectious agent is *Plasmodium falciparum* and the antigen is selected from the group consisting of: CSP, SSP2, EXP1, LSA1.
23. The method of any claims 1-4, wherein the selected variant and the at least one remaining variant comprise different primary anchor residues of the same motif or supermotif.
24. The method of any of claims 1-4, wherein the motif or supermotif is selected from the group consisting of those in Tables 1-2.
25. The method of any of claims 1-4, wherein the conserved non-anchor residues are at any of positions 3-7 of said variant.
26. The method of any of claims 1-4, wherein the variant comprises only 1-3 conserved non-anchor residues compared to at least one remaining variant.
27. The method of any of claims 26, wherein the variant comprises only 1-2 conserved non-anchor residues compared to at least one remaining variant.
28. The method of any of claims 27, wherein the variant comprises only 1 conserved non-anchor residue compared to at least one remaining variant.
29. The method of claim 16, wherein the infectious agent is HPV, and further wherein, the HPV infectious agent is selected from the group consisting of HPV strains 16, 18, 31, 33, 45, 52, 56, and 58.
30. The method of any of claims 1-29, wherein the variants are a population of naturally occurring variants.

## METHODS OF IDENTIFYING OPTIMAL VARIANTS OF PEPTIDE EPITOPES

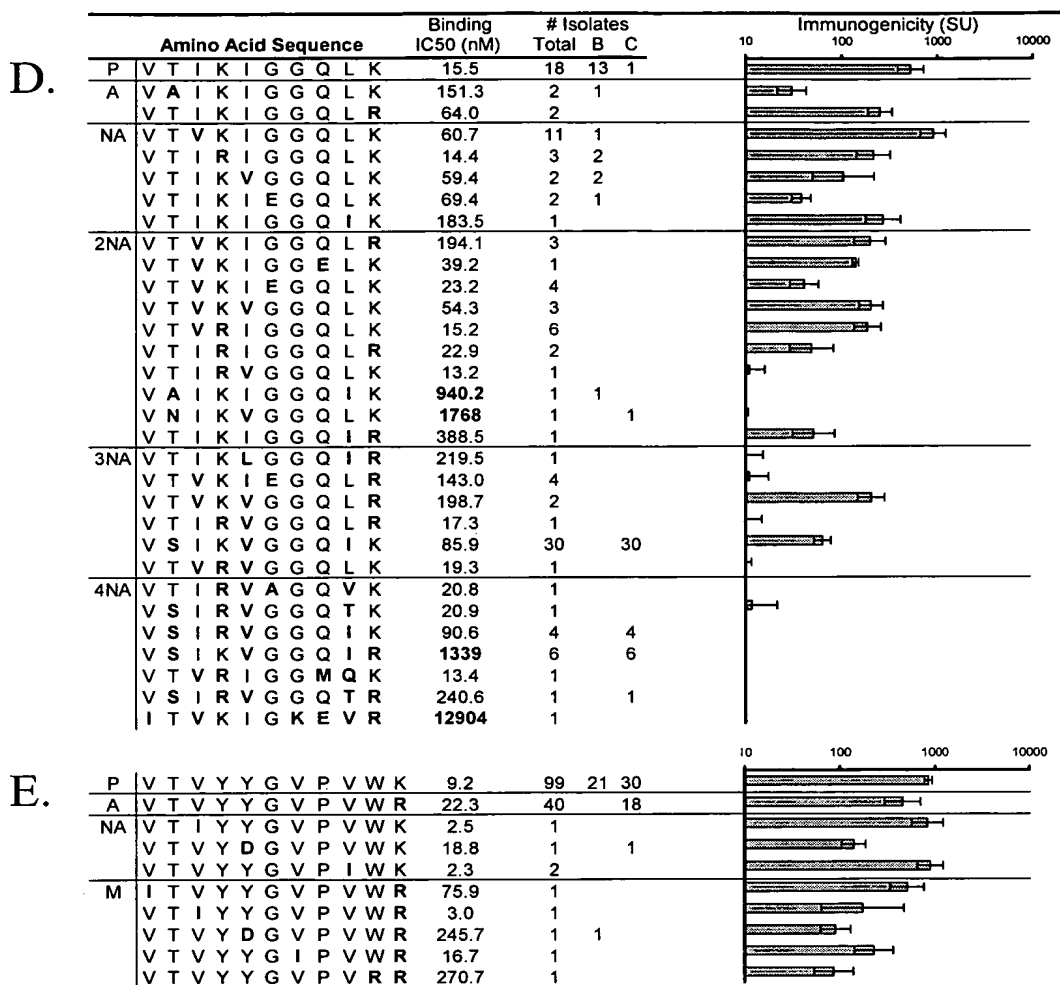
### ABSTRACT OF THE DISCLOSURE

The present invention is directed to methods for selecting a variant of a peptide epitope which induces a CTL response against another variant(s) of the peptide epitope, by determining whether the variant comprises only conserved residues, as defined herein, at non-anchor positions in comparison to the other variant(s). The present invention is also directed to variants identified by the methods above; peptides comprising such variants; nucleic acids encoding such variants and peptides; cells comprising such variants, and/or peptides, and/or nucleic acids; compositions comprising such variants, and/or peptides, and/or nucleic acids, and/or cells; as well as therapeutic and diagnostic methods for using such variants, peptides, nucleic acids, cells, and compositions.

FIGS. 1A-1C

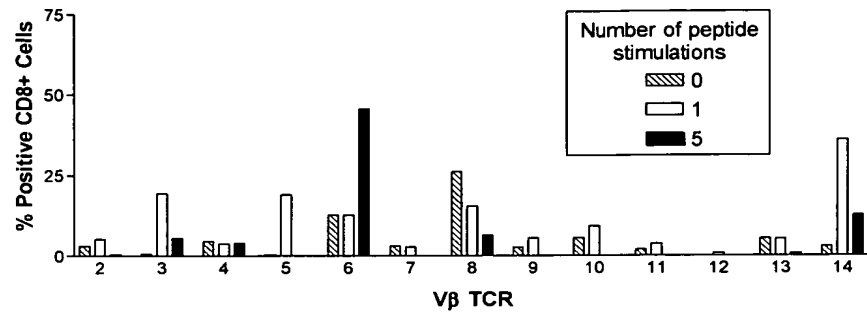


FIGS. 1D-1E

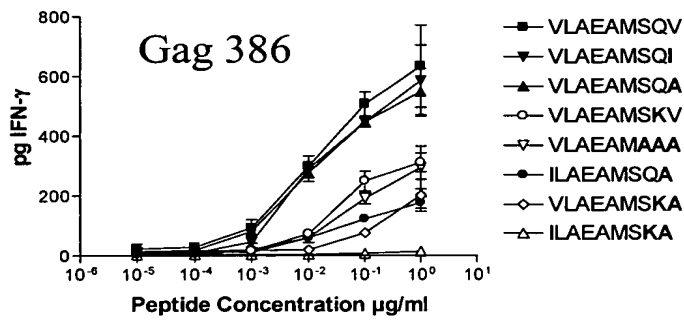


FIGS. 2A-2C

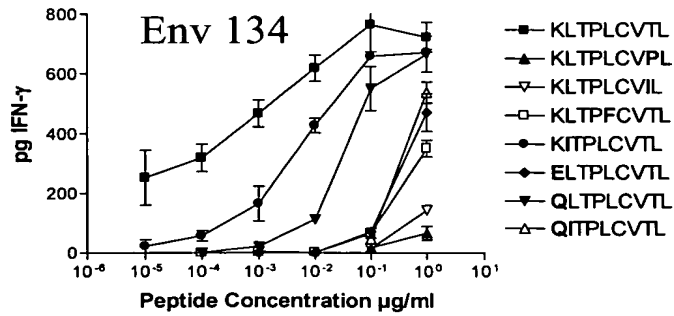
A.



B.



C.





FIGS. 3A-3B

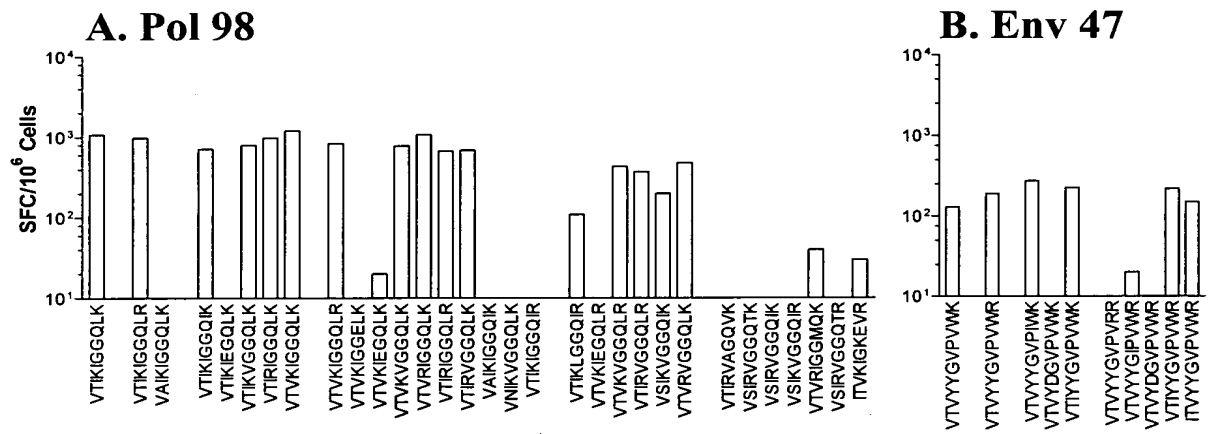


FIG. 4

